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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 0.439826 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-11

Perfect score: 15

Sequence: 1 RXRS 4

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pap:*
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4: /cgn2_6/ptodata/1/iaa/6B.COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/PTCUS.COMB.pap:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	4	2	US-08-387-942C-14
2	15	100.0	4	3	US-08-894-173-17
3	15	100.0	4	3	US-09-398-193-17
4	15	100.0	4	4	US-09-443-780C-82
5	15	100.0	4	4	US-09-079-723-263
6	15	100.0	5	2	US-08-637-759B-84
7	15	100.0	5	3	US-08-871-355A-84
8	15	100.0	5	3	US-08-894-173-40
9	15	100.0	5	3	US-09-398-193-40
10	15	100.0	5	3	US-09-201-945-84
11	15	100.0	5	4	US-09-638-202A-79
12	15	100.0	5	4	US-09-638-202A-85
13	15	100.0	5	4	US-09-638-202A-87
14	15	100.0	5	4	US-09-638-202A-91
15	15	100.0	5	4	US-09-367-777-130
16	15	100.0	5	4	US-09-367-791A-106
17	15	100.0	5	4	US-09-096-749A-79
18	15	100.0	5	4	US-09-096-749A-85
19	15	100.0	5	4	US-09-096-749A-87
20	15	100.0	5	4	US-09-096-749A-91
21	15	100.0	5	4	US-09-637-614-79
22	15	100.0	5	4	US-09-637-614-85
23	15	100.0	5	4	US-09-637-614-87
24	15	100.0	5	4	US-09-637-614-91
25	15	100.0	5	4	US-09-933-999A-24
26	15	100.0	5	4	US-09-933-999A-29
27	15	100.0	6	1	US-08-030-077-3

28	15	100.0	6	1	US-08-064-111C-4	Sequence 4, Appli
29	15	100.0	6	1	US-08-537-069-9	Sequence 9, Appli
30	15	100.0	6	1	US-08-537-069-10	Sequence 10, Appli
31	15	100.0	6	1	US-08-537-069-11	Sequence 11, Appli
32	15	100.0	6	1	US-08-537-069-12	Sequence 12, Appli
33	15	100.0	6	1	US-08-537-069-13	Sequence 13, Appli
34	15	100.0	6	2	US-08-733-505A-4	Sequence 4, Appli
35	15	100.0	6	2	US-08-733-505A-5	Sequence 5, Appli
36	15	100.0	6	2	US-08-733-505A-7	Sequence 7, Appli
37	15	100.0	6	2	US-08-387-942C-12	Sequence 12, Appli
38	15	100.0	6	3	US-08-843-659-6	Sequence 6, Appli
39	15	100.0	6	4	US-08-171-384A-6	Sequence 6, Appli
40	15	100.0	6	4	US-09-122-144-8	Sequence 8, Appli
41	15	100.0	6	4	US-09-579-894-3	Sequence 3, Appli
42	15	100.0	7	1	US-08-537-069-14	Sequence 14, Appli
43	15	100.0	7	3	US-09-049-691-68	Sequence 68, Appli
44	15	100.0	7	3	US-09-049-691-70	Sequence 70, Appli
45	15	100.0	7	3	US-09-258-754-393	Sequence 393, App

ALIGNMENTS

RESULT 1
US-08-387-942C-14
; Sequence 14, Application US/08387942C
; Patent No. 5939289
; GENERAL INFORMATION:
; APPLICANT: ERTSVAG, HELGA
; APPLICANT: VALLA, SVEIN
; APPLICANT: SKJAK-BRAEK, GUDMUND
; APPLICANT: LARSEN, BJORN
; TITLE OF INVENTION: DNA COMPOUNDS COMPRISING SEQUENCES
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP
; STREET: P.O.BOX 747
; CITY: FALLS CHURCH
; STATE: VA
; COUNTRY: USA
; ZIP: 22042
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,942C
; FILING DATE: 09-MAY-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY JR, GERALD M.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1809-106P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-205-8000
; TELEFAX: 703-205-8050
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-387-942C-14

Query Match 100.0%; Score 15; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
|:|:|

Db 1 RARS 4

RESULT 2

US-08-894-173-17
; Sequence 17, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P4716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mouse
; OTHER INFORMATION: STRANDEDNESS : Single
; FEATURE:
; OTHER INFORMATION: TOPOLOGY : Linear
; FEATURE:
; OTHER INFORMATION: MOLECULE TYPE : Peptide
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
; FEATURE:
; OTHER INFORMATION: ANTI-SENSE : NO
; US-08-894-173-17

Query Match 100.0%; Score 15; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4

Db 1 RARS 4

RESULT 3

US-09-398-193-17
; Sequence 17, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; OTHER INFORMATION: STRANDEDNESS : Single
; FEATURE:
; OTHER INFORMATION: TOPOLOGY : Linear
; FEATURE:
; OTHER INFORMATION: MOLECULE TYPE : Peptide
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
; FEATURE:
; OTHER INFORMATION: ANTI-SENSE : NO
; US-09-398-193-17

Query Match 100.0%; Score 15; DB 3; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4

Db 1 RARS 4

RESULT 4

US-09-443-780C-82
; Sequence 82, Application US/09443780C
; Patent No. 6699973
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J
; APPLICANT: Seveso, Michela
; TITLE OF INVENTION: Antibodies To Peptides That Target GIT Receptors And Related Methc
; FILE REFERENCE: E1067/20037
; CURRENT APPLICATION NUMBER: US/09/443,780C
; CURRENT FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: US 60/109,036
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 4
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: binding 4 mer fragment L-form
; US-09-443-780C-82

Query Match 100.0%; Score 15; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4

Db 1 RARS 4

RESULT 5

US-09-079-723-263
; Sequence 263, Application US/09079723
; Patent No. 6703362
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Vernon L.
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Singleton, Judith
; APPLICANT: Patterson, Catherine A.
; APPLICANT: Cagney, Gerard M.
; APPLICANT: Belinka, Benjamin A.
; APPLICANT: Carter, John M.
; TITLE OF INVENTION: RANDOM PEPTIDES THAT BIND TO GASTRO-
; TITLE OF INVENTION: INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA: US/09/079,723
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-219
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-790-9090
; TELEFAX: 212-869-9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 263:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-09-079-723-263

Query Match 100.0%; Score 15; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4
|:|
DB 1 RVRS 4

RESULT 6
US-08-637-759B-84
; Sequence 84, Application US/08637759B
; Patent No. 5876931
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 03-MAY-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: PCT/GB95/02875

US-08-637-759B-84
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-637-759B-84

Query Match 100.0%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4
|:|

Db 1 RRRS 4

RESULT 7
US-08-871-355A-84
; Sequence 84, Application US/08871355A
; Patent No. 6013669
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 09-JUN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: PCT/GB95/02875
; FILING DATE: 11-DEC-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101 CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
US-08-871-355A-84

Query Match 100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4
|:|
DB 1 RRRS 4

RESULT 8
US-08-894-173-40
; Sequence 40, Application US/08894173A
; Patent No. 6090612
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P14716C
; CURRENT APPLICATION NUMBER: US/08/894,173A
; CURRENT FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT

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; ORGANISM: Mouse
; FEATURE:
; OTHER INFORMATION: STRANDEDNESS : Single
; FEATURE:
; OTHER INFORMATION: TOPOLOGY : Linear
; FEATURE:
; OTHER INFORMATION: MOLECULE TYPE : Peptide
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
; FEATURE:
; OTHER INFORMATION: ANTI-SENSE : NO
;
US-08-894-173-40
Query Match 100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
Db 2 RSRS 5

RESULT 9
US-09-398-193-40
; Sequence 40, Application US/09398193
; Patent No. 6197581
; GENERAL INFORMATION:
; APPLICANT: Medical Research Council
; TITLE OF INVENTION: Adenylate cyclase and uses therefor
; FILE REFERENCE: P24360-
; CURRENT APPLICATION NUMBER: US/09/398,193
; CURRENT FILING DATE: 1999-09-17
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; OTHER INFORMATION: STRANDEDNESS : Single
; FEATURE:
; OTHER INFORMATION: TOPOLOGY : Linear
; FEATURE:
; OTHER INFORMATION: MOLECULE TYPE : Peptide
; FEATURE:
; OTHER INFORMATION: HYPOTHETICAL : NO
; FEATURE:
; OTHER INFORMATION: ANTI-SENSE : NO
;
US-09-398-193-40
Query Match 100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
Db 2 RSRS 5

RESULT 10
US-09-201-945-84
; Sequence 84, Application US/09201945
; Patent No. 6342215
; GENERAL INFORMATION:
; APPLICANT: David William Holden
; TITLE OF INVENTION: Identification of Genes
; NUMBER OF SEQUENCES: 501
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
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; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/201,945
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/637,759
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: RPMS 101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8794
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 84:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
;
US-09-201-945-84
Query Match 100.0%; Score 15; DB 3; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
Db 1 RRRS 4

RESULT 11
US-09-638-202A-79
; Sequence 79, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koleda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnine
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
```

TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 79:

Query Match 100.0%; Score 15; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4
|:|
DB 2 RXRS 5

RESULT 12
US-09-638-202A-85
; Sequence 85, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 85:

Query Match 100.0%; Score 15; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RXRS 4
|:|
DB 2 RXRS 5

RESULT 13
US-09-638-202A-87
; Sequence 87, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.
; STREET: 121 South Eighth Street, Ste. 1600
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/638,202A
; FILING DATE: 11-Aug-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/096,749
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Ann S. Viksnins
; REGISTRATION NUMBER: 37,748
; REFERENCE/DOCKET NUMBER: 109.034US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (612) 373-6900
; TELEFAX: (612) 339-3061
; INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 87:

Query Match 100.0%; Score 15; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRS 4
|:|
DB 2 RXRS 5

RESULT 14
US-09-638-202A-91
; Sequence 91, Application US/09638202A
; Patent No. 6462189
; GENERAL INFORMATION:
; APPLICANT: Koieda, Shohei
; TITLE OF INVENTION: ARTIFICIAL ANTIBODY POLYPEPTIDES
; NUMBER OF SEQUENCES: 118
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schwegman, Lundberg, Woessner & Kluth P.A.

STREET: 121 South Eighth Street, Ste. 1600
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/638, 202A
FILING DATE: 11-Aug-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/096, 749
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ann S. Viksnins
REGISTRATION NUMBER: 37,748
REFERENCE/DOCKET NUMBER: 109.034US1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 373-6900
TELEFAX: (612) 339-3061
INFORMATION FOR SEQ ID NO: 91:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 91:
US-09-638-202A-91

Query Match 100.0%; Score 15; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
|:|
Db 2 RYRS 5

RESULT 15
US-09-367-777-130
; Sequence 130, Application US/0936777
; Patent No. 6562598
; GENERAL INFORMATION:
; APPLICANT: Himmelspach, Michele
; Pfleiderer, Michael
; Falkner, Falko-Gunter
; Bibl, Johann
; Dörner, Friedrich
; Schlokot, Uwe
; TITLE OF INVENTION: Factor X Deletion Mutants
; and Analogues Thereof
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/367,777
FILING DATE: 10-No. 6562598-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AT A 336/97
FILING DATE: 27-FEB-1997
APPLICATION NUMBER: WO PCT/AT98/00046
FILING DATE: 27-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Ausenhus, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 20695D-000900US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 130:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 130:
US-09-367-777-130

Query Match 100.0%; Score 15; DB 4; Length 5;
Best Local Similarity 75.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
|:|
Db 2 RYRS 5

Search completed: March 8, 2005, 05:53:48
Job time : 1.43983 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 1.85451 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-11
Perfect score: 15
Sequence: 1 RXRS 4

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15	100.0	4	2	AAR22517 Peptide o
2	15	100.0	4	2	Aaw74084 Fragment
3	15	100.0	4	2	Aay34297 Consensus
4	15	100.0	4	2	Aay34295 Consensus
5	15	100.0	4	5	Aag68362 Tomato mo
6	15	100.0	4	5	Aag68364 Tomato mo
7	15	100.0	4	5	Abg78063 ITALY, LO
8	15	100.0	4	6	Abp55115 Human pot
9	15	100.0	4	8	Adm72392 cAMP and
10	15	100.0	4	8	Adr45631 Human STM
11	15	100.0	5	2	Aaw56878 Enzyme in
12	15	100.0	5	2	Aay21060 Human p53
13	15	100.0	5	2	Aay34296 Consensus
14	15	100.0	5	2	Aay34298 Consensus
15	15	100.0	5	2	AAW98065 Sorting s
16	15	100.0	5	2	AAW98060 Staphyloc
17	15	100.0	5	2	AAW94174 BC loop s
18	15	100.0	5	3	AAAB10342 Human and
19	15	100.0	5	3	AAAB11071 S. apyoge
20	15	100.0	5	3	AAAB11076 S. pyogen
21	15	100.0	5	5	ABB94435 Ubiquitin
22	15	100.0	5	5	ABB94441 Ubiquitin
23	15	100.0	5	5	ABB94443 Ubiquitin
24	15	100.0	5	5	ABB94447 Ubiquitin
25	15	100.0	5	6	AAE36595 Staphyloc

26	15	100.0	5	6	AAE36600 Staphyloc
27	15	100.0	5	6	ABU64640 Motif-ape
28	15	100.0	5	6	ABU61779 S. aureus
29	15	100.0	5	6	ABU61774 S. aureus
30	15	100.0	5	6	ABR55100 MMP subet
31	15	100.0	5	7	ADI10868 Cell surf
32	15	100.0	5	7	ADI10841 Cell surf
33	15	100.0	5	7	ADI10848 Cell surf
34	15	100.0	5	7	ADI10554 Cell surf
35	15	100.0	5	7	ADI10838 Cell surf
36	15	100.0	5	7	ADI10844 Cell surf
37	15	100.0	5	7	ADI10846 Cell surf
38	15	100.0	5	7	ADI10553 Cell surf
39	15	100.0	5	7	ADI10552 Cell surf
40	15	100.0	5	7	ADI10555 Cell surf
41	15	100.0	5	7	ADI10842 Cell surf
42	15	100.0	5	7	ADI10849 Cell surf
43	15	100.0	5	8	ADI32462 Phage dis
44	15	100.0	5	8	ADI32466 Phage dis
45	15	100.0	5	8	ADI32454 Phage dis

ALIGNMENTS

RESULT 1
AAR22517
ID AAR22517 standard; peptide; 4 AA.
XX AAR22517;
AC AAR22517;
XX 20-NOV-1992 (first entry)
DT
XX
DE Peptide or peptide-analogue kininogenase inhibitor.
XX
KW Kininogenase inhibitor; kallikrein; antinflammatory; antiaesthmic;
KW antiallergic; hay fever; antispasmodic; smooth muscle spasm;
KW antihypotensive; hypotension; oedema; pain; analgesia; irritation.
XX
OS Synthetic.

XX Key Location/Qualifiers
FT Modified-site 1 /note= "D-Arg"
FT Modified-site 4 /note= "Ser-NH2"
FT
XX WO9204371-A.
XX
XX 19-MAR-1992.
XX
XX 02-SEP-1991; 91WO-GB001479.
XX
XX 07-SEP-1990; 90GB-00019558.
XX (FERR) FERRING PEPTIDE RES.
XX
XX Szelke M, Evans DM, Jones DM;
XX
XX WPI, 1992-114296/14.
XX
XX New di:peptide analogues not exceeding size of hexa:peptide - are
XX kininogenase inhibitors for treating inflammatory disorders and
XX hypertension, etc.

XX Disclosure; Page 21; 70pp; English.

XX The peptide is one specific example of a group of highly generic peptide
XX analogues not exceeding the size of a hexapeptide, based on the known
XX amino acid sequence of the kininogens at cleavage site 1, which analogues
XX have sufficient similarity to the cleavage site sequence to bind to the
XX active site of the kininogenase but are not hydrolysable and therefore
XX remain bound, inactivating the enzyme. The kininogenase inhibitors are

CC useful for the treatment or prophylaxis of inflammatory disorders (esp.
 CC allergic inflammation disorders such as asthma and hay fever), smooth
 CC muscle spasms, hypotension, oedema, pain and irritation
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 15; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RXRS 4
 | : | |
 Db 1 RFRS 4

RESULT 2
 AAW74084
 ID AAW74084 standard; peptide; 4 AA.
 XX
 AC AAW74084;
 XX
 DT 04-MAY-1999 (first entry)
 XX
 DE Fragment of gastro-intestinal transport receptor binding peptide.
 XX
 KW Gastro-intestinal transport receptor; binding protein; hSI; HPT1; D2H;
 KW hPEPT1; human; GI tract receptor; sucrose-isomaltase complex;
 KW intestinal peptide-associated transporter; hypertension; diabetes;
 KW osteoporosis; haemophilia; anaemia; cancer; migraine; angina pectoris;
 KW therapeutic agent delivery; therapy.
 XX
 OS Homo sapiens.
 XX
 PN WO9851325-A2.
 XX
 PD 19-NOV-1998.
 XX
 PF 15-MAY-1998; 98WO-US010088.
 XX
 PR 15-MAY-1997; 97US-0046595P.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (ELAN-) ELAN CORP PLC.
 XX
 PI Alvarez VL, Mahony DJ, Lambkin IJ, Patterson CA, Singleton J;
 PI Belinka BA, Carter JM, Cagney GM;
 XX
 DR WPI; 1999-009568/01.
 XX
 PT New proteins that bind specifically to receptors in the gastro-intestinal
 PT tract and related nucleic acid - chimaeras and antibodies, used to
 PT deliver therapeutic or diagnostic agents to, or through, the
 PT gastrointestinal tract, e.g. insulin or leuprolide.
 XX
 PS Claim 20; Page 237; 294pp; English.
 XX
 CC This sequence represents a fragment of a protein of the invention. The
 CC invention relates to purified proteins (I) that bind specifically to at
 CC least one of the gastro-intestinal (GI) tract receptors human intestinal
 CC peptide-associated transporter (HPT1), hPEPT1, D2H and human sucrose-
 CC isomaltase complex (hSI). (I) provide active transport of therapeutic
 CC agents through human and animal GI tissue (into the blood) for in vivo
 CC delivery, particularly for treatment or prevention of hypertension,
 CC diabetes, osteoporosis, haemophilia, anaemia, cancer, migraine, or angina
 CC pectoris. Specifically they are used to deliver insulin or leuprolide,
 CC but many other suitable therapeutic agents are disclosed, including genes
 CC or inhibitory nucleic acid, imaging agents and antigens. (I) may also
 CC provide targeting to the GI tract. Other uses of (I) are: (i) to
 CC determine the level of specified receptors in a sample (in a binding
 CC assay); and (ii) to screen for molecules that bind (I). Immunogenic
 CC analogues or derivatives of (I) are used to raise antibodies and in
 CC immunoassays. The antibodies are used to locate, detect and measure (I),
 CC e.g. for imaging, monitoring treatment, tissue analysis etc., also for

CC peptide purification and immobilisation
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 15; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RXRS 4
 | : | |
 Db 1 RFRS 4

RESULT 3
 AAY34297
 ID AAY34297 standard; peptide; 4 AA.
 XX
 AC AAY34297;
 XX
 DT 19-NOV-1999 (first entry)
 XX
 DE Consensus binding site for antibody ABX-CBL.
 XX
 KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.
 XX
 OS Synthetic.
 XX
 PN WO9945031-A2.
 XX
 PD 10-SEP-1999.
 XX
 PF 03-MAR-1999; 99WO-US004583.
 XX
 PR 03-MAR-1998; 98US-00034607.
 PR 03-FEB-1999; 99US-00244253.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
 XX
 DR WPI; 1999-540816/45.
 XX
 PT New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.
 XX
 PS Claim 24; Page 131; 245pp; English.
 XX
 CC This sequence represents a consensus binding site for the antibody of the
 CC invention. The antibody is a monoclonal antibody (Mab) with an isotype on
 CC that fixes complement and a variable region that binds to the epitope on
 CC CD147 bound by the IGM Mab ABX-CBL, providing that the antibody is not
 CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells
 CC or resting or activated monocytes. The products and methods can be used
 CC for treating diseases involving activated T-cells or B-cells or
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
 CC (e.g. arthritis)
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 15; DB 2; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RXRS 4
 | : | |
 Db 1 RFRS 4

```
RESULT 4
RAY34295
ID AAY34295 standard; peptide; 4 AA.
XX
XX AAY34295;
AC
XX
XX 19-NOV-1999 (first entry)
DT
XX
XX Consensus binding site for antibody ABX-CBL.
XX
XX Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocytic; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH Key
FT Misc-difference 2
FT /note= "unspecified amino acid"
XX
XX WO9945031-A2.
XX
XX 10-SEP-1999.
PD
XX
XX 03-MAR-1999; 99WO-US004583.
PF
XX
XX 03-MAR-1998; 98US-00034607.
PR
XX 03-FEB-1999; 99US-00244253.
XX
XX (ABGE-) ABGENIX INC.
PA
XX
XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
PI
XX WPI; 1999-540816/45.
DR
XX
XX New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
PT
XX
XX Claim 24; Page 131; 245pp; English.
PS
XX
XX This sequence represents a consensus binding site for the antibody of the
CC invention. The antibody is a monoclonal antibody (Mab) with an isotype
CC that fixes complement and a variable region that binds to the epitope on
CC CD147 bound by the IGM Mab ABX-CBL, providing that the antibody is not
CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells
CC or resting or activated monocytes. The products and methods can be used
CC for treating diseases involving activated T-cells or B-cells or
CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
CC (e.g. arthritis)
XX
XX Sequence 4 AA;
SQ
Query Match 100.0%; Score 15; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RXRS 4
Db 1 RXRS 4

RESULT 5
AAG68362
ID AAG68362 standard; peptide; 4 AA.
XX
XX AAG68362;
AC
```

```
XX
DT 01-MAR-2002 (first entry)
XX
XX Tomato mosaic virus related peptide #2.
XX
XX Tomato mosaic virus; vaccine K; low-virulent vaccine K genome;
KW point mutation; replicase; motor protein; plant virus genome;
KW genetic engineering; viral disease; plant.
XX
XX Tomato mosaic virus.
OS
XX
XX CN1306090-A.
PN
XX
XX 01-AUG-2001.
PD
XX
XX 14-JAN-2000; 2000CN-00100211.
PF
XX
XX 14-JAN-2000; 2000CN-00100211.
PR
XX
XX (MICR-) INST MICROBIOLOGY CHINESE ACAD SCI.
PA
XX
XX Qiu B, Yang G, Tian B;
PI
XX WPI; 2002-000227/01.
DR
XX
XX Low-virulent vaccine K genom sequence of tomato mosaic.
PT
XX
XX Example 7; Page 10 (Disclosure); 22pp; Chinese.
PS
XX
XX The present invention describes the genome separated and cloned from
CC tomato mosaic virus, which is modified into low-virulent vaccine K genome
CC by point mutation. The nucleotide sequence of its coded replicase and
CC motor protein has the mutation, so it can be used to modify the plant
CC virus genome and prepare genetically engineered vaccine for effectively
CC preventing and treating the viral diseases of plants. The present
CC sequence represents a peptide which is used in an example from the
CC present invention
XX
XX Sequence 4 AA;
SQ
Query Match 100.0%; Score 15; DB 5; Length 4;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy 1 RXRS 4
Db 1 RXRS 4

RESULT 6
AAG68364
ID AAG68364 standard; peptide; 4 AA.
XX
XX AAG68364;
AC
XX
XX 01-MAR-2002 (first entry)
DT
XX
XX Tomato mosaic virus related peptide #4.
XX
XX Tomato mosaic virus; vaccine K; low-virulent vaccine K genome;
KW point mutation; replicase; motor protein; plant virus genome;
KW genetic engineering; viral disease; plant.
XX
XX Tomato mosaic virus.
OS
XX
XX CN1306090-A.
PN
XX
XX 01-AUG-2001.
PD
XX
XX 14-JAN-2000; 2000CN-00100211.
PF
XX
XX 14-JAN-2000; 2000CN-00100211.
PR
XX
```


OS Homo sapiens;
 XX WO200281657-A2.
 XX
 XX PD 17-OCT-2002.
 XX
 XX PF 01-APR-2002; 2002WO-US009743.
 XX
 XX PR 30-MAR-2001; 2001US-00820923.
 XX
 XX PA (PEKE) PE CORP NY.
 XX PA (BEAS/) BEASLEY E M.
 XX PA (WEIM/) WEI M.
 XX PA (KETC/) KETCHUM K A.
 XX PA (DFRA/) DI FRANCESCO V.
 XX
 XX PI Beasley EM, Wei M, Ketchum KA, Di Francesco V;
 XX
 XX DR WPI; 2003-058533/05.
 XX
 XX PT Novel isolated human transporter peptide useful for treating disorder
 PT characterized by absence of, in appropriate or unwanted expression of the
 PT transporter protein, and as immunogens to raise antibodies.
 XX
 XX PS Disclosure; Fig 2A; 75pp; English.
 XX
 XX CC The present sequence is that of a cAMP- and cGMP-dependent protein kinase
 CC phosphorylation site located at amino acid residues 120-123 of a novel
 CC human transporter protein (see ABP55112) of the invention. Unique peptide
 CC sequences from the transporter protein, and nucleic acids encoding them,
 CC can be used as models for the development of human therapeutic targets,
 CC aid in the identification of therapeutic proteins, and serve as targets
 CC for the development of therapeutic agents that modulate transporter
 CC activity in cells and tissues that express the transporter
 XX
 XX SQ Sequence 4 AA;
 XX
 XX Query Match 100.0%; Score 15; DB 6; Length 4;
 XX Best Local Similarity 75.0%; Pred. NO. 1.8e+06;
 XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 RXRS 4
 XX Db |||||
 XX 1 RRRS 4
 XX
 XX RESULT 9
 XX ADM72392
 XX ID ADM72392 standard; peptide; 4 AA.
 XX AC ADM72392;
 XX
 XX DT 01-JUL-2004 (first entry)
 XX
 XX DE cAMP and cGMP-dependent protein phosphorylation site.
 XX
 XX KW Plant; nematode-regulated polypeptide; calcium dependent protein kinase;
 KW CDPK; nematode-responsive transcription factor 1; NRTP1;
 KW nematode-responsive protein; NRP; caffeic acid 7-O-methyltransferase;
 KW 7OM; inositol 5-phosphatase; IPP; nematocidal; gene therapy;
 KW nematode resistance; enzyme.
 XX
 XX OS Synthetic.
 XX
 XX PN WO2004029222-A2.
 XX
 XX PD 08-APR-2004.
 XX
 XX PF 30-SEP-2003; 2003WO-US031029.
 XX
 XX PR 30-SEP-2002; 2002US-0414771P.
 XX
 XX PA (PION-) PIONEER HI-BRED INT INC.

XX Hu X, Lu G;
 XX WPI; 2004-316104/29.
 XX
 XX PT New isolated nucleic acid molecules encoding nematode-responsive
 PT proteins, useful for conferring or improving nematode resistance in
 PT plants.
 XX
 XX PS Disclosure; SEQ ID NO 30; 143pp; English.
 XX
 XX CC The invention relates to pathogen-responsive genes that encode a nematode
 CC regulated polypeptides. The proteins of the invention include calcium
 CC dependent protein kinase (CDPK), nematode-responsive transcription factor
 CC 1 (NRTP1), nematode-responsive protein (NRP), caffeic acid 7-O-
 CC methyltransferase (7OM) or inositol 5-phosphatase (IPP) polypeptides. The
 CC nucleic acid molecule encoding the polypeptides are operably linked to a
 CC promoter that drives expression in a host cell. The composition and
 CC methods are useful for conferring or improving nematode resistance in
 CC plants. The present sequence represents a cAMP and cGMP-dependent protein
 CC phosphorylation site peptide fragment.
 XX
 XX SQ Sequence 4 AA;
 XX
 XX Query Match 100.0%; Score 15; DB 8; Length 4;
 XX Best Local Similarity 75.0%; Pred. NO. 1.8e+06;
 XX Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 XX
 XX QY 1 RXRS 4
 XX Db |||||
 XX 1 RRRS 4
 XX
 XX RESULT 10
 XX ADR45631
 XX ID ADR45631 standard; peptide; 4 AA.
 XX
 XX AC ADR45631;
 XX
 XX DT 02-DEC-2004 (first entry)
 XX
 XX DE Human STMST-2 cGMP-dependent protein kinase phosphorylation site #4.
 XX
 XX KW Human; ITALY; Lysyl Oxidase Related-2; LOR-2; STRIFE; TRASH;
 KW Brain-derived Signaling Factor; BDSF; Leucine-rich Surface Glycoprotein;
 KW LRSG; Seven Transmembrane Signal Transducer; STMST; cancer; obesity;
 KW gastritis; diarrhoea; constipation; haemorrhoid; asthma; anaemia;
 KW thrombocytopaenia; graft-versus-host disease; allergy; cystic fibrosis;
 KW hypogonadism; cardiovascular disorder; arthritis; osteoarthritis;
 KW arteriosclerosis; hypertension; bacterial infection; psoriasis;
 KW diabetes mellitus; hepatitis; Alzheimer's disease; Huntington's disease;
 KW Parkinson's disease; systemic lupus erythematosus;
 KW Chediak-Higashi syndrome; AIDS; tuberculosis; viral infection; malaria;
 KW goitre; infertility; endometriosis; wound; muscular disorder;
 KW Interleukin ten Associated Locus Yang.
 XX
 XX OS Homo sapiens.
 XX
 XX PN US2004176296-A1.
 XX
 XX PD 09-SEP-2004.
 XX
 XX PF 22-MAR-2004; 2004US-00806018.
 XX
 XX PR 27-JAN-1998; 98US-00014195.
 XX PR 27-JAN-1998; 98US-00014348.
 XX PR 27-MAR-1998; 98US-00049799.
 XX PR 21-APR-1998; 98US-00063950.
 XX PR 29-MAY-1998; 98US-00086892.
 XX PR 29-MAY-1998; 98US-00087121.
 XX PR 27-JAN-1999; 99US-0117580P.
 XX PR 25-MAR-1999; 99US-00276400.
 XX PR 21-APR-1999; 99US-00296208.

PR 23-NOV-1999; 99US-00448076.
 PR 27-JAN-2000; 2000WO-US002125.
 PR 28-APR-2000; 2000US-00561381.
 PR 28-APR-2000; 2000US-00561810.
 PR 28-SEP-2000; 2000US-00672721.
 PR 13-FEB-2001; 2001US-00782980.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX
 XX Holtzman DA, McCarthy SA, Macbeth KJ, Busfield SJ, Pan Y;
 PI White D, Khodadoust MW, Gu W;
 XX
 XX WPI; 2004-661401/64.
 DR
 XX
 XX New ITALY, LOR-2, STRIFE, TRASH, BDSF, LRSG and STMST polypeptide and
 PT encoding nucleic acid molecule, useful in diagnosing or treating cancer,
 PT diabetes, psoriasis, hepatitis and Alzheimer's disease.
 XX
 XX Example 13; SEQ ID NO 103; 259pp; English.
 PS
 XX
 XX The invention relates to an isolated Interleukin Ten Associated Locus
 CC Yang (ITALY), Lyseal Oxidase Related-2 (LOR-2), STRIFE, TRASH, Brain-
 CC derived Signaling Factor (BDSF), Leucine-rich Surface Glycoprotein (LRSG)
 CC and Seven Transmembrane Signal Transducer (STMST) nucleic acid molecule
 CC and their encoded proteins. Also included are a host cell which contains
 CC any of the above nucleic acids, a non-human mammalian host cell
 CC containing any of the above nucleic acids, an isolated polypeptide
 CC encoded by the isolated nucleic acid molecule as cited above (or their
 CC complement), an antibody which selectively binds with the polypeptide, a
 CC method for producing the polypeptide, a method for detecting the presence
 CC of a polypeptide in a sample, a method for detecting the presence of any
 CC of the above nucleic acids in a sample, a kit comprising a compound which
 CC selectively binds with a polypeptide or a compound which selectively
 CC hybridizes with the nucleic acid molecule cited above (and instructions
 CC for use), a method for identifying a compound which binds with a
 CC polypeptide, a method for modulating the activity of a polypeptide, a
 CC method for identifying a compound which modulates the activity of a
 CC polypeptide, and a method of making an antibody substance which
 CC selectively binds with the polypeptide. The nucleic acid molecules and
 CC the encoded polypeptides and compositions are useful in diagnosing,
 CC preventing, and treating cancer, obesity, gastritis, diarrhoea,
 CC constipation, haemorrhoids, asthma, anaemia, thrombocytopaenia, graft-
 CC versus-host reactions, allergic reactions, cystic fibrosis, hypogonadism,
 CC cardiovascular disorders, arthritis, osteoarthritis, arteriosclerosis,
 CC hypertension, bacterial infections, psoriasis, diabetes mellitus,
 CC hepatitis, Alzheimer's disease, Huntington's disease, Parkinson's
 CC disease, systemic lupus erythematosus, Chediak-Higashi syndrome, AIDS,
 CC tuberculosis, viral infections, malaria, goitre, infertility,
 CC endometriosis, wounds, or muscular disorders. The present sequence
 CC represents motif/domain/region identified in one of the novel proteins of
 CC the invention.
 XX
 SQ Sequence 4 AA;
 Query Match 100.0%; Score 15; DB 8; Length 4;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RXRS 4
 Db 1 RRRS 4
 ||||
 ||||
 RESULT 11
 AAWS6878
 ID AAWS6878 standard; peptide; 5 AA.
 XX
 AC AAWS6878;
 XX
 XX 28-JUL-1998 (first entry)
 DT
 XX Enzyme inhibitor peptide SEQ ID NO:79.
 DE
 XX

KW Enzyme inhibitor; t-PA; u-PA; chymotrypsin; serine protease; active;
 KW latent; substrate subtraction phage display peptide library;
 KW identification; kinase; phosphatase; serpin.
 XX
 OS Homo sapiens.
 XX
 XX WO9747314-A1.
 PN
 XX 18-DEC-1997.
 PD
 XX 10-JUN-1997; 97WO-US009760.
 PF
 XX 10-JUN-1996; 96US-0019495P.
 PR
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX Madison EL, Ke S;
 XX
 XX WPI; 1998-062746/06.
 DR
 XX
 XX Substrate subtraction phage display peptide libraries - used to
 PT distinguish between active and latent forms of enzyme, e.g. serine
 PT protease.
 XX
 PS Claim 25; Page 66; 138pp; English.
 XX
 CC The present sequence represents an enzyme inhibitor peptide used in the
 CC method of the invention to distinguish between t-PA and u-PA. The present
 CC invention describes a substrate subtraction library for the
 CC identification of peptide substrates selective between a first enzyme
 CC (E1) and a second enzyme (E2), comprising a collection of different
 CC peptides, substantially lacking peptides that are effective substrates
 CC for E1. Also described are: (1) a method (M1) for identifying peptide
 CC substrates selective between a first enzyme (E1) and a second enzyme (E2)
 CC ; (2) a compound comprising the amino acid sequence of a peptide
 CC identified by M1; (3) a polypeptide for use as an enzyme inhibitor
 CC comprising one of 237 amino acid sequences (see AAW56801 to AAW56947, and
 CC AAW56949 to AAW57038); (4) a recombinant DNA vector comprising DNA (I)
 CC encoding a protease inhibitor including the sequence identified by the M1
 CC ; (5) a prokaryotic or eukaryotic cell containing the vector of (4); (6)
 CC an antibody (Ab) immunoreactive with at least one of the peptides
 CC identified by M1; and (7) a diagnostic assay for distinguishing between
 CC active and latent forms of protease inhibitors, that uses (Ab). The
 CC library and method are used for distinguishing between active and latent
 CC forms of enzyme inhibitors, e.g. proteases, kinases and phosphatases.
 CC (Ab) are used for affinity purification of recombinant peptides and in
 CC the identification of naturally occurring protease inhibitors. Enzyme-
 CC inhibiting peptides identified can be used to treat a serpin deficiency
 CC or a disorder of serine proteases
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 15; DB 2; Length 5;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RXRS 4
 Db 1 RGRS 4
 ||||
 ||||
 RESULT 12
 AAY21060
 ID AAY21060 standard; protein; 5 AA.
 XX
 AC AAY21060;
 XX
 XX 22-JUL-1999 (first entry)
 DT
 XX Human p53 cellular tumour antigen mutant protein fragment 7.
 DE
 XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
 KW frameshift mutation; age-related disease; neurodegenerative disorder;

KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
 KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
 KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
 KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofilament-M;
 KW neurofilament-F; presenilin I; presenilin II; cellular tumour antigen;
 KW glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
 KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
 KW high mobility group protein-C; neuroendocrine specific protein A.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 XX
 PN W09845322-A2.
 XX
 PD 15-OCT-1998.
 XX
 XX
 XX 02-APR-1998; 98WO-IB000705.
 XX
 XX 10-APR-1997; 97US-0043163P.
 XX
 XX (ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
 PA (UYRO-) UNIV ROTTERDAM ERASMUS.
 PA (UYUT-) RIJKSUNIV UTRECHT.
 XX
 PI Van Leeuwen FW, Grosveld FG, Burbach JPH;
 XX
 XX WPI; 1998-609901/51.
 DR N-PSDB; AAX75765.
 XX
 XX Diagnosing disease by detecting frameshift mutations in RNA or
 PT corresponding protein mutations - used to diagnose cancer and
 PT neurological diseases, particularly Alzheimer's disease, and also for
 PT treatment and prevention with specific ribozymes or wild-type RNA.
 XX
 XX Disclosure; Fig 14; 258pp; English.
 XX
 CC This invention describes a novel method for the diagnosis of a disease
 CC caused by, or associated with, an RNA molecule that has a frameshift
 CC mutation. The method is used to diagnose age-related diseases, especially
 CC cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's
 CC disease, Down's syndrome, myotonic dystrophy, Huntington's disease,
 CC multiple sclerosis, alcoholic liver disease, diabetes mellitus type II
 CC and many others listed) or susceptibility to these disorders. The method
 CC allows a definitive diagnosis of Alzheimer's disease in living patients,
 CC at an early stage. It is based on the observation that disease may be
 CC caused by mutations in RNA rather than DNA. The invention describes the
 CC use of neuronal system RNA molecules, specifically proteins including
 CC beta-amyloid precursor protein (beta-APP), the microtubule associated
 CC proteins tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule
 CC associated protein 2 (MAP2), neurofilament-L, neurofilament-M,
 CC neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic
 CC protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma
 CC 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group
 CC protein-C (HMGP-C) and neuroendocrine specific protein A
 XX
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 15; DB 2; Length 5;
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RXRS 4
 Db 1 RPRS 4
 RESULT 13
 AAY34296
 ID AAY34296 standard; peptide; 5 AA.
 XX
 XX AAY34296;
 AC
 XX 19-NOV-1999 (first entry)
 DT

XX Consensus binding site for antibody ABX-CBL.
 DE
 XX Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocytic; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 2 /note= "unspecified amino acid"
 FT
 XX W09945031-A2.
 PN
 XX 10-SEP-1999.
 PD
 XX 03-MAR-1999; 99WO-US004583.
 PF
 XX 03-MAR-1998; 98US-00034607.
 PR
 XX 03-FEB-1999; 99US-00244253.
 PR
 XX (ABGE-) ABGENIX INC.
 PA
 XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
 PI WPI; 1999-540816/45.
 XX
 DR New monoclonal antibody, used for treating e.g. graft versus host
 XX disease, cancer, autoimmune diseases and inflammatory diseases.
 FT
 XX Claim 24; Page 131; 245pp; English.
 PS
 XX This sequence represents a consensus binding site for the antibody of the
 CC invention. The antibody is a monoclonal antibody (MAB) with an isotype
 CC that fixes complement and a variable region that binds to the epitope on
 CC CD147 bound by the IGM MAB ABX-CBL, providing that the antibody is not
 CC CBL1. The MAB can selectively kill activated T-cells, activated B-cells
 CC or resting or activated monocytes. The products and methods can be used
 CC for treating diseases involving activated T-cells or B-cells or
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
 CC (e.g. arthritis)
 CC
 SQ Sequence 5 AA;
 Query Match 100.0%; Score 15; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 RXRS 4
 Db 1 RXRS 4
 RESULT 14
 AAY34298
 ID AAY34298 standard; peptide; 5 AA.
 XX
 XX AAY34298;
 AC
 XX 19-NOV-1999 (first entry)
 DT
 XX Consensus binding site for antibody ABX-CBL.
 DE
 XX Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocytic; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.

```

XX OS Synthetic.
XX PN WO9945031-A2.
XX PD 10-SEP-1999.
XX PF 03-MAR-1999; 99WO-US004583.
XX PR 03-MAR-1998; 98US-00034507.
XX PR 03-FEB-1999; 99US-00244253.
XX PA (ABGE-) ABGENIX INC.
XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;
XX WPI; 1999-540816/45.
XX PD New monoclonal antibody, used for treating e.g. graft versus host
XX PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX PT
XX PS Claim 24; Page 131; 245pp; English.
XX
XX This sequence represents a consensus binding site for the antibody of the
XX invention. The antibody is a monoclonal antibody (Mab) with an isotype
XX CC that fixes complement and a variable region that binds to the epitope on
XX CC CD147 bound by the Igm Mab ABX-CBL, providing that the antibody is not
XX CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells
XX CC or resting or activated monocytes. The products and methods can be used
XX CC for treating diseases involving activated T-cells or B-cells or
XX CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
XX CC rejection diseases (e.g. renal transplant, ocular transplant) cancers
XX CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
XX CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
XX CC (e.g. arthritis)
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
Db 1 RVRS 4

RESULT 15
AAW98065
XX ID AAW98065 standard; peptide; 5 AA.
XX AC AAW98065;
XX XX
XX DT 21-JUN-1999 (first entry)
XX DE Sorting signal charged tail.
XX KW Sortase-transamidase; Gram-positive bacterium; peptidoglycan; antibiotic;
KW screening; peptide display; protein display; infection; diagnosis;
KW therapy; vaccine; sorting signal; proteinase.
XX OS Synthetic.
XX PN WO9909145-A1.
XX PD 25-FEB-1999.
XX PF 03-AUG-1998; 98WO-US016229.
XX PR 14-AUG-1997; 97US-0055662P.
XX PA (REGC ) UNIV CALIFORNIA.

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XX PI Schneewind O, Mazmanian S, Ton-That H;
XX DR WPI; 1999-190156/16.
XX PD New isolated sortase-transamidase enzyme - obtained from Staphylococcus
XX PT aureus, used to develop products for treating infections or for
XX PT displaying polypeptides on gram-positive bacteria.
XX PS Disclosure; Page 16; 98pp; English.
XX
XX This synthetic peptide is useable as the charged tail portion of a sorting
XX signal. Novel sortase-transamidase (S-T) enzymes of the invention (see
XX CC AAW98038 and AAW98040) catalyse a reaction that covalently cross-links
XX CC the C-terminus of a protein having a sorting signal to the peptidoglycan
XX CC of a Gram-positive bacterium. The sorting signal has: (a) a motif (see
XX CC AAW98037) that is cleaved by the S-T; (b) a hydrophobic domain (see
XX CC AAW98045-50) of at least 31 amino acids carboxyl to the motif; and (c) a
XX CC charged tail region (see AAW98051-66). Novel isolated S-T enzymes are
XX CC utilised in methods of surface display of peptides and proteins, and can
XX CC also be utilised in the production of vaccines against antigens that can
XX CC be covalently bound to the surfaces of Gram-positive bacteria, and in
XX CC methods for the diagnosis and treatment of bacterial infections
XX SQ Sequence 5 AA;

Query Match 100.0%; Score 15; DB 2; Length 5;
Best Local Similarity 75.0%; Pred. No. 1.8e+06;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRS 4
Db 1 RSRS 4

Search completed: March 8, 2005, 06:16:59
Job time : 3.85451 secs

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time: 0.355347 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-13

Perfect score: 23

Sequence: 1 RXRSH 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	42	1	WIBP17
2	23	100.0	42	2	gene 1.1 protein -
3	23	100.0	46	1	hypothetical prote
4	23	100.0	46	2	ribosomal protein
5	23	100.0	46	2	50s ribosomal prot
6	23	100.0	46	2	50S ribosomal subu
7	23	100.0	46	2	50S ribosomal subu
8	23	100.0	47	1	hypothetical prote
9	23	100.0	47	2	ribosomal protein
10	23	100.0	50	2	50S ribosomal prot
11	23	100.0	50	2	aspartic proteinas
12	23	100.0	51	2	ribosomal protein
13	23	100.0	58	2	hypothetical prote
14	23	100.0	63	2	hypothetical prote
15	23	100.0	68	2	hypothetical prote
16	23	100.0	68	2	hypothetical prote
17	23	100.0	92	2	protamine 2 precur
18	23	100.0	100	2	hypothetical prote
19	23	100.0	102	2	hypothetical prote
20	23	100.0	105	2	hypothetical prote
21	23	100.0	108	2	hypothetical prote
22	23	100.0	114	2	phytochrome - Meso
23	23	100.0	115	2	protamine 2 precur
24	23	100.0	118	2	hypothetical prote
25	23	100.0	118	2	hypothetical prote
26	23	100.0	119	2	hypothetical prote
27	23	100.0	123	2	hypothetical prote
28	23	100.0	124	2	hypothetical prote
29	23	100.0	125	2	hypothetical prote
			127	2	hypothetical prote
			127	2	T13521

30	23	100.0	129	2	T03248
31	23	100.0	130	2	calmodulin-binding
32	23	100.0	130	2	hypothetical prote
33	23	100.0	131	1	hypothetical prote
34	23	100.0	132	1	spermatid transiti
35	23	100.0	132	2	conserved hypothet
36	23	100.0	133	2	hypothetical prote
37	23	100.0	134	2	hypothetical 2b pr
38	23	100.0	136	2	hypothetical prote
39	23	100.0	139	2	finger protein (cl
40	23	100.0	141	2	hypothetical prote
41	23	100.0	141	2	unknown protein en
42	23	100.0	141	2	hypothetical prote
43	23	100.0	141	2	hypothetical prote
44	23	100.0	141	2	hypothetical prote
45	23	100.0	141	2	unknown protein en

ALIGNMENTS

RESULT 1

WIBP17

gene 1.1 protein - phase T7

C:Species: phase T7

C>Date: 28-Feb-1981 #sequence revision 01-Sep-1981 #text_change 09-Jul-2004

C:Accession: E43002; E43004; A93851; S42290; A04404

R:Dunn, J.J.; Thompson, K.

submitted to the Nucleic Acid Sequence Database, September 1982

A:Reference number: A94615

A:Accession: E43002

A:Molecule type: DNA

A:Residues: 1-42 <DUN>

A:Cross-references: UNIPROT:P03779

R:Dunn, J.J.; Studier, F.W.

J. Mol. Biol. 148, 303-330, 1981

A:Title: Nucleotide sequence from the genetic left end of bacteriophage T7 DNA to the be

A:Reference number: A92866; MUID:82078034; PMID:7310871

A:Accession: E43004

A:Molecule type: DNA

A:Residues: 1-42 <DU2>

A:Cross-references: GB:V01127; NID:g15498; PIDN:CAA24334.1; PID:g15506

R:Saito, H.; Tabor, S.; Tamanoi, F.; Richardson, C.C.

Proc. Natl. Acad. Sci. U.S.A. 77, 3917-3921, 1980

A:Title: Nucleotide sequence of the primary origin of bacteriophage T7 DNA replication: 1

A:Reference number: A93851; MUID:81054683; PMID:6254001

A:Accession: A93851

A:Molecule type: DNA

A:Residues: 1-42 <SAI>

A:Cross-references: GB:V01126; NID:g15495; PIDN:CAA24324.1; PID:g15496

R:Dunn, J.J.; Studier, F.W.

J. Mol. Biol. 166, 477-535, 1983

A:Title: Complete nucleotide sequence of bacteriophage T7 DNA and the locations of T7 ge

A:Reference number: S42283; MUID:83241725; PMID:6864790

A:Accession: S42290

A:Molecule type: DNA

A:Residues: 1-42 <DUW>

A:Cross-references: EMBL:V01146; NID:g431187; PIDN:CAA24391.1; PID:g15570

C:Comment: The function of this early gene protein is unknown.

C:Genetics:

A:Gene: 1.1

A:Map position: 15.02-15.33

C:Superfamily: phase T7 gene 1.1 protein

Query Match 100.0%; Score 23; DB 1; Length 42;

Best Local Similarity 80.0%; Pred. No. 81;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5

|:|

31 RDRSH 35

Db

RESULT 2

F82691
 C:Species: Xylella fastidiosa (strain 9a5c)
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: F82691
 R:anonymouse, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence
 Nature 406, 151-157, 2000
 A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
 A:Reference number: A02515; MUID:20365717; PMID:10910347
 A:Note: for a complete list of authors see reference number A59328 below
 A:Accession: F82691
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-42 <SIM>
 A:Cross-references: UNIPROT:Q9PDM8; GB:AE003967; GB:AE003849; NID:g9106347; PIDN:AAF8416
 A:Experimental source: strain 9a5c
 R:Simpson, A.J.G.; Reinach, P.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
 Briones, M.R.S.; Bueno, M.R.P.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
 as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
 submitted to GenBank, June 2000
 A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
 J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
 chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
 A:Authors: Martins, E.M.F.; Matukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
 F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
 Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
 A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
 M.; Tsuchino, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
 A:Reference number: A59328
 A:Contents: annotation
 C:Genetics:
 A:Gene: XF1351

Query Match 100.0%; Score 23; DB 2; Length 42;

Best Local Similarity 80.0%; Pred. No. 81;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5

|:|:|

Db 24 KTRSH 28

RESULT 3

R5EC34
 C:Species: Escherichia coli
 C:Date: 12-Aug-1981 #sequence_revision 12-Aug-1991 #text_change 09-Jul-2004
 C:Accession: C21915; A02836; S11620; H65172
 R:Hansen, F.G.; Hansen, E.B.; Aclung, T.
 EMBO J. 1, 1043-1048, 1982
 A:Title: The nucleotide sequence of the dnaA gene promoter and of the adjacent rpmH gene
 A:Reference number: A21915; MUID:84236082; PMID:6329723
 A:Accession: C21915
 A:Molecule type: DNA
 A:Residues: 1-46 <HAN>
 A:Cross-references: UNIPROT:P02437; GB:J01602; NID:q145758; PIDN:AAB59148.1; PID:gl45759
 R:Chen, R.

Hoppe-Seyler's Z. Physiol. Chem. 357, 873-886, 1976

A:Title: The sequence determination of a protein in a micro scale: the sequence analysis

A:Reference number: A02836; MUID:76258983; PMID:783033

A:Accession: A02836

A:Molecule type: protein

A:Residues: 1-46 <CHE>

A:Experimental source: strain K12

R:Kashiwagi, K.; Igarashi, K.

Biochim. Biophys. Acta 911, 180-190, 1987

A:Title: Nonspecific inhibition of Escherichia coli ornithine decarboxylase by various

A:Reference number: S11620; MUID:87101185; PMID:3542048

A:Accession: S11620

A:Molecule type: protein

A:Residues: 1-46 <KAS>

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: H65172

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-46 <BLAT>

A:Cross-references: GB:AE000447; GB:U00096; NID:q2367266; PIDN:AAC76726.1; PID:gl790138;

A:Experimental source: strain K-12, substrain MG1655

R:Arnold, R.J.; Reilly, J.P.

Anal. Biochem. 269, 105-112, 1999

A:Title: Observation of Escherichia coli ribosomal proteins and their posttranslational

A:Reference number: A59071; MUID:99196679; PMID:10094780

A:Contents: annotation; mass spectrographic analysis

A:Note: no post-translational modifications were observed in mass spectrographic analysis

C:Genetics:

A:Gene: rpmH

A:Map position: 83 min

C:Complex: the ribosome is composed of the large (50S) and small (30S) subunit; the large

S rRNA and 22 distinct proteins

C:Complex: large subunit ribosomal proteins: L1 (PIR:R5EC1), L3 (PIR:R5EC1), L2 (PIR:R5EC

(PIR:R5EC1), L13 (PIR:R5EC13), L14 (PIR:R5EC14), L15 (PIR:R5EC15), L16 (PIR:R5EC16), L1:

C:Function:

A:Pathway: protein biosynthesis

C:Superfamily: Escherichia coli ribosomal protein L34

C:Keywords: protein biosynthesis; ribosome

F:1-46/Product: ribosomal protein L34 #status experimental <MAT>

Query Match 100.0%; Score 23; DB 1; Length 46;

Best Local Similarity 80.0%; Pred. No. 88;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5

|:|:|

Db 12 RNRSH 16

RESULT 4

AH0957
 50s ribosomal protein L34 [imported] - Salmonella enterica subsp. enterica serovar Typhi
 C:Species: Salmonella enterica subsp. enterica serovar Typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
 C:Accession: AH0957
 R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
 th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
 S.; Moule, S.; O'Gaora, P.
 Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A:Reference number: AB0502; MUID:21534947; PMID:11677608

A:Accession: AH0957

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-46 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03156.1; PID:gl6504791; GSPDB:GN00176

C:Genetics:

A:Gene: rpmH

C:Superfamily: Escherichia coli ribosomal protein L34

Query Match 100.0%; Score 23; DB 2; Length 46;

Best Local Similarity 80.0%; Pred. No. 88;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5

|:|:|

Db 12 RNRSH 16

RESULT 5

H86054
 50S ribosomal subunit protein L34 [imported] - Escherichia coli (strain O157:H7, substra

C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H86054
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H86054
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-46 <STO>
A:Cross-references: UNIPROT:P02437; GB:AE005174; NID:G12518542; PIDN:AA658900.1; GSPDB:C
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: rpmH
C:Superfamily: Escherichia coli ribosomal protein L34

Query Match 100.0%; Score 23; DB 2; Length 46;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
Db 12 RNRSH 16

RESULT 6
F91208
50S ribosomal subunit protein L34 [imported] - Escherichia coli (strain O157:H7, substra
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: F91208
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: F91208
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-46 <HAY>
A:Cross-references: UNIPROT:P02437; GB:BA000007; PIDN:BA838061.1; PID:G13364113; GSPDB:C
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: EC84638
C:Superfamily: Escherichia coli ribosomal protein L34

Query Match 100.0%; Score 23; DB 2; Length 46;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
Db 12 RNRSH 16

RESULT 7
D71317
hypothetical protein TP0504 - syphilis spirochete
C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C:Accession: D71317
R:Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
raon, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A>Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A:Reference number: A71250; MUID:98332770; PMID:9665876
A:Accession: D71317
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-46 <COL>

A:Cross-references: UNIPROT:O83517; GB:AE001226; GB:AE000520; NID:G3322785; PIDN:AA6549;
A:Experimental source: strain Nichols
C:Genetics:
A:Gene: TP0504

Query Match 100.0%; Score 23; DB 2; Length 46;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
Db 10 RARSH 14

RESULT 8
JC1154
ribosomal protein L34 - Buchnera aphidicola
C:Species: Buchnera aphidicola
C>Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C:Accession: JC1154
R:Lai, C.Y.; Baumann, P.
Gene 113, 175-181, 1992
A>Title: Genetic analysis of an aphid endosymbiont DNA fragment homologous to the rnpA-r
A:Reference number: JC1154; MUID:92241666; PMID:1572539
A:Accession: JC1154
A:Molecule type: DNA
A:Residues: 1-47 <LAI>
A:Cross-references: UNIPROT:P29437; GB:M80817; NID:G144144; PIDN:AAA73148.1; PID:G144148
C:Genetics:
A:Gene: rpmH
C:Superfamily: Escherichia coli ribosomal protein L34
C:Keywords: protein biosynthesis; ribosome

Query Match 100.0%; Score 23; DB 1; Length 47;
Best Local Similarity 80.0%; Pred. No. 90;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
Db 12 RNRSH 16

RESULT 9
E84931
50S ribosomal protein L34 [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: E84931
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A>Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: E84931
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-47 <STO>
A:Cross-references: GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: rpmH; BU013
C:Superfamily: Escherichia coli ribosomal protein L34

Query Match 100.0%; Score 23; DB 2; Length 47;
Best Local Similarity 80.0%; Pred. No. 90;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
Db 12 RNRSH 16

RESULT 10
JT0399

aspartic proteinase (EC 3.4.23.-) NM1 - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 12-Apr-1995
C:Accession: J70399
R:Lu, Q.; Wolfe, K.H.; McConnell, D.J.
Gene 71, 135-146, 1988
A:Title: Molecular cloning of multiple bovine aspartyl protease genes.
A:Reference number: J70397; MUID:89108032; PMID:3145907
A:Accession: J70399
A:Molecule type: DNA
A:Residues: 1-50 <LUQ>
C:Superfamily: peptin
C:Keywords: aspartic proteinase; gastric juice; hydrolase; protein digestion; stomach

Query Match 100.0%; Score 23; DB 2; Length 50;
Best Local Similarity 80.0%; Pred. No. 95;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
|:|:|
Db 32 RXRSH 36
|:|:|

RESULT 11
E69082
ribosomal protein L39 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: E69082
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. K.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: functional reference number: A69000; MUID:98037514; PMID:9371463
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: E69082
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-51 <MTH>
A:Cross-references: UNIPROT:Q27650; GB:AE000920; GB:AE000666; NID:g2622729; PIDN:AAB8608
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1613
C:Superfamily: rat ribosomal protein L39

Query Match 100.0%; Score 23; DB 2; Length 51;
Best Local Similarity 80.0%; Pred. No. 97;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
|:|:|
Db 34 RXRSH 38
|:|:|

RESULT 12
AI3030
hypothetical protein Atu3853 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AI3030
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AI3030
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-58 <KUR>
A:Cross-references: UNIPROT:Q8U975; GB:AE000689; PIDN:AAL44663.1; PID:g1742289; GSPDB:G

A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu3853
A:Map position: linear chromosome

Query Match 100.0%; Score 23; DB 2; Length 58;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
|:|:|
Db 50 RLRSH 54
|:|:|

RESULT 13
B70638
hypothetical protein Rv1950c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C:Accession: B70638
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence: reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: B70638
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-63 <COL>
A:Cross-references: UNIPROT:P95264; GB:Z84498; GB:AL123456; NID:g3261701; PIDN:CAB06511.1
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv1950c

Query Match 100.0%; Score 23; DB 2; Length 63;
Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
|:|:|
Db 38 RNRSH 42
|:|:|

RESULT 14
S72952
hypothetical protein - Mycobacterium leprae
C:Species: Mycobacterium leprae
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S72952
R:Smith, D.R.; Robison, K.
submitted to the EMBL Data Library, November 1993
A:Description: Mycobacterium leprae cosmid L247.
A:Reference number: S72589
A:Accession: S72952
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <SML>
A:Cross-references: UNIPROT:Q49883; EMBL:U00021; NID:g467141; PIDN:AAA50912.1; PID:g46714.1
C:Genetics:
A:Start codon: GTG

Query Match 100.0%; Score 23; DB 2; Length 68;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
|:|:|
Db 26 RLRSH 30
|:|:|

RESULT 15

G65037
hypothetical protein b2596 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C:Accession: G65037
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: G65037
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-68 <BLAT>
A:Cross-references: UNIPROT:P76595; GB:AE000346; GB:U00096; NID:G2367141; PIDN:AAC75645.
A:Experimental source: strain K-12, substrain MG1655

Query Match 100.0%; Score 23; DB 2; Length 68;
Best Local Similarity 80.0%; Pred.No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
|:|
Db 18 RYRSH 22

Search completed: March 8, 2005, 06:39:19
Job time : 2.40535 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 1.86725 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-13
Perfect score: 23
Sequence: 1 RXRSH 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	23	100.0	35	Q7BQA7	Q7bqa7 mycobacteri
2	23	100.0	41	O60686	O60686 homo sapien
3	23	100.0	42	V11_BPT7	P03779 bacterioph
4	23	100.0	42	Q6WY56	Q6wy56 bacterioph
5	23	100.0	42	Q6WYGO	Q6wygo bacterioph
6	23	100.0	42	Q9PDM8	Q9pdm8 xylella fas
7	23	100.0	45	Q7U525	Q7u525 synechococc
8	23	100.0	45	Q7V0S1	Q7v0s1 prochloroco
9	23	100.0	45	Q8EKT3	Q8ekt3 shewanella
10	23	100.0	46	RL34_ECOLI	P02437 escherichia
11	23	100.0	46	RL34_YERPE	O829u5 versinia pe
12	23	100.0	46	Y504_TREPA	O83517 treponema p
13	23	100.0	46	Q663T0	Q663t0 yersinia ps
14	23	100.0	46	Q7MXZ2	Q7mxz2 photorhabdu
15	23	100.0	46	Q6CYR2	P57129 buchnera ap
16	23	100.0	47	RL34_BUCAI	P29437 buchnera ap
17	23	100.0	47	RL34_BUCBP	Q89b35 buchnera ap
18	23	100.0	47	RL34_BUCBP	Q89b35 buchnera ap
19	23	100.0	51	RL39_METTH	O27650 methanobact
20	23	100.0	53	Q6Z7G2	Q6z7g2 oryza sativ
21	23	100.0	57	Q7YVK1	Q7yvk1 trypanosoma
22	23	100.0	58	Q8U975	Q8u975 agrobacteri
23	23	100.0	59	Q8VWS3	Q8vws3 narcissus p
24	23	100.0	60	Q8YSD3	Q8yds3 oryza sativ
25	23	100.0	62	HSPI_PLATE	O18748 planigale t
26	23	100.0	62	Q8EIF5	Q8eif5 homo sapien
27	23	100.0	62	Q63326	Q63326 rattus norv
28	23	100.0	63	RL32_ACHLA	Q81395 acholeplasm
29	23	100.0	63	P95264	P95264 mycobacteri
30	23	100.0	63	Q7CZ82	Q7cz82 mycobacteri
31	23	100.0	64	Q6W4W0	Q6w4w0 homo sapien

32	23	100.0	66	2	Q6DTY1	Q6dty1 homo sapien
33	23	100.0	66	2	Q6L982	Q6l982 homo sapien
34	23	100.0	66	2	Q6Z9W1	Q6z9w1 oryza sativ
35	23	100.0	66	2	Q62BX6	Q62bx6 burkholderi
36	23	100.0	67	2	Q91ER3	Q91er3 cydia pomon
37	23	100.0	68	2	Q96GH5	Q96gh5 homo sapien
38	23	100.0	68	2	Q9M676	Q9m676 cucumis mel
39	23	100.0	68	2	Q49883	Q49883 mycobacteri
40	23	100.0	68	2	P76595	P76595 escherichia
41	23	100.0	68	2	Q8C1N3	Q8c1n3 mus musculu
42	23	100.0	70	2	Q6EP25	Q6ep25 oryza sativ
43	23	100.0	70	2	Q67720	Q67720 human adeno
44	23	100.0	72	2	Q7N4I3	Q7n4i3 photorhabdu
45	23	100.0	72	2	Q7U2F8	Q7u2f8 mycobacteri

ALIGNMENTS

RESULT 1
Q7BQA7 PRELIMINARY; PRT; 35 AA.
AC Q7BQA7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Alkanal monooxygenase-like protein (Fragment).
OS Mycobacterium phlei.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1771;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 354;
RA Kim B.-K., Choi K.-P., Daniels L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 354;
RA Kim B.-K., Choi K.-P., Purwantini E., Bae Y.-M., Cho P., Kang S.-A.,
RA Simpson D.R., Daniels L.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152397; AAR92169.1; -.
KW Monooxygenase.
FT NON TER 1
SQ SEQUENCE 35 AA; 4068 MW; 87A1P4A0990C209F CRC64;
Query Match 100.0%; Score 23; DB 2; Length 35;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RXRSH 5
Db 22 RLRSH 26
RESULT 2
O60686 PRELIMINARY; PRT; 41 AA.
AC O60686;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Erythroid alpha-spectrin (Fragment).
GN Name=SPTA1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99224641; PubMed=10215350;

RA Galluzzi L., Patardini M., Magnani M., Nicolas G., Lecomte M.C.,
RA Harper S., Speicher D.W.;
RT "cDNA sequence of the human erythroid alpha-spectrin: identification
of a base deletion in the sequence database.";
RL Blood 93:2421-2422(1999).
DR EMBL; AF060556; AAC15757.1; -.
FT NON TER 1
SQ SEQUENCE 41 AA; 4677 MW; EAA3BFF0EB3CD36D CRC64;

Query Match 100.0%; Score 23; DB 2; Length 41;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 21 RGRSH 25

RESULT 3
V11_BPT7 STANDARD; PRT; 42 AA.
AC P03779;
DT 21-JUL-1996 (Rel. 01, Created)
DT 21-JUL-1996 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Gene 1.1 protein.
GN Name=1.1;
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83241725; PubMed=6864790;
RA Dunn J.J., Studier F.W.;
RT "Complete nucleotide sequence of bacteriophage T7 DNA and the
locations of T7 genetic elements.";
RL J. Mol. Biol. 166:477-535(1983).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82078034; PubMed=7310871;
RA Dunn J.J., Studier F.W.;
RT "Nucleotide sequence from the genetic left end of bacteriophage T7 DNA
to the beginning of gene 4.";
RL J. Mol. Biol. 148:303-330(1981).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=81054683; PubMed=6254001;
RA Saito H., Tabor S., Tamanoi F., Richardson C.C.;
RT "Nucleotide sequence of the primary origin of bacteriophage T7 DNA
replication: relationship to adjacent genes and regulatory elements.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:3917-3921(1980).
CC -!- FUNCTION: Function of this early gene protein is unknown.
CC -----
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CC -----
DR EMBL; V01146; CAA24391.1; -.
DR EMBL; V01126; CAA24324.1; -.
DR EMBL; V01127; CAA24334.1; -.
DR PIR; E43002; W1BP17.
KW Early protein.
SQ SEQUENCE 42 AA; 5181 MW; 26FDF241A530F76F CRC64;

Query Match 100.0%; Score 23; DB 1; Length 42;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 31 RDRSH 35

RESULT 4
Q6WY56 PRELIMINARY; PRT; 42 AA.
AC Q6WY56;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gene 1.1.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
viral genome.";
RL J. Mol. Evol. 57:241-248(2003).
DR EMBL; AY264778; AAP34125.1; -.
DR EMBL; AY264777; AAP34071.1; -.
SQ SEQUENCE 42 AA; 5162 MW; 26PDE29BC530F76F CRC64;

Query Match 100.0%; Score 23; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 31 RDRSH 35

RESULT 5
Q6WYGO PRELIMINARY; PRT; 42 AA.
AC Q6WYGO;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gene 1.1.
OS Bacteriophage T7.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
OC T7-like viruses.
OX NCBI_TaxID=10760;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22990536; PubMed=14629033;
RA Bull J.J., Badgett M.R., Rokyta D., Molineux I.J.;
RT "Experimental evolution yields hundreds of mutations in a functional
viral genome.";
RL J. Mol. Evol. 57:241-248(2003).
DR EMBL; AY264776; AAP34021.1; -.
DR EMBL; AY264775; AAP33970.1; -.
SQ SEQUENCE 42 AA; 5251 MW; 51E022AFABC0EFD8 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 42;
Best Local Similarity 80.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 31 RDRSH 35

RESULT 6
Q9PDM8 PRELIMINARY; PRT; 42 AA.
AC Q9PDM8;
ID Q9PDM8;

DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocusNames=Xf1351;
 OS Xylella fastidiosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
 OC Xanthomonadaceae; Xylella.
 OX NCBI_TaxID=2371;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=9a5c;
 RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
 RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
 RA Valvargem R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
 RA Barros M.P., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
 RA Bueno M.R.H., Canagaro A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
 RA Coutinho N.B., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,
 RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
 RA Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
 RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
 RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
 RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
 RA Krieger J.E., Kuramae E.E., Laigret P., Lambais M.R., Leite L.C.C.,
 RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
 RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
 RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
 RA Menci C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
 RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
 RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
 RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
 RA Peixoto B.R., Pereira A.G.G., Pereira H.A. Jr., Pesquero J.B.,
 RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
 RA de Rosa J.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
 RA da Silva A.C.R., da Silva A.M., da Silva P.R., Silva W.A. Jr.,
 RA da Silva J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
 RA de Souza A.P., Terezi M.F., Truffi D., Tsai S.M., Tshako M.H.,
 RA Vallada H., Van Sluys M.A., Verjovsky-Almeida S., Vettore A.L.,
 RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
 RT "The genome sequence of the plant pathogen Xylella fastidiosa";
 RL Nature 406:151-159(2000).
 DR EMBL; AF003967; AAF84160.1; --
 DR PIR; P82691; P82691.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 42 AA; 4915 MW; 0F9E51F876F60C9E CRC64;

Query Match 100.0%; Score 23; DB 2; Length 42;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
 Db 24 RTRSH 28

RESULT 7
 Q7U525 PRELIMINARY; PRT; 45 AA.
 AC Q7U525
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE 50S ribosomal protein L34.
 GN Name=rp134; Synonyms=rpnh; OrderedLocusNames=SYNW1887;
 OS Synecococcus sp. (strain WH8102).
 OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
 OX NCBI_TaxID=84588;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22825697; PubMed=12917641; DOI=10.1038/nature01943;
 RA Palenik B., Brahamsha B., Larimer F.W., Land M.L., Hauser L.,
 RA Chain P., Lamerding J.E., Regala W., Allen E.E., McCarren J.,
 RA Paulsen I.T., Dufresne A., Partensky F., Webb E.A., Waterbury J.

RT "The genome of a motile marine Synecococcus";
 RL Nature 424:1037-1042(2003).
 CC -1- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
 DR EMBL; BX569694; CAE08402.1; --
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR000271; Ribosomal_L34.
 DR Pfam; PF00468; Ribosomal_L34; 1.
 DR ProDom; PD003101; Ribosomal_L34; 1.
 DR TIGRFAMs; TIGR01030; rpnh_bact; 1.
 KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
 SQ SEQUENCE 45 AA; 5366 MW; 33407F46A03E39BE CRC64;

Query Match 100.0%; Score 23; DB 2; Length 45;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
 Db 22 RMRSH 26

RESULT 8
 Q7V0S1 PRELIMINARY; PRT; 45 AA.
 AC Q7V0S1
 DT 01-OCT-2003 (TReMBLrel. 25, Created)
 DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE 50S ribosomal protein L34.
 GN Name=rp134; Synonyms=rpnh; OrderedLocusNames=PMW1183;
 OS Prochlorococcus marinus subsp. pastoris (strain CCMP 1378 / MED4).
 OC Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae;
 OC Prochlorococcus.
 OX NCBI_TaxID=53919;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22825698; PubMed=12917642; DOI=10.1038/nature01947;
 RA Rocap G., Larimer F.W., Lamerding J.E., Malfatti S., Chain P.,
 RA Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R.,
 RA Johnson Z.I., Land M.L., Lindell D., Post A.F., Regala W., Shah M.,
 RA Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A.,
 RA Webb E.A., Zinser E.R., Chisholm S.W.;
 RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation";
 RL Nature 424:1042-1047(2003).
 CC -1- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
 DR EMBL; BX572093; CAE19642.1; --
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR000271; Ribosomal_L34.
 DR Pfam; PF00468; Ribosomal_L34; 1.
 DR ProDom; PD003101; Ribosomal_L34; 1.
 DR TIGRFAMs; TIGR01030; rpnh_bact; 1.
 KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
 SQ SEQUENCE 45 AA; 5400 MW; 3BE2FA307AA339B0 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 45;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
 Db 22 RMRSH 26

RESULT 9
 Q8EKT3 PRELIMINARY; PRT; 45 AA.
 ID Q8EKT3
 AC Q8EKT3
 DT 01-MAR-2003 (TReMBLrel. 23, Created)

DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
 DE Ribosomal protein L34.
 GN Name=rpM; OrderedLocusNames=SO00007;
 OS Shewanella oneidensis.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
 CC Shewanellaceae; Shewanella.
 OX NCBI_TaxID=70863;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MR-1;
 RX MEDLINE=22297686; PubMed=12369813; DOI=10.1038/nbt749;
 RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
 RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
 RA Clayton R.A., Meyer T., Tespin A., Scott J., Beanan M.J.,
 RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
 RA Hatt D.H., Kolonay J.F., Madupu R., Peterson J.D., Unayam L.A.,
 RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
 RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
 RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
 RA Venter J.C., Neillson K.H., Fraser C.M.,
 RA "Genome sequence of the dissimilatory metal ion-reducing bacterium
 RT Shewanella oneidensis.";
 RT Nat. Biotechnol. 20:1118-1123(2002).
 CC -!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
 RL EMBL; AE015452; AAN53094.1; -.
 DR TIGR; SO0007; -.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; P:protein biosynthesis; IEA.
 DR InterPro; IPR000271; Ribosomal L34.
 DR Pfam; PF00468; Ribosomal L34; 1.
 DR ProDom; PD003101; Ribosomal L34; 1.
 DR TIGRFAMs; TIGR01030; rpM_bact; 1.
 DR PROSITE; PS00784; RIBOSOMAL L34; 1.
 KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
 SQ SEQUENCE 45 AA; 5125 MW; 54E7F91C32438C CRC64;

Query Match 100.0%; Score 23; DB 2; Length 45;
 Best Local Similarity 80.0%; Pred. No. 2.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
 |::|
 Db 13 RXRSH 17

RESULT 10
 RL34 ECOLI
 ID RL34 ECOLI STANDARD; PRT; 46 AA.
 AC P02437;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 25-JAN-2005 (Rel. 46, Last annotation update)
 DE 50S ribosomal protein L34.
 GN Name=rpM; Synonyms=xr1M, ssaE;
 GN OrderedLocusNames=B3703; c4627, 25194, ECs4638, STM3839, STY3939.1,
 GN t3680, SF3761, S4010; ORFNames=STY3939A;
 OS Escherichia coli,
 OS Escherichia coli O6,
 OS Escherichia coli O157:H7,
 OS Salmonella typhimurium,
 OS Salmonella typhi, and
 OS Shigella flexneri.
 CC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 CC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562, 217992, 83334, 602, 601, 623;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=84236082; PubMed=6329723;
 RA Hansen F.G., Hansen E.B., Atlung T.;

RT "The nucleotide sequence of the dnaA gene promoter and of the adjacent
 RT rpmH gene, coding for the ribosomal protein L34, of Escherichia
 RL coli.";
 RL EMBL J. 1:1043-1048(1982).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli;
 RX MEDLINE=86056995; PubMed=2415431; DOI=10.1016/0378-1119(85)90206-9;
 RA Hansen F.G., Hansen E.B., Atlung T.;
 RA "Physical mapping and nucleotide sequence of the rnpA gene that
 RT encodes the protein component of ribonuclease P in Escherichia coli.";
 RL Gene 38:85-93(1985).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=K12 / MG1655;
 RX MEDLINE=93315143; PubMed=7686882;
 RA Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;
 RA "DNA sequence and analysis of 136 kilobases of the Escherichia coli
 RT genome: organizational symmetry around the origin of replication.";
 RL Genomics 16:551-561(1993).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
 RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.352529799;
 RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 RA Raske D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 RA Rayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RA "Extensive mosaic structure revealed by the complete genome sequence
 RT of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
 RX MEDLINE=21074935; PubMed=1208551; DOI=10.1038/35054089;
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RA "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533(2001).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=E.coli; STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RA "Complete genome sequence of enterohemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:11-22(2001).
 RN [7]
 RP SEQUENCE.
 RC SPECIES=E.coli; STRAIN=K12;
 RX MEDLINE=76258983; PubMed=7830333;
 RA Chen R.;
 RT "The sequence determination of a protein in a micro scale: the
 RL sequence analysis of ribosomal protein L34 of Escherichia coli.";
 RN Hoppe-Seyler's Z. Physiol. Chem. 357:873-886(1976).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhimurium; STRAIN=LT2 / SC5C1412 / ATCC 700720;
 RX MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
 RA McClelland M., Wollink S., Ali J., Dante M., Du F., Hou S., Layman D.,
 RA Courtney L., Porwollik S., Scott K., Holmes A., Grewal N., Mulvaney E.,
 RA Leonard S., Nguyen C., Scott K., Miller W., Stoneking T., Nhan M.,
 RA Ryan E., Sun H., Florea L., Wilson R.K.;
 RA Waterston R., Wilson R.K.;
 RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
 RT LT2.";

RL Nature 413:852-856(2001).
 RN [9]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=CT18;
 RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
 RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
 RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
 RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
 RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
 RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
 RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
 RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
 RA Whitehead S., Barrall B.G.;
 RA "Complete genome sequence of a multiple drug resistant Salmonella
 RT enterica serovar Typhi CT18.";
 RL Nature 413:848-852(2001).
 RN [10]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
 RX MEDLINE=22531367; PubMed=12644504;
 RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
 RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
 RA "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
 RT and CT18.";
 RL J. Bacteriol. 185:2330-2337(2003).
 RN [11]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
 RX MEDLINE=2272406; PubMed=12384590; DOI=10.1093/nar/gkf566;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RA "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=2457T / ATCC 700930 / Serotype 2a;
 RX MEDLINE=22590274; PubMed=12704152;
 RA Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
 RA Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
 RA Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
 RA Schwartz D.C., Blattner F.R.;
 RA "Complete genome sequence and comparative genomics of Shigella
 RT flexneri serotype 2a strain 2457T.";
 RL Infect. Immun. 71:2775-2786(2003).
 RN [13]
 RP MASS SPECTROMETRY.
 RC SPECIES=E.coli; STRAIN=K12 / ATCC 25404;
 RX MEDLINE=99196579; PubMed=10094780; DOI=10.1006/abio.1998.3077;
 RA Arnold R.J., Reilly J.P.;
 RA "Observation of Escherichia coli ribosomal proteins and their
 RT posttranslational modifications by mass spectrometry.";
 RL Anal. Biochem. 269:105-112(1999).
 CC -1- MASS SPECTROMETRY: MW=5380.5; METHOD=WALDI; RANGE=1-46;
 CC -1- NOTE=Ref.13.
 CC -1- SIMILARITY: Belongs to the ribosomal protein L34P family.
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 CC -----
 DR EMBL: J01602; AAB59148.1; -;
 DR EMBL: X01861; CA245982.1; -;
 DR EMBL: M11056; AAA24566.1; -;

DR EMBL: L10328; AAA62054.1; -;
 DR EMBL: U00096; AAC76726.1; -;
 DR EMBL: AE016769; AAN83058.1; -;
 DR EMBL: AP005601; AAG58900.1; -;
 DR EMBL: AP002566; BAB38061.1; -;
 DR EMBL: AE008879; AAL22698.1; -;
 DR EMBL: AL627280; CAD03156.1; -;
 DR EMBL: AE016846; AAO71176.1; -;
 DR EMBL: AE015383; AAN45204.1; -;
 DR EMBL: AE016991; AAP18993.1; -;
 DR PIR: C21915; R5EC34.
 DR PIR: F91208; F91208.
 DR PIR: H86054; H86054.
 DR ECHOBASE; EB0885; -;
 DR EcoGene; EG10892; rpmH.
 DR STyGene; SG77777; rpmH.
 DR HAMAP; MF_00391; -;
 DR InterPro; IPR000271; Ribosomal_L34.
 DR Pfam; PF00468; Ribosomal_L34; 1.
 DR PRODOM; PD003101; Ribosomal_L34; 1.
 DR TIGRFAMs; TIGR01030; rpmH_bact; 1.
 DR PROSITE; PS00784; RIBOSOMAL_L34; 1.
 KW Complete proteome; Direct protein sequencing; Ribosomal protein.
 SQ SEQUENCE 46 AA; 5380 MW; 600916E398939412 CRC64;
 Query Match 100.0%; Score 23; DB 1; Length 46;
 Best Local Similarity 80.0%; Pred. No. 2.9e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RXRS 5
 DB 12 RNRSH 16
 RESULT 11
 RL34_YERPE STANDARD; PRT; 46 AA.
 ID RL34_YERPE STANDARD; PRT; 46 AA.
 AC Q829U5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE S0S ribosomal protein L34.
 GN Name=rpml; OrderedLocNames=YPO4100, Y4114, YP4007;
 OS Versinia pestis.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Versinia.
 OX NCBI_TaxID=632;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / Biovar Orientalis;
 RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
 RA Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L.,
 RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.-M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
 RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrall B.G.;
 RT "Genome sequence of Versinia pestis, the causative agent of plague.";
 RL Nature 413:523-527(2001).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN=KIMS / Biovar Mediaevalis;
 RX MEDLINE=22137863; PubMed=12142430;
 RX DOI=10.1128/JB.184.16.4601-4611.2002;
 RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
 RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
 RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
 RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
 RA Perry R.D.;
 RT "Genome sequence of Versinia pestis KIM.";
 RL J. Bacteriol. 184:4601-4611(2002).
 RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN=91001 / Biovar Mediaevalis;
RA Song Y., Tong Z., Wang L., Han Y., Zhang J., Pei D., Wang J., Zhou D.,
RA Han Y., Pang X., Zhai J., Chen F., Qin H., Wang J., Li S., Guo Z.,
RA Ye C., Du Z., Lin W., Wang J., Yu J., Yang H., Wang J., Huang P.,
RA Yang R.;
RC Submitted (Apr-2003) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ribosomal protein L34P family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ414160; CAC93549.1; -.
DR EMBL; AE014013; AAM87656.1; -.
DR EMBL; AE017142; AAS64146.1; -.
DR HMAP; MF_00391; -.
DR InterPro; IPR000271; Ribosomal_L34.
DR Pfam; PF00468; Ribosomal_L34; 1.
DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpmH_bact; 1.
DR PROSITE; PS00784; RIBOSOMAL_L34; 1.
KW Complete proteome; Ribosomal protein.
KW NCBI_TaxID=160;
SQ SEQUENCE 46 AA; 5426 MW; 714D16E398938C72 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 46;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 12 RNRSH 16

RESULT 12
Y504_TREPA
ID Y504_TREPA STANDARD; PRT; 46 AA.
AC 083517;
DR 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein TP0504.
GN OrderedLocusNames=TP0504;
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
RA Fraser C.M., Norris S.J., Weinstein G.M., White O., Sutton G.G.,
RA Dodson R.J., Winn M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod W.P., Salzberg S.L., Peterson J.D.,
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Utterback T.R., McDonald L.A., Artlich P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete";
RL Science 281:375-388 (1998).
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
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DR EMBL; AE001226; AAC65493.1; -.
DR PIR; D71317; D71317.
DR TIGR; TP0504; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 46 AA; 5038 MW; 5BFA08088568ACC3 CRC64;

Query Match 100.0%; Score 23; DB 1; Length 46;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 10 RARSH 14

RESULT 13
Q663T0
ID Q663T0 PRELIMINARY; PRT; 46 AA.
AC Q663T0;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 50S ribosomal protein L34.
GN Name=rpMh; Synonyms=rmaA, ssaF; ORFNames=YPTB3945;
OS Versinia pseudotuberculosis IP 32953.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Versinia.
OX NCBI_TaxID=273123;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=IP 32953;
RX PubMed=15358858;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Verges L.M., Land M.L., Motin L.V.,
RA Brubaker R.R., Fowler J., Hinnebusch B.J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francoise V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the genome evolution of Versinia pseudotuberculosis";
RT genome comparison with Versinia pseudotuberculosis";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
DR EMBL; BX936398; CAH23183.1; -.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR00271; Ribosomal_L34.
DR Pfam; PF00468; Ribosomal_L34; 1.
DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpmH_bact; 1.
DR PROSITE; PS00784; RIBOSOMAL_L34; 1.
DR Ribonucleoprotein; Ribosomal protein.
KW Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 46 AA; 5426 MW; 714D16E398938C72 CRC64;

Query Match 100.0%; Score 23; DB 2; Length 46;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 12 RNRSH 16

RESULT 14
Q7MXZ2
ID Q7MXZ2 PRELIMINARY; PRT; 46 AA.
AC Q7MXZ2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 50S ribosomal protein L34.
GN Name=rpMh; OrderedLocusNames=plu4909;
OS Photorhabdus luminescens (subsp. laumondii).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Photorhabdus.
OX NCBI_TaxID=141679;
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RN SEQUENCE FROM N.A.
RC STRAIN=TT01;
RA MEDLINE=22957627; PubMed=14528314;
RA Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
RA Taourit S., Bocs S., Boursaux-Rude C., Chandler M., Charles J.-P.,
RA Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
RA Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
RA Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
RT "The genome sequence of the entomopathogenic bacterium Photobacterium
RT luminescens."
RL Nat. Biotechnol. 21:1307-1313 (2003).
CC -!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
DR EMBL; BX571875; CAB17281.1; -.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000271; Ribosomal_L34.
DR Pfam; PF00468; Ribosomal_L34; 1.
DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpmH_bact; 1.
DR PROSITE; PS00784; RIBOSOMAL_L34; 1.
KW Complete proteome; Ribonucleoprotein; Ribosomal protein.
SQ SEQUENCE 46 AA; 5410 MW; 600916E398938862 CRC64;

Query Match      100.0%; Score 23; DB 2; Length 46;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
Db 12 RNRSH 16

Search completed: March 8, 2005, 06:35:42
Job time : 4.86725 secs

[1]
SEQUENCE FROM N.A.
STRAIN=TT01;
MEDLINE=22957627; PubMed=14528314;
Duchaud E., Rusniok C., Frangeul L., Buchrieser C., Givaudan A.,
Taourit S., Bocs S., Boursaux-Rude C., Chandler M., Charles J.-P.,
Dassa E., Derose R., Derzelle S., Freyssinet G., Gaudriault S.,
Medigue C., Lanois A., Powell K., Sigulier P., Vincent R., Wingate V.,
Zouine M., Glaser P., Boemare N., Danchin A., Kunst F.;
"The genome sequence of the entomopathogenic bacterium Photobacterium
luminescens."
Nat. Biotechnol. 21:1307-1313 (2003).
-!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
EMBL; BX571875; CAB17281.1; -.
GO; GO:0005840; C:ribosome; IEA.
GO; GO:0003735; F:structural constituent of ribosome; IEA.
GO; GO:0006412; P:protein biosynthesis; IEA.
InterPro; IPR000271; Ribosomal_L34.
Pfam; PF00468; Ribosomal_L34; 1.
ProDom; PD003101; Ribosomal_L34; 1.
TIGRFAMs; TIGR01030; rpmH_bact; 1.
PROSITE; PS00784; RIBOSOMAL_L34; 1.
Complete proteome; Ribonucleoprotein; Ribosomal protein.
SEQUENCE 46 AA; 5410 MW; 600916E398938862 CRC64;

RESULT 15
Q6CYR2 PRELIMINARY; PRT; 46 AA.
ID Q6CYR2;
AC Q6CYR2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 508 ribosomal protein L34.
GN OrderedLocustNames=ECA443;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
SEQUENCE FROM N.A.
STRAIN=SCRI 1043 / ATCC BAA-672;
RC PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors."
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).
CC -!- SIMILARITY: Belongs to the L34P family of ribosomal proteins.
DR EMBL; BX950851; CAG77339.1; -.
DR GO; GO:0005840; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR000271; Ribosomal_L34.
DR Pfam; PF00468; Ribosomal_L34; 1.
DR ProDom; PD003101; Ribosomal_L34; 1.
DR TIGRFAMs; TIGR01030; rpmH_bact; 1.
DR PROSITE; PS00784; RIBOSOMAL_L34; 1.
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 2.31814 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-13

Perfect score: 23

Sequence: 1 RXRSH 5

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	23	100.0	5	2	AY34296	Aay34296 Consensus
2	23	100.0	5	2	AY34298	Aay34298 Consensus
3	23	100.0	8	2	AY39453	Aay39453 CD147 bin
4	23	100.0	10	4	AAG96802	Aag96802 Human com
5	23	100.0	10	4	AAG96808	Aag96808 Human com
6	23	100.0	10	8	ADR21474	Adr21474 N-myc dow
7	23	100.0	11	6	AAE14841	Aae14841 LAMP-1 cy
8	23	100.0	12	2	AY39460	Aay39460 CD147 bin
9	23	100.0	15	2	AY39463	Aay39463 CD147 bin
10	23	100.0	15	2	AY01569	Aay01569 Antigenic
11	23	100.0	15	5	AAE27041	Aae27041 Mouse TCR
12	23	100.0	15	5	AAO19143	Aao19143 Truncated
13	23	100.0	15	8	ADOO5885	Adoo5885 Rat MOGI-
14	23	100.0	16	7	ADM47488	Adm47488 Bioactive
15	23	100.0	18	5	AAE19258	Aae19258 Human rec
16	23	100.0	18	7	ADD84768	Add84768 Alpha-gal
17	23	100.0	18	7	ADI28365	Adi28365 Human TTE
18	23	100.0	18	8	ADJ88294	Adj88294 Tobacco m
19	23	100.0	18	8	ADM48698	Adm48698 Human rga
20	23	100.0	19	6	ABP82361	Abp82361 G protein
21	23	100.0	20	2	AAW00869	Aaw00869 T-cell re
22	23	100.0	22	5	AAE19256	Aae19256 Human rec
23	23	100.0	22	7	ADD84766	Add84766 Alpha-gal
24	23	100.0	22	8	ADJ88292	Adj88292 Tobacco m
25	23	100.0	22	8	ADM48696	Adm48696 Human rga

26	23	100.0	23	6	ABO12112	Abol2112 Human zin
27	23	100.0	23	6	ABO13097	Abol3097 Mouse zin
28	23	100.0	24	5	AAE19259	Aae19259 Human rec
29	23	100.0	24	7	ADD84769	Add84769 Alpha-gal
30	23	100.0	24	8	ADJ88295	Adj88295 Tobacco m
31	23	100.0	24	8	ADM48699	Adm48699 Human rga
32	23	100.0	25	4	AAU01685	Aau01685 Gene 28 h
33	23	100.0	25	5	AAE27040	Aae27040 Mouse TCR
34	23	100.0	25	5	AAO19142	Aao19142 Truncated
35	23	100.0	26	5	ABG95061	Abg95061 Human tra
36	23	100.0	26	5	ABG95098	Abg95098 Human tra
37	23	100.0	26	5	ABE19254	Abe19254 Human rec
38	23	100.0	26	7	ADD84764	Add84764 Alpha-gal
39	23	100.0	26	8	ADJ88290	Adj88290 Tobacco m
40	23	100.0	26	8	ADM48694	Adm48694 Human rga
41	23	100.0	27	8	ABO58949	Abo58949 Human gen
42	23	100.0	28	5	AAE19257	Aae19257 Human rec
43	23	100.0	29	2	AAE66180	Aae66180 Portion o
44	23	100.0	29	4	ABB40852	Abb40852 Peptide #
45	23	100.0	29	4	AAW34620	Aaw34620 Peptide #

ALIGNMENTS

RESULT 1

AAAY34296

ID AAY34296 standard; peptide; 5 AA.

XX

AC AAY34296;

DT 19-NOV-1999 (first entry)

DE Consensus binding site for antibody ABX-CBL.

KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 2 /note= "unspecified amino acid"

XX WO9945031-A2.

XX PD 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

XX Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX New monoclonal antibody, used for treating e.g. graft versus host

XX disease, cancers, autoimmune diseases and inflammatory diseases.

XX Claim 24; Page 131; 245pp; English.

PS This sequence represents a consensus binding site for the antibody of the
XX invention. The antibody is a monoclonal antibody (Mab) with an isotype
CC that fixes complement and a variable region that binds to the epitope on
CC CD147 bound by the IgM Mab ABX-CBL, providing that the antibody is not
CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells
CC or resting or activated monocytes. The products and methods can be used

CC for treating diseases involving activated T-cells or B-cells or
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
 CC (e.g. arthritis)
 XX
 SQ Sequence 5 AA;

Query Match 100.0%; Score 23; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
 |||||
 Db 1 RXRSH 5

RESULT 2
 AAY34298
 ID AAY34298 standard; peptide; 5 AA.

XX AAY34298;

XX 19-NOV-1999 (first entry)

XX Consensus binding site for antibody ABX-CBL.

XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Synthetic.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX Claim 24; Page 131; 245pp; English.

XX This sequence represents a consensus binding site for the antibody of the
 CC invention. The antibody is a monoclonal antibody (Mab) with an isotype
 CC that fixes complement and a variable region that binds to the epitope on
 CC CD147 bound by the IgM Mab ABX-CBL, providing that the antibody is not
 CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells
 CC or resting or activated monocytes. The products and methods can be used
 CC for treating diseases involving activated T-cells or B-cells or
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
 CC (e.g. arthritis)

XX Sequence 5 AA;

Query Match 100.0%; Score 23; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 RXRSH 5
 |||||
 Db 1 RVRSH 5

RESULT 3

AAY39453

ID AAY39453 standard; peptide; 8 AA.

XX AAY39453;

XX 19-NOV-1999 (first entry)

XX CD147 binding site for antibody ABX-CBL.

XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Synthetic.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX Example 12; Page 75; 245pp; English.

XX This sequence represents a binding site for the antibody of the
 CC invention. The antibody is a monoclonal antibody (Mab) with an isotype
 CC that fixes complement and a variable region that binds to the epitope on
 CC CD147 bound by the IgM Mab ABX-CBL, providing that the antibody is not
 CC CBL1. The Mab can selectively kill activated T-cells, activated B-cells
 CC or resting or activated monocytes. The products and methods can be used
 CC for treating diseases involving activated T-cells or B-cells or
 CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
 CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
 CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
 CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
 CC (e.g. arthritis)

XX Sequence 8 AA;

Query Match 100.0%; Score 23; DB 2; Length 8;
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
 |||||
 Db 4 RVRSH 8

RESULT 4

AAG96802

ID AAG96802 standard; peptide; 10 AA.

XX

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AC AAG96802;
XX
XX 18-SEP-2001 (first entry)
XX
DE Human complementary peptide, SEQ ID NO: 2996.
XX
XX Human; complementary peptide; ligand; drug discovery; drug design.
XX
XX OS Homo sapiens.
XX
XX PN WO200142277-A2.
XX
XX PD 14-JUN-2001.
XX
XX PF 13-DEC-2000; 2000WO-GB004776.
XX
XX PR 13-DEC-1999; 99GB-00029464.
XX
XX PA (PROT-) PROTEOM LTD.
XX
XX PI Roberts GW, Heal JR;
XX
XX DR WPI; 2001-408419/43.
XX
XX PT A set of peptide ligands consisting of specific complementary peptides to
XX PT proteins encoded by genes of the human genome, useful in an assay for
XX PT screening and identifying of one or more novel peptides which are drug
XX PT candidates or pro-drugs.
XX
XX PS Example 4; Page 473; 646pp; English.
XX
XX CC The invention relates to a set of complementary peptide ligands generated
XX CC from the human genome. The complementary peptides interact with their
XX CC relevant target proteins encoded in the human genome. They can be used as
XX CC reagents in drug discovery and as lead ligands to facilitate drug design
XX CC and development. The present sequence is a complementary peptide provided
XX CC in the specification
XX
XX SQ Sequence 10 AA;

Query Match 100.0%; Score 23; DB 4; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
Db |:|:|
2 RSRSH 6

RESULT 6
ADR21474
ID ADR21474 standard; peptide; 10 AA.
XX
XX AC ADR21474;
XX
XX DT 21-OCT-2004 (first entry)
XX
XX DE N-myc downstream-regulated gene 2 C-terminal repeat sequence.
XX
XX KW anorectic; anabolic; eating disorder; antidiabetic; muscular; cardiac;
XX KW antiinflammatory; immunomodulator; cerebroprotective; antiseborrheic;
XX KW dermatological; antianginal; antiarthritic; respiratory;
XX KW gastrointestinal; endocrine; central nervous system; gene therapy;
XX KW gene expression; hypothalamus tissue; obese animal; lean animal;
XX KW fasted animal; fed animal; myopathy; obesity; anorexia;
XX KW weight maintenance; diabetes; mitochondrial dysfunction disorder;
XX KW genetic disorder; cancer impaired muscle development; heart disease;
XX KW inflammation; immune system disorder; infertility; brain disease;
XX KW metabolic energy level; acne; angina; arthritis; aspiration pneumonia;
XX KW emphysema; gastroenteritis; intestinal flu; Digeorge syndrome;
XX KW Job syndrome; Bruton disease; complement deficiency; Varicocoele;
XX KW Young's syndrome; Myotonic dystrophy; Cystic fibrosis; Kennedy's disease;
XX KW Turner's syndrome; Cushing's syndrome; fat sand rat.
XX
XX OS Homo sapiens.
XX OS Mus sp.
XX
XX PN WO2004063218-A1.
XX
XX PD 29-JUL-2004.
XX
XX PF 13-JAN-2004; 2004WO-AU0000043.
XX
XX PR 13-JAN-2003; 2003US-0439767P.
XX
XX PA (AUTO-) AUTOGEN RES PTY LTD.
XX PA (UYDE-) UNIV DEAKIN.
XX
XX PI Collier G, Walder K, Segal D, Foletta VC;
XX
XX DR WPI; 2004-553717/53.
XX
XX PT New isolated nucleic acid molecule, useful for treating e.g., myopathy,
```

PT obesity, anorexia, weight maintenance, diabetes, disorders associated
 PT with mitochondrial dysfunction, genetic disorders, heart disease and
 PT inflammation.

XX Example 4; SEQ ID NO 13; 210pp; English.

XX The invention relates to an isolated nucleic acid molecule (I) comprising
 CC a sequence of nucleotides encoding or complementary to a sequence
 CC encoding a molecule or its derivative or homologue where (I) is expressed
 CC in a larger amount in hypothalamus tissue of obese animals compared to
 CC lean animals or in fasted animals compared to fed animals. A method
 CC comprising administering to the mammal an agent for a time and under
 CC conditions to modulate the expression or activity of AGT-701, AGT-702,
 CC AGT-704, AGT-705, AGT-706, AGT-707, AGT-708, AGT-709 and/or AGT-710, is
 CC useful for treating a mammal suffering from a condition characterized by
 CC one or more symptoms or inter alia a myopathy, obesity, anorexia, weight
 CC maintenance, diabetes, disorders associated with mitochondrial
 CC dysfunction, genetic disorders, cancer impaired muscle development, heart
 CC disease, inflammation, disorders associated with the immune system,
 CC infertility, disease associated with the brain, and metabolic energy
 CC levels. Examples of inflammatory diseases include acne, angina,
 CC arthritis, aspiration pneumonia, emphysema, gastroenteritis and
 CC intestinal flu. Disorders associated with the immune system include
 CC DiGeorge syndrome, Job syndrome, Bruton disease, and Complement
 CC deficiencies. Examples of disorders associated with infertility are
 CC Varicocele, Young's syndrome, Myotonic dystrophy, Cystic fibrosis,
 CC Kennedy's disease, Turner's syndrome and Cushing's syndrome. This
 CC sequence corresponds to a repeat peptide sequence found in the N-myc
 CC downstream-regulated gene 2 (NDRG2) protein C-terminal region conserved
 CC in human and mouse NDRG2 proteins. The protein encoded by the AGT-701
 CC nucleic acid sequence of the invention has sequence homology to the NDRG2
 CC protein sequence.

XX Sequence 10 AA;

Query Match 100.0%; Score 23; DB 8; Length 10;
 Best Local Similarity 80.0%; Pred. No. 1.5e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
 Db 3 RSRSH 7

RESULT 7

AAE14841
 ID AAE14841 standard; peptide; 11 AA.

AC AAE14841;

DT 24-MAR-2003 (first entry)

XX LAMP-1 cytoplasmic tail.

XX Chimera; vaccine; trafficking domain; endosome; lysosome; cancer;

KW autoimmune disease; allergic reaction; transplant; graft;

KW hypersensitivity; congenital disease; luminal domain; LAMP-1;

KW lysosomal associated membrane protein; immune response; cytoplasmic tail.

XX Unidentified.

XX Key Location/Qualifiers

FT Domain 8..11

FT /label= Tyr_motif

FT /note= "Targets molecules to lysosome"

FN WO200280851-A2.

PD 17-OCT-2002.

XX 05-APR-2002; 2002WO-US010757.

XX 05-APR-2001; 2001US-0281607P.

PR 05-APR-2001; 2001US-0281608P.
 PR 05-APR-2001; 2001US-0281621P.

XX (UWJO) UNIV JOHNS HOPKINS.

PI August T, Marques B;

XX WPI; 2003-058464/05.

XX Novel chimeric protein for treating cancer, comprises antigen sequence,
 PT and trafficking domain that directs both membrane and non-membrane
 PT proteins to endosomal compartment or trafficking domain of endocytic
 PT receptor.

PS Disclosure; Page 32; 102pp; English.

XX The invention provides chimeric proteins and nucleic acids encoding these
 CC which can be used to generate vaccines against selected antigens. The
 CC chimeric protein comprises an antigen domain having at least one epitope,
 CC and a trafficking domain that directs both membrane and non-membrane
 CC proteins to an endosomal/lysosomal compartment in a cell and/or to a
 CC lysosome-related organelle. The antigen used in the chimeric protein is
 CC taken from a pathogenic organism, e.g. HIV, a cancer-specific polypeptide
 CC or a molecule associated with an abnormal physiological response (e.g.
 CC autoimmune disease, an allergic reaction, cancer, reaction to a
 CC transplant or graft, hypersensitivity reaction, or congenital disease).
 CC The trafficking domain comprises a luminal domain of a lysosomal
 CC associated membrane protein (LAMP). Alternatively, or additionally, the
 CC protein comprises a trafficking domain of an endocytic receptor. The
 CC vaccine (DNA, RNA, protein) can be used to modulate an immune response
 CC against any kind of antigen. The invention also provides a method for
 CC treating a patient with cancer by providing a chimeric protein comprising
 CC cancer-specific antigen or a nucleic acid encoding the protein. The
 CC present sequence is lysosomal associated membrane protein (LAMP)-1
 CC cytoplasmic tail used in the chimeric protein of the invention

XX Sequence 11 AA;

Query Match 100.0%; Score 23; DB 6; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5

Db 1 RKRSH 5

RESULT 8

AAV39460

ID AAV39460 standard; peptide; 12 AA.

AC AAV39460;

DT 19-NOV-1999 (first entry)

XX CD147 binding site for antibody ABX-CBL.

XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Synthetic.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

```

PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
PI WPI; 1999-540816/45.
XX
XX New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
XX Example 12; Page 76; 245pp; English.
XX
XX This sequence represents a binding site for the antibody of the
CC invention. The antibody is a monoclonal antibody (MAB) with an isotype
CC that fixes complement and a variable region that binds to the epitope on
CC CD147 bound by the Igm MAB ABX-CBL, providing that the antibody is not
CC CBL1. The MAB can selectively kill activated T-cells, activated B-cells
CC or resting or activated monocytes. The products and methods can be used
CC for treating diseases involving activated T-cells or B-cells or
CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
CC (e.g. arthritis)
XX
SQ Sequence 12 AA;
Query Match 100.0%; Score 23; DB 2; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RQRSH 5
DB |:|
7 RQRSH 11
RESULT 9
AAAY39463
ID AAY39463 standard; peptide; 15 AA.
XX
AC AAY39463;
XX
DT 19-NOV-1999 (first entry)
XX
DE CD147 binding site for antibody ABX-CBL.
XX
KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Synthetic.
XX
PN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
XX
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
XX WPI; 1999-540816/45.
XX
XX New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
XX Example 12; Page 77; 245pp; English.
XX

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XX This sequence represents a binding site for the antibody of the
CC invention. The antibody is a monoclonal antibody (MAB) with an isotype
CC that fixes complement and a variable region that binds to the epitope on
CC CD147 bound by the Igm MAB ABX-CBL, providing that the antibody is not
CC CBL1. The MAB can selectively kill activated T-cells, activated B-cells
CC or resting or activated monocytes. The products and methods can be used
CC for treating diseases involving activated T-cells or B-cells or
CC monocytes, e.g. graft versus host disease (GVHD), organ transplant
CC rejection diseases (e.g. renal transplant, ocular transplant), cancers
CC (e.g. cancers of the blood (e.g. leukaemia's and lymphomas) and
CC pancreatic), autoimmune diseases (e.g. lupus), and inflammatory diseases
CC (e.g. arthritis)
XX
SQ Sequence 15 AA;
Query Match 100.0%; Score 23; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 RKRSH 5
DB |:|
11 RVRSH 15
RESULT 10
AAAY01569
ID AAY01569 standard; peptide; 15 AA.
XX
AC AAY01569;
XX
DT 17-OCT-2003 (revised)
DT 18-JUN-1999 (first entry)
XX
DE Antigenic peptide of streptokinase.
XX
KW Antigenic peptide; streptokinase; streptokinase-specific antibody;
KW thrombolytic activity; thrombolytic therapy; glomerulonephritis;
KW rheumatic fever.
XX
OS Streptococcus dysgalactiae subsp. equisimilis.
XX
PN WO9908698-A1.
XX
PD 25-FEB-1999.
XX
PF 18-AUG-1998; 98WO-US017114.
XX
PR 18-AUG-1997; 97US-0055911P.
XX
PA (HARD ) HARVARD COLLEGE.
PA (GEHO ) GEN HOSPITAL CORP.
XX
XX Reed GL, Parhami-Seren B;
XX
XX WPI; 1999-190113/16.
XX
XX New polypeptides which bind streptokinase-specific antibodies - useful in
PT thrombolytic therapy.
XX
XX Example 1; Fig 1; 44pp; English.
XX
XX The present sequence represents an antigenic peptide of streptokinase.
CC The specification describes a polypeptide which binds to a streptokinase-
CC specific antibody and prevents the antibody binding to native
CC streptokinase. The specification also describes a synthetic polypeptide
CC (PI) comprising an epitope which binds to an streptokinase-specific
CC antibody and reduces thrombolytic activity of streptokinase. PI is used
CC in thrombolytic therapy, and to prevent or treat glomerulonephritis and
CC rheumatic fever. (Updated on 17-OCT-2003 to standardise OS field)
XX
SQ Sequence 15 AA;

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Query Match      100.0%; Score 23; DB 2; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RARSH 6

RESULT 11
AAE27041
ID AAE27041 standard; peptide; 15 AA.
XX
AC AAE27041;
XX
DT 13-DEC-2002 (first entry)
XX
DE Mouse TCR intronic JalphaTA39 gene peptide #2.
XX
KW Mouse; T cell receptor; TCR; mesenchymal cell growth; cell therapy;
KW carcinoma; wound healing; intronic J region; joining region; J region;
KW constant domain; C domain; receptor; JalphaTA39.
XX
OS Mus sp.
XX
PN WO200266636-A2.
XX
PD 29-AUG-2002.
XX
PF 20-FEB-2002; 2002WO-IL000130.
XX
PR 20-FEB-2001; 2001IL-00141539.
XX
PA (YEDA ) YEDA RES & DEV CO LTD.
XX
PY (UYBA-) UNIV BAR-ILAN.
XX
PI Zipori D, Rozenszajn AL, Barda-Saad M, Shav-Tal Y;
XX
DR WPI; 2002-667067/71.
XX
PT New isolated polynucleotide comprising a transcript of a T cell receptor
PT gene, useful for transfecting mesenchymal cells for wound healing or
PT suppression of carcinomas.
XX
PS Claim 20; Page 39; 63pp; English.
XX
CC The invention relates to polynucleotide transcripts of T cell receptor
CC (TCR) gene, as well as protein sequences encoded by these transcripts,
CC and their use in the modulation of mesenchymal cell growth. The invention
CC also concerns cDNA molecules encoded by a TCR gene lacking V region
CC sequences and comprising a constant (C) domain and joining (J) region
CC sequences and a 5' intronic J' sequences upstream to the J region sequence
CC including an in-frame methionine. Polynucleotides of the invention are
CC useful for transfecting mesenchymal cells for wound healing or
CC suppression of carcinomas. Antibodies of the invention are useful as
CC markers of mesenchymal cells. The invention is useful in cell therapy.
CC The present sequence is a peptide encoded by intronic JalphaTA39 gene of
CC mouse TCR
XX
SQ Sequence 15 AA;
Query Match      100.0%; Score 23; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 5 RERSH 9

RESULT 12
AAO19143
ID AAO19143 standard; peptide; 15 AA.
XX

```

```

XX AAO19143;
AC
DT 27-NOV-2002 (first entry)
XX
DE Truncated T cell receptor variant peptide from mesenchymal cell #15.
XX
KW Immunoglobulin; Ig; T cell receptor; TCR; variant; mesenchymal cell;
KW haematopoiesis; haematopoietic stem cell; mu heavy chain; mouse;
KW gene therapy; vulnery; cytostatic; wound healing; cancer.
XX
OS Unidentified.
XX
PN WO200266648-A2.
XX
PD 29-AUG-2002.
XX
PF 20-FEB-2002; 2002WO-IL000129.
XX
PR 20-FEB-2001; 2001IL-00141539.
XX
PR 25-SEP-2001; 2001IL-00145658.
XX
PA (YEDA ) YEDA RES & DEV CO LTD.
XX
PY Zipori D, Shav-Tal Y, Barda-Saad M;
XX
DR WPI; 2002-674947/72.
XX
PT New isolated polynucleotide comprising a transcript of an immunoglobulin
PT gene, useful for transfection of mesenchymal cells, for wound healing, or
PT for inducing hemopoiesis after bone marrow transplantation or
PT chemotherapy.
XX
PS Claim 19; Page 16; 48pp; English.
XX
CC The present invention relates to an isolated polynucleotide comprising a
CC transcript of an immunoglobulin (Ig) gene. The polynucleotide lacks
CC variable (V) region sequences and comprises a constant (C) domain and
CC joining (J) region sequences, and a 5' intronic J sequence upstream to
CC the J region sequence including an in-frame methionine codon. The
CC polynucleotides are useful for the transfection of mesenchymal cells, for
CC wound healing, for inducing haematopoiesis after bone marrow
CC transplantation or chemotherapy, for the suppression of cancer, and for
CC treating disorders involving the proliferation and differentiation of
CC haematopoietic stem cells. The present sequence is a peptide described in
CC the invention
XX
SQ Sequence 15 AA;
Query Match      100.0%; Score 23; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 5 RERSH 9

RESULT 13
ADO05885
ID ADO05885 standard; protein; 15 AA.
XX
AC ADO05885;
XX
DT 15-JUL-2004 (first entry)
XX
DE Rat MOG1-125 C-terminal peptide fragment.
XX
KW MOG; multiple sclerosis; MS; allergic encephalomyelitis; EAE;
KW myelin/oligodendrocyte glycoprotein; rat.
XX
OS Rattus sp.
XX

```


PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI Garger SJ, Turpen TH, Kumagai MH;
XX
DR WPI; 2002-195873/25.
XX
PT New glucocerebrosidase and alpha-galactosidase having a post-
PT translational modification, useful in enzyme replacement therapy for
PT treating lysosomal storage diseases, e.g. Gaucher disease, Niemann-Pick
PT disease, Fabry disease.
XX
XX Example 11; Fig 5; 102pp; English.
XX
CC The invention relates to production of lysosomal enzymes in plants by
CC transient expression. The invention particularly relates to
CC glucocerebrosidase and alpha-galactosidase having a post-translational
CC modification. The enzymes are useful in enzyme replacement therapy for
CC treating lysosomal storage diseases (e.g. Gaucher disease, Niemann-Pick
CC disease, Fabry disease and Tay-Sachs disease), in researches for
CC developing new approaches to medical treatment of lysosomal storage
CC diseases and in industrial processes involving enzymatic substrate
CC hydrolysis. The present sequence is human recombinant alpha-
CC galactosidase-A C-terminal modified peptide
XX
SQ Sequence 18 AA;

Query Match 100.0%; Score 23; DB 5; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
Db 3 RLRS 7

Search completed: March 8, 2005, 06:17:01
Job time : 4.31814 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 2.65337 Seconds
(without alignments)

620.051 Million cell updates/sec

Title: US-09-784-950-13

Perfect score: 23

Sequence: 1 RXRSH 5

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	7	11	US-09-855-604-23
2	23	100.0	8	17	US-10-808-187-1281
3	23	100.0	10	10	US-09-572-404B-2996
4	23	100.0	10	10	US-09-572-404B-3002
5	23	100.0	15	15	US-10-682-420-61
6	23	100.0	15	15	US-10-682-420-84
7	23	100.0	15	15	US-10-409-613-61
8	23	100.0	15	15	US-10-409-613-84
9	23	100.0	15	15	US-10-442-180-61
10	23	100.0	15	15	US-10-442-180-84
11	23	100.0	15	16	US-10-643-982-22
12	23	100.0	15	17	US-10-683-451-38
13	23	100.0	15	17	US-10-775-337-61

14	23	100.0	15	17	US-10-775-337-84	Sequence 84, Appl
15	23	100.0	16	14	US-10-267-251-25	Sequence 25, Appl
16	23	100.0	18	9	US-09-993-059-29	Sequence 29, Appl
17	23	100.0	18	14	US-10-103-327-29	Sequence 29, Appl
18	23	100.0	18	14	US-10-123-626-29	Sequence 29, Appl
19	23	100.0	18	15	US-10-602-219-29	Sequence 29, Appl
20	23	100.0	18	15	US-10-602-220-29	Sequence 29, Appl
21	23	100.0	18	15	US-10-684-300-9	Sequence 9, Appl
22	23	100.0	18	15	US-10-684-349-9	Sequence 9, Appl
23	23	100.0	19	14	US-10-225-567A-1034	Sequence 1034, Ap
24	23	100.0	22	9	US-09-993-059-27	Sequence 27, Appl
25	23	100.0	22	14	US-10-103-327-27	Sequence 27, Appl
26	23	100.0	22	15	US-10-602-219-27	Sequence 27, Appl
27	23	100.0	22	15	US-10-602-220-27	Sequence 27, Appl
28	23	100.0	22	15	US-10-684-300-7	Sequence 7, Appl
29	23	100.0	22	15	US-10-684-349-7	Sequence 7, Appl
30	23	100.0	24	9	US-09-993-059-30	Sequence 30, Appl
31	23	100.0	24	14	US-10-164-359-13	Sequence 13, Appl
32	23	100.0	24	14	US-10-103-327-30	Sequence 30, Appl
33	23	100.0	24	15	US-10-602-219-30	Sequence 30, Appl
34	23	100.0	24	15	US-10-602-220-30	Sequence 30, Appl
35	23	100.0	24	15	US-10-684-300-10	Sequence 10, Appl
36	23	100.0	24	15	US-10-684-349-10	Sequence 10, Appl
37	23	100.0	25	16	US-10-643-982-21	Sequence 21, Appl
38	23	100.0	26	9	US-09-993-059-25	Sequence 25, Appl
39	23	100.0	26	14	US-10-103-327-25	Sequence 25, Appl
40	23	100.0	26	15	US-10-602-219-25	Sequence 25, Appl
41	23	100.0	26	15	US-10-602-220-25	Sequence 25, Appl
42	23	100.0	26	15	US-10-684-300-5	Sequence 5, Appl
43	23	100.0	26	15	US-10-684-349-5	Sequence 5, Appl
44	23	100.0	27	14	US-10-029-386-32583	Sequence 32583, A
45	23	100.0	28	15	US-10-684-300-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1

US-09-855-604-23
; Sequence 23, Application US/09855604
; Publication No. US20040214165A1
; GENERAL INFORMATION:
; APPLICANT: GICQUEL, BRIGITTE
; APPLICANT: PORTNOI, DENIS
; APPLICANT: LIM, ENG-MONG
; APPLICANT: PELICIC, VLADIMIR
; APPLICANT: GUIGUENO, AGNES
; APPLICANT: GOGUET DE LA SALMONIERE, YVES
; TITLE OF INVENTION: POLYPEPTIDE NUCLEIC SEQUENCES EXPORTED FROM MYCOBACTERIA,
; TITLE OF INVENTION: VECTORS COMPRISING SAME AND USES FOR DIAGNOSING AND
; TITLE OF INVENTION: PREVENTING TUBERCULOSIS
; FILE REFERENCE: 03715.0062-01000
; CURRENT APPLICATION NUMBER: US/09/855,604
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 09/485,536
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/FR98/01813
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: FR 97 10404
; PRIOR FILING DATE: 1997-08-14
; PRIOR APPLICATION NUMBER: FR 97 11325
; PRIOR FILING DATE: 1997-09-11
; NUMBER OF SEQ ID NOS: 935
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-855-604-23

Query Match 100.0%; Score 23; DB 11; Length 7;

Best Local Similarity 80.0%; Pred. No. 1.3e+06; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0;

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;
;
; OTHER INFORMATION: sequence located in SFRS3 OR SRP20 OR X16 at 187-196 and may inter
; OTHER INFORMATION: with Sequence 2995 in this patent.
US-09-572-404B-2996

Query Match      100.0%; Score 23; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
DB 1 RSRSH 5

RESULT 4
US-09-572-404B-3002
; Sequence 3002, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3002
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in SFRS3 OR SRP20 OR X16 at 186-195 and may inter
; OTHER INFORMATION: with Sequence 3001 in this patent.
US-09-572-404B-3002

Query Match      100.0%; Score 23; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
DB 2 RSRSH 6

RESULT 5
US-10-682-420-61
; Sequence 61, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PMD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
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;
; OTHER INFORMATION: sequence located in SFRS3 OR SRP20 OR X16 at 187-196 and may inter
; OTHER INFORMATION: with Sequence 2995 in this patent.
US-09-572-404B-2996

Query Match      100.0%; Score 23; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
DB 1 RSRSH 5

RESULT 4
US-09-572-404B-3002
; Sequence 3002, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572.404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 3002
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in SFRS3 OR SRP20 OR X16 at 186-195 and may inter
; OTHER INFORMATION: with Sequence 3001 in this patent.
US-09-572-404B-3002

Query Match      100.0%; Score 23; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
DB 2 RSRSH 6

RESULT 5
US-10-682-420-61
; Sequence 61, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PMD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 61
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; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-10-682-420-61

Query Match      100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RPRSH 6

RESULT 6
US-10-682-420-84
; Sequence 84, Application US/10682420
; Publication No. US20040062775A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/682,420
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: US/10/637,011
; PRIOR FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-682-420-84

Query Match      100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RPRSH 6

RESULT 7
US-10-409-613-61
; Sequence 61, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-409-613-84

Query Match      100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RPRSH 6

RESULT 8
US-10-409-613-84
; Sequence 84, Application US/10409613
; Publication No. US20040076635A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Phillipe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
; TITLE OF INVENTION: DISEASE (PWD)
; FILE REFERENCE: 065691/0176
; CURRENT APPLICATION NUMBER: US/10/409,613
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US/09/514,245B
; PRIOR FILING DATE: 2000-02-28
; PRIOR APPLICATION NUMBER: FR 97/15396
; PRIOR FILING DATE: 1997-12-05
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-10-409-613-84

Query Match      100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
Db 2 RPRSH 6

RESULT 9
US-10-442-180-61
; Sequence 61, Application US/10442180
; Publication No. US20040091502A1
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
```

APPLICANT: Le Cann, Pierre
APPLICANT: BLANCHARD, Philippe
APPLICANT: HUTET, Evelyne
APPLICANT: ARNAULD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: CARIOLET, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISEASE (PMD)
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/10/442,180
CURRENT FILING DATE: 2003-05-21
PRIOR APPLICATION NUMBER: US/09/514,245
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PatentIn version 3.0
SEQ ID NO 61
LENGTH: 15
TYPE: PRT
ORGANISM: Type B PWD circovirus
US-10-442-180-61

Query Match 100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
|:|
Db 2 RPRSH 6

RESULT 10
US-10-442-180-84

Sequence 84, Application US/10442180
Publication No. US20040091502A1

GENERAL INFORMATION:

APPLICANT: JESTIN, Andre

APPLICANT: ALBINA, Emanuel

APPLICANT: Le Cann, Pierre

APPLICANT: BLANCHARD, Philippe

APPLICANT: HUTET, Evelyne

APPLICANT: ARNAULD, Claire

APPLICANT: TRUONG, Catherine

APPLICANT: MAHE, Dominique

APPLICANT: CARIOLET, Roland

APPLICANT: MADEC, Francois

TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS

TITLE OF INVENTION: DISEASE (PMD)

FILE REFERENCE: 065691/0176

CURRENT APPLICATION NUMBER: US/10/442,180

CURRENT FILING DATE: 2003-05-21

PRIOR APPLICATION NUMBER: US/09/514,245

PRIOR FILING DATE: 2000-02-28

PRIOR APPLICATION NUMBER: FR 97/15396

PRIOR FILING DATE: 1997-12-05

NUMBER OF SEQ ID NOS: 170

SOFTWARE: PatentIn version 3.0

SEQ ID NO 84

LENGTH: 15

TYPE: PRT

ORGANISM: Type A PWD circovirus

US-10-442-180-84

Query Match 100.0%; Score 23; DB 15; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
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Db 2 RPRSH 6

RESULT 11

US-10-643-982-22

Sequence 22, Application US/10643982

Publication No. US20040101931A1

GENERAL INFORMATION:

APPLICANT: Zipori, Dov

APPLICANT: Shav-Tal, Yaron

APPLICANT: Barda-Saad, Mira

TITLE OF INVENTION: IMMUNOGLOBULIN SUPERFAMILY VARIANTS EXPRESSED IN MESENCHYMAL CELLS

FILE REFERENCE: 85189-5000

CURRENT APPLICATION NUMBER: US/10/643,982

CURRENT FILING DATE: 2003-08-20

PRIOR APPLICATION NUMBER: PCT/IL02/00129

PRIOR FILING DATE: 2002-02-20

PRIOR APPLICATION NUMBER: IL141539

PRIOR FILING DATE: 2001-02-20

PRIOR APPLICATION NUMBER: IL145658

PRIOR FILING DATE: 2001-09-25

NUMBER OF SEQ ID NOS: 42

SEQ ID NO 22

LENGTH: 15

TYPE: PRT

ORGANISM: Mus musculus

US-10-643-982-22

Query Match 100.0%; Score 23; DB 15; Length 15;

Best Local Similarity 80.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
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Db 5 RERSH 9

RESULT 12

US-10-683-451-38

Sequence 38, Application US/10683451

Publication No. US20050009096A1

GENERAL INFORMATION:

APPLICANT: GENAIN, CLAUDE P.

APPLICANT: VON BUDINGEN, HANS-CHRISTIAN

APPLICANT: MENGE, TIL P.

TITLE OF INVENTION: A METHOD FOR DIAGNOSIS AND PROGNOSIS OF MULTIPLE SCLEROSIS

FILE REFERENCE: 305T-300410US

CURRENT APPLICATION NUMBER: US/10/683,451

CURRENT FILING DATE: 2003-10-10

PRIOR APPLICATION NUMBER: US 60/418,001

PRIOR FILING DATE: 2002-10-11

NUMBER OF SEQ ID NOS: 38

SOFTWARE: PatentIn version 3.2

SEQ ID NO 38

LENGTH: 15

TYPE: PRT

ORGANISM: Rattus rattus

US-10-683-451-38

Query Match 100.0%; Score 23; DB 17; Length 15;

Best Local Similarity 80.0%; Pred. No. 3.6e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RXRSH 5
|:|
Db 6 RSRSH 10

RESULT 13

US-10-775-337-61

Sequence 61, Application US/10775337

Publication No. US20050008651A1

GENERAL INFORMATION:

APPLICANT: JESTIN, Andre

APPLICANT: ALBINA, Emanuel
APPLICANT: Le CANN, Pierre
APPLICANT: BLANCHARD, Philippe
APPLICANT: HUTET, Evelyne
APPLICANT: ARNAULD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: CARIOLET, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISEASE (PWD)
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/10/775,337
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: US/09/514,245
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patent in version 3.0
SEQ ID NO 61
LENGTH: 15
TYPE: PRT
ORGANISM: Type B PWD circovirus
US-10-775-337-61

Query Match 100.0%; Score 23; DB 17; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRSH 5
|:|
|:|
|:|
DB 2 RRRSH 6

RESULT 14
US-10-775-337-84
Sequence 84, Application US/10775337
Publication No. US20050008651A1
GENERAL INFORMATION:
APPLICANT: JESTIN, Andre
APPLICANT: ALBINA, Emanuel
APPLICANT: Le CANN, Pierre
APPLICANT: BLANCHARD, Philippe
APPLICANT: HUTET, Evelyne
APPLICANT: ARNAULD, Claire
APPLICANT: TRUONG, Catherine
APPLICANT: MAHE, Dominique
APPLICANT: CARIOLET, Roland
APPLICANT: MADEC, Francois
TITLE OF INVENTION: CIRCOVIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS
TITLE OF INVENTION: DISEASE (PWD)
FILE REFERENCE: 065691/0176
CURRENT APPLICATION NUMBER: US/10/775,337
CURRENT FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: US/09/514,245
PRIOR FILING DATE: 2000-02-28
PRIOR APPLICATION NUMBER: FR 97/15396
PRIOR FILING DATE: 1997-12-05
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patent in version 3.0
SEQ ID NO 84
LENGTH: 15
TYPE: PRT
ORGANISM: Type A PWD circovirus
US-10-775-337-84

Query Match 100.0%; Score 23; DB 17; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRSH 5
|:|
|:|
|:|

Db 2 RRRSH 6

RESULT 15
US-10-267-251-25
Sequence 25, Application US/10267251
Publication No. US20030134329A1
GENERAL INFORMATION:
APPLICANT: No. US20030134329Alman, Thea
TITLE OF INVENTION: CROSS-SPECIES BIOACTIVE PEPTIDES
FILE REFERENCE: 14184-011001
CURRENT APPLICATION NUMBER: US/10/267,251
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US 60/328,340
PRIOR FILING DATE: 2001-10-09
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 25
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated peptide
US-10-267-251-25

Query Match 100.0%; Score 23; DB 14; Length 16;
Best Local Similarity 80.0%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRSH 5
|:|
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|:|
DB 4 RRRSH 8

Search completed: March 8, 2005, 07:05:46
Job time : 2.65337 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 0.549782 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-13

Perfect score: 23

Sequence: 1 RXRSH 5

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2_6/ptodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	11	1	US-08-006-845-1
2	23	100.0	14	1	US-08-006-845-28
3	23	100.0	15	4	US-09-514-245-61
4	23	100.0	15	4	US-09-514-245-84
5	23	100.0	20	1	US-08-416-336-4
6	23	100.0	21	3	US-09-109-957-9
7	23	100.0	29	5	PCT-US94-05150-37
8	23	100.0	32	4	US-09-270-767-61126
9	23	100.0	33	4	US-09-270-767-40082
10	23	100.0	33	4	US-09-270-767-55298
11	23	100.0	36	3	US-08-789-333F-22
12	23	100.0	36	3	US-09-169-015-32
13	23	100.0	36	3	US-09-133-944-21
14	23	100.0	36	3	US-09-208-827-23
15	23	100.0	36	4	US-08-787-738B-22
16	23	100.0	36	4	US-09-157-748-24
17	23	100.0	36	4	US-09-800-170-75
18	23	100.0	36	4	US-09-626-581D-35
19	23	100.0	36	4	US-09-415-765B-35
20	23	100.0	36	4	US-09-626-580C-35
21	23	100.0	36	4	US-09-749-959-31
22	23	100.0	36	4	US-10-043-074-23
23	23	100.0	36	4	US-09-285-912A-84
24	23	100.0	36	4	US-09-578-030-26
25	23	100.0	36	4	US-09-916-940-22
26	23	100.0	36	4	US-09-419-381-69
27	23	100.0	36	4	US-10-142-662-36

28	23	100.0	36	4	US-10-096-550-22	Sequence 22, Appl
29	23	100.0	39	4	US-09-443-780C-31	Sequence 31, Appl
30	23	100.0	39	4	US-09-079-723-15	Sequence 15, Appl
31	23	100.0	46	4	US-09-732-210-938	Sequence 938, App
32	23	100.0	46	4	US-09-711-164-423	Sequence 423, App
33	23	100.0	47	4	US-09-732-210-936	Sequence 936, App
34	23	100.0	50	4	US-09-270-767-36886	Sequence 36886, A
35	23	100.0	50	4	US-09-270-767-52103	Sequence 52103, A
36	23	100.0	50	4	US-09-270-767-57158	Sequence 57158, A
37	23	100.0	51	4	US-09-732-210-1015	Sequence 1015, Ap
38	23	100.0	62	4	US-09-513-999C-5909	Sequence 5909, Ap
39	23	100.0	63	4	US-09-489-039A-11322	Sequence 11322, A
40	23	100.0	63	4	US-09-489-039A-12618	Sequence 12618, A
41	23	100.0	65	4	US-09-489-039A-11132	Sequence 11132, A
42	23	100.0	65	4	US-09-248-796A-24384	Sequence 24384, A
43	23	100.0	65	4	US-09-640-211A-604	Sequence 604, App
44	23	100.0	67	4	US-09-489-039A-9965	Sequence 9965, Ap
45	23	100.0	68	4	US-09-621-976-6572	Sequence 6572, Ap

ALIGNMENTS

RESULT 1
US-08-006-845-1
; Sequence 1, Application US/08006845
; Patent No. 5633234
; GENERAL INFORMATION:
; APPLICANT: August, Thomas J.
; APPLICANT: Pardoll, Drew M.
; APPLICANT: Guarneri, Frank G.
; TITLE OF INVENTION: LYSSOMAL TARGETING OF IMMUNOGENS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner, Birch, McKie and Beckett
; STREET: 1001 G Street, N.W., Eleventh Floor
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001-4597
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/006.845
; FILING DATE: 19930122
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Posorske, Laurence H.
; REGISTRATION NUMBER: 34,698
; REFERENCE/DOCKET NUMBER: 1107.041541
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: C-terminal
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; US-08-006-845-1

Query Match 100.0%; Score 23; DB 1; Length 11;
Best Local Similarity 80.0%; Pred. No. 57;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5

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Db      1 RKRSH 5
; TITLE OF INVENTION:  CIRCOWIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE:      065691/0176
; CURRENT APPLICATION NUMBER:  US/09/514,245
; CURRENT FILING DATE:  2000-02-28
; PRIOR APPLICATION NUMBER:    FR 97/15396
; PRIOR FILING DATE:  1997-12-05
; NUMBER OF SEQ ID NOS:  170
; SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 61
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type B PWD circovirus
US-09-514-245-61
Query Match      100.0%; Score 23; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRSH 5
Db      2 RPRSH 6

RESULT 4
US-09-514-245-84
; Sequence 84, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
; TITLE OF INVENTION:  CIRCOWIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE:      065691/0176
; CURRENT APPLICATION NUMBER:  US/09/514,245
; CURRENT FILING DATE:  2000-02-28
; PRIOR APPLICATION NUMBER:    FR 97/15396
; PRIOR FILING DATE:  1997-12-05
; NUMBER OF SEQ ID NOS:  170
; SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-84
Query Match      100.0%; Score 23; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRSH 5
Db      2 RPRSH 6

RESULT 5
US-08-416-336-4
; Sequence 4, Application US/08416336
; Patent No. 5807714
; GENERAL INFORMATION:
; APPLICANT: Ishizaka, Kimishige
; APPLICANT: Ishii, Yasuyuki
; TITLE OF INVENTION:  METHOD OF PRODUCTION OF ANTIGEN-SPECIFIC
; TITLE OF INVENTION:  GLYCOSYLATION INHIBITING FACTOR
; NUMBER OF SEQUENCES:  8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Fish & Richardson P.C.

Db      1 RKRSH 5
; TITLE OF INVENTION:  CIRCOWIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE:      065691/0176
; CURRENT APPLICATION NUMBER:  US/09/514,245
; CURRENT FILING DATE:  2000-02-28
; PRIOR APPLICATION NUMBER:    FR 97/15396
; PRIOR FILING DATE:  1997-12-05
; NUMBER OF SEQ ID NOS:  170
; SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-84
Query Match      100.0%; Score 23; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRSH 5
Db      4 RKRSH 8

RESULT 3
US-09-514-245-61
; Sequence 61, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois

Db      1 RKRSH 5
; TITLE OF INVENTION:  CIRCOWIRUS SEQUENCES ASSOCIATED WITH PIGLET WEIGHT LOSS DISEASE
; FILE REFERENCE:      065691/0176
; CURRENT APPLICATION NUMBER:  US/09/514,245
; CURRENT FILING DATE:  2000-02-28
; PRIOR APPLICATION NUMBER:    FR 97/15396
; PRIOR FILING DATE:  1997-12-05
; NUMBER OF SEQ ID NOS:  170
; SOFTWARE:  PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Type A PWD circovirus
US-09-514-245-84
Query Match      100.0%; Score 23; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RKRSH 5
Db      4 RKRSH 8

RESULT 3
US-09-514-245-61
; Sequence 61, Application US/09514245
; Patent No. 6703023
; GENERAL INFORMATION:
; APPLICANT: JESTIN, Andre
; APPLICANT: ALBINA, Emanuel
; APPLICANT: Le CANN, Pierre
; APPLICANT: BLANCHARD, Philippe
; APPLICANT: HUTET, Evelyne
; APPLICANT: ARNAULD, Claire
; APPLICANT: TRUONG, Catherine
; APPLICANT: MAHE, Dominique
; APPLICANT: CARIOLET, Roland
; APPLICANT: MADEC, Francois
```

STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,336
FILING DATE: 04-APR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa H.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07246/010001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-416-336-4

Query Match 100.0%; Score 23; DB 1; Length 20;
Best Local Similarity 80.0%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 4; Conservative 1;

QY 1 RXRSH 5
|:|
DB 11 RSRSH 15

RESULT 6
US-09-109-957-9
Sequence 9, Application US/09109957
Patent No. 6136533
GENERAL INFORMATION:
APPLICANT: Bekkaoui, Faouzi
APPLICANT: Modrusan, Zora D.
APPLICANT: Pische, Isabelle A.
APPLICANT: Duck, Peter D.
APPLICANT: Cloney, Lynn P.
APPLICANT: Wong, Alfred C.K.
TITLE OF INVENTION: ADDITIVES FOR USE IN CYCLING PROBE REACTIONS
FILE REFERENCE: 480094.419
CURRENT APPLICATION NUMBER: US/09/109,957
CURRENT FILING DATE: 1998-07-02
NUMBER OF SEQ ID NOS: 11
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 21
TYPE: PRT
ORGANISM: Escherichia coli
US-09-109-957-9

Query Match 100.0%; Score 23; DB 3; Length 21;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
DB 12 RNRSH 16

RESULT 7
PCT-US94-05150-37
Sequence 37, Application PC/TUS9405150

GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Purified Mammalian Flt3 Ligands and Agonists and Antagonists
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05150
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/162,413
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,111
FILING DATE: 19-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/112,391
FILING DATE: 24-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/106,340
FILING DATE: 13-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/092,549
FILING DATE: 16-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,263
FILING DATE: 07-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/065,231
FILING DATE: 19-MAY-1993
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US94-05150-37

Query Match 100.0%; Score 23; DB 5; Length 29;
Best Local Similarity 80.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
DB 12 RCRSH 16

RESULT 8
US-09-270-767-61126
Sequence 61126, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7328-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 61126
LENGTH: 32
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-61126

Query Match 100.0%; Score 23; DB 4; Length 32;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 RXRSH 5
    |:|||
Db 2 RXRSH 6

RESULT 9
US-09-270-767-40082
; Sequence 40082, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 40082
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-40082

Query Match 100.0%; Score 23; DB 4; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
    |:|||
Db 14 RFRSH 18

RESULT 10
US-09-270-767-55298
; Sequence 55298, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55298
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
US-09-270-767-55298

Query Match 100.0%; Score 23; DB 4; Length 33;
Best Local Similarity 80.0%; Pred. No. 1.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
    |:|||
Db 14 RFRSH 18

RESULT 11
US-08-789-333F-22
; Sequence 22, Application US/08789333F
; Patent No. 6153380
; GENERAL INFORMATION:
; APPLICANT: No. 6153380an, Garry P
; APPLICANT: Rothenberg, S. M.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT INTRACELLULAR
; FILE REFERENCE: A642601DIBRMSDSS
; CURRENT APPLICATION NUMBER: US/08/789,333F
; CURRENT FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: lysosomal
; OTHER INFORMATION: membrane sequence.
US-08-789-333F-22

Query Match 100.0%; Score 23; DB 3; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
    |:|||
Db 26 RXRSH 30

RESULT 12
US-09-169-015-32
; Sequence 32, Application US/09169015
; Patent No. 6180343
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; TITLE OF INVENTION: Green Fluorescent Protein Fusions with Random Peptides
; FILE REFERENCE: A66900/DJB/RMS/SJR
; CURRENT APPLICATION NUMBER: US/09/169,015
; CURRENT FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; PUBLICATION INFORMATION:
; JOURNAL: Cell. Mol. Biol. Res.
; ISSUE: 41
; PAGES: 405-
; DATE: 1995
US-09-169-015-32

Query Match 100.0%; Score 23; DB 3; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
    |:|||
Db 26 RXRSH 30

RESULT 13
US-09-133-944-21
; Sequence 21, Application US/09133944
; Patent No. 6280937
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Pei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHUTTLE VECTORS
; FILE REFERENCE: A66252/DJB/DAV
; CURRENT APPLICATION NUMBER: US/09/133,944
; CURRENT FILING DATE: 1999-08-14
; EARLIER APPLICATION NUMBER: 09/133,949
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 39
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; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: lysosomal
; OTHER INFORMATION: membrane sequence
; PUBLICATION INFORMATION:
; JOURNAL: Cell. Mol. Biol. Res.
; VOLUME: 41
; PAGES: 405-405
; DATE: 1995
US-09-133-944-21

Query Match 100.0%; Score 23; DB 3; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
Db 26 RKRSH 30

RESULT 14
US-09-208-827-23
; Sequence 23, Application US/09208827
; Patent No. 6391582
; GENERAL INFORMATION:
; APPLICANT: Luo, Ying
; APPLICANT: Yu, Fei Wen
; APPLICANT: Lorens, James
; TITLE OF INVENTION: SHUTTLE VECTORS
; FILE REFERENCE: A66252-1/DJB/DAV
; CURRENT APPLICATION NUMBER: US/09/208,827
; CURRENT FILING DATE: 1998-12-09
; EARLIER APPLICATION NUMBER: 09/133,949
; EARLIER FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: lysosomal
; OTHER INFORMATION: membrane sequence
; PUBLICATION INFORMATION:
; JOURNAL: Cell. Mol. Biol. Res.
; VOLUME: 41
; PAGES: 405-405
; DATE: 1995
US-09-208-827-23

Query Match 100.0%; Score 23; DB 3; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
Db 26 RKRSH 30

RESULT 15
US-08-787-738B-22
; Sequence 22, Application US/08787738B
; Patent No. 6455247
; GENERAL INFORMATION:
; APPLICANT: No. 6455247an, Garry P
; APPLICANT: Rothenburg, Michael S.
; TITLE OF INVENTION: METHODS FOR SCREENING FOR TRANSDOMINANT EFFECTOR
; TITLE OF INVENTION: PEPTIDES AND RNA MOLECULES
; FILE REFERENCE: A-64259-1 correction

; CURRENT APPLICATION NUMBER: US/08/787,738B
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 08/589,108
; PRIOR FILING DATE: 1996-01-23
; PRIOR APPLICATION NUMBER: 08/589,911
; PRIOR FILING DATE: 1996-01-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 22
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Cricetulus griseus
US-08-787-738B-22

Query Match 100.0%; Score 23; DB 4; Length 36;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 RXRSH 5
|:|
Db 26 RKRSH 30

Search completed: March 8, 2005, 05:53:49
Job time : 1.54978 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.5692 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083
Sequence: 1 GLLKPSETLSLTCVAVGSGP.....LPKSDVMQGTDEHVVVTSKGE 205

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	87.5	231	B23746	Ig Fab region IV-J
2	749.5	69.2	627	S14683	Ig mu chain precu
3	599.5	55.4	143	B49028	Ig heavy chain v-I
4	553.5	51.1	592	B25705	Ig mu chain - shee
5	524	48.4	146	GIH0H2	Ig heavy chain pre
6	521	48.1	140	S78052	Ig gamma-1 heavy c
7	518.5	47.9	220	A49444	Ig heavy chain v r
8	513	47.4	126	S47010	Ig heavy chain v r
9	512.5	47.3	140	A49045	Ig mu chain - huma
10	495.5	45.8	116	B37456	Ig heavy chain VDJ
11	494.5	45.7	288	S29690	Ig heavy chain - h
12	488.5	45.1	155	S31512	Ig heavy chain - h
13	488.5	45.1	155	S31511	Ig heavy chain v r
14	480	44.3	122	JL0047	Ig heavy chain v r
15	478	44.1	137	S31676	Ig heavy chain v r
16	477.5	44.1	114	I72667	cold agglutinin FS
17	475.5	43.9	130	S31690	Ig heavy chain v r
18	475.5	43.9	140	I37782	Ig variable region
19	469	43.3	97	S26898	Ig heavy chain v r
20	463	42.8	97	S26805	Ig heavy chain v r
21	460	42.5	97	S14474	Ig heavy chain v r
22	459	42.4	97	G34964	Ig heavy chain v-I
23	456.5	42.2	146	S09711	Ig heavy chain v r
24	456	42.1	97	S26806	Ig heavy chain v r
25	455	42.0	139	S31586	Ig heavy chain v r
26	453	41.8	130	S30534	Ig heavy chain v r
27	452.5	41.8	135	S78051	Ig heavy chain pre
28	452	41.7	145	S78055	Ig heavy chain pre
29	450	41.6	106	S37454	Ig mu chain - huma

30	450	41.6	452	1	MHHU	Ig mu chain C regi
31	450	41.6	453	2	S37768	Ig mu chain C regi
32	450	41.6	473	1	MHHUM	Ig mu chain C regi
33	450	41.6	474	2	S15590	Ig heavy chain - h
34	446	41.2	470	2	S22080	Ig heavy chain pre
35	444	41.0	568	2	A34891	Ig heavy chain pre
36	443.5	41.0	146	2	S09710	Ig heavy chain v r
37	442	40.8	231	2	PC4155	Ig gamma-2b chain
38	440.5	40.7	147	2	S13519	Ig heavy chain v r
39	440	40.6	129	2	S44114	Ig heavy chain v r
40	435.5	40.2	127	2	S19668	Ig heavy chain v r
41	434	40.1	97	2	JH0428	Ig gamma chain v r
42	433.5	40.0	123	2	S30529	Ig heavy chain v r
43	433	40.0	118	2	S24443	Ig heavy chain v r
44	431.5	39.8	123	2	S30530	Ig heavy chain v r
45	431.5	39.8	134	2	S54906	Ig heavy chain v r

ALIGNMENTS

RESULT 1

B23746

Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000

C:Accession: B23746

R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.

J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin

A:Reference number: A23746; MUID:91131575; PMID:1993660

A:Accession: B23746

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-231 <LEO>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F140-209/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 948; DB 2; Length 231;

Best Local Similarity 87.9%; Pred. No. 1.8e-67;

Matches 188; Conservative 7; Mismatches 7; Indels 14; Gaps 3;

QY	1	GLLKPSETLSLTCVAVGSGFSGYWSWIRQPPGKGLWIGEINHSGSTYNPFLSKSRVTI	60
DB	9	GLLKPSETLSLTGAVYGGSDYWSWIRQPPGKGLWIGEINHSGSTYNPFLSKSRVTI	68
QY	61	SVDTSKNQFSLKSSVTADTAATVYCAR---GTTEVYYYGYMDVWGQGTTVTVSGGSAS	117
DB	69	SVDTSKNQFSLKSSVTADTAATVYCARPPHDTSGHYWNY-----WGQGTTLVTVSGGSAS	123
QY	118	APTLPPLVSCENSPSDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSSTRGPPSVLRGKG	177
DB	124	APTLPPLVSCENSPSDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSSTRGPPSVLRGKG	183
QY	178	YAATSQVLLPKSDVMQGTDEHVV-----TGSKE 205	
DB	184	YAATSQVLLPKSDVMQGTDEHVVCKVQHPNGNKE 217	

RESULT 2

S14683

Ig mu chain precursor, membrane-bound (clone 201) - human

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999

C:Accession: S14683; S08047

R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990

A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.

A:Reference number: S14683; MUID:90332450; PMID:2115996

A:Accession: S14683

A:Molecule type: mRNA

A:Residues: 1-627 <FRI>

A:Cross-References: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451

Db 90 SLDTSKNLFSLKLSVTAADTAIVYVCARGLLRGWHDVDYYGMDVWGQGTIVTVSS 146

RESULT 6

S78052
Ig heavy chain precursor V-D-J region (clone mAb 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S23717
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAR>
A:CROSS-references: EMBL:X54441; NID:g937815; PIDN:CRA38308.1; PID:g930118
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and H
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23717
A:Molecule type: mRNA
A:Residues: 15-111 <HAW>
A:CROSS-references: EMBL:X54441
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:29-111/Domain: immunoglobulin homology <IMM>

Query Match 48.1%; Score 521; DB 2; Length 140;
Best Local Similarity 86.3%; Pred. No. 3.9e-34;
Matches 101; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

QY 1 GLLKPESETLSLTCVAVGSGFSGYVSWIRQPPGKGLEWIGEINHSNSTYNPSLKSRTVI 60

DB 24 GLLKPESETLSLTCVAVGSGFSGYVSWIRQPPGKGLEWIGEINHSNSTYNPSLKSRTVI 83

QY 61 SVDTSKNPFSLKLSVTAADTAIVYVCARGTTTETVY----YVYVYVMDVWGQGTIVTVSS 113

DB 84 SVDTSKNPFSLKLSVTAADTAIVYVCARGSVLRFLWLLYPAPDYWGQGTIVTVSS 140

RESULT 7

A49444
Ig Gamma-1 heavy chain (New) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999
C:Accession: A49444
R:Saul, F.A.; Poljak, R.J.
Proteins 14, 363-371, 1992
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res
A:Reference number: A49444; MUID:93066153; PMID:1438175
A:Accession: A49444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-220 <SAU>
A:Note: this sequence modified after extraction from NCBI backbone
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 47.9%; Score 518.5; DB 2; Length 220;
Best Local Similarity 51.5%; Pred. No. 1e-33;
Matches 103; Conservative 36; Mismatches 50; Indels 11; Gaps 5;

QY 1 GLLKPESETLSLTCVAVGSGFSGYVSWIRQPPGKGLEWIGEINHSNSTYNPSLKSRTVI 60

DB 10 GLVRSQTLSTLTCTVSGTSDYVYVWVQPPGKGLEWIGYVYGTITLLDPSLRGVTM 69

QY 61 SVDTSKNPFSLKLSVTAADTAIVYVCARGTTTETVYVYVYVMDVWGQGTIVTVSSGSASAPT 120

Db 70 LVNTSKNPFSLKLSVTAADTAIVYVCARNLIA-----GGIDVWGQSLTVSSASTKGFS 124

QY 121 LFPVLVSCENSPSDTSSVAVGCLAQDFLPDXITFFSKYKKNISDISSTRGPPSVLR-GGKYA 179

DB 125 VFPLAPSSKSTSG-CTAALGCLVKDYFPEPTVSM--NSGALTSGVHTTTPAVLQSSGLYS 181

QY 180 ATSQVLLPSKDVWQGTDBHV 199

DB 182 LSSVTVTPSSSL--GTQTYI 199

RESULT 8

S47010
Ig heavy chain V4.21-UniqueJ5 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S47010
R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bind
A:Reference number: S47009
A:Accession: S47010
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <MAH>
A:CROSS-references: EMBL:Z35492; NID:g517254; PIDN:CAA84625.1; PID:g517255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 47.4%; Score 513; DB 2; Length 126;
Best Local Similarity 82.1%; Pred. No. 1.5e-33;
Matches 101; Conservative 2; Mismatches 4; Indels 16; Gaps 2;

QY 1 GLLKPESETLSLTCVAVGSGFSGYVSWIRQPPGKGLEWIGEINHSNSTYNPSLKSRTVI 60

DB 10 GLLKPESETLSLTCVAVGSGFSGYVSWIRQPPGKGLEWIGEINHSNSTYNPSLKSRTVI 69

QY 61 SVDTSKNPFSLKLSVTAADTAIVYVCARG-----TTEVYVYVYVMDVWGQGTIVTV 110

DB 70 SVDTSKNPFSLKLSVTAADTAIVYVCARGGQCPKXSCVTKWPF-----DPWGQGTIVTV 123

QY 111 VSS 113

DB 124 VSS 126

RESULT 9

A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rasseenti, L.Z.; Labaune, S.; Silvermar
Eur. J. Immunol. 22, 1781-1788, 1992
A:Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i blc
A:Reference number: A49045; MUID:92324290; PMID:1623923

Query Match 47.3%; Score 512.5; DB 2; Length 140;
Best Local Similarity 85.6%; Pred. No. 1.8e-33;
Matches 101; Conservative 1; Mismatches 5; Indels 11; Gaps 2;

QY 1 GLLKPESETLSLTCVAVGSGFSGYVSWIRQPPGKGLEWIGEINHSNSTYNPSLKSRTVI 60

Db 29 GLLKPSSETISLTCAVYGGSPGYIWSIRQPPCKGLEWIGEINHGSGTNPINSLKSRVTI 88

Qy 61 SVDTSKNQPSLKLSSVTAADTAIVYCARG-----TTEYYYYYYYGMDVWGCGTTVTVSS 113

Db 89 SVDTSKNQPSLKLSSVTAADTAIVYCARGFAATIVESF-----DYWGGLPLTVTSS 140

RESULT 10
S37456
Ig mu chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C/Accession: S37456
R/McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A/Description: Cloning and analysis of human IGM anti-Thyroglobulin autoantibodies from
A/Reference number: S37453
A/Accession: S37456
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-116 <MCri>
A/Cross-references: EMBL:X75024; NID:G404313; PIDN:CAA52932.1; PID:G758095
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: immunoglobulin
F:6-90/Domain: immunoglobulin homology <IMM>

```

RESULT 11
S29690
I9 heavy chain VDJ region - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C/Accession: S29690
R/Damers, P.M.; Bos, N.A.; Kroese, F.G.M.
Submitted to the EMBL Data Library, October 1992
A/Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.
A/Reference number: S29690
A/Accession: S29690
A/Molecule type: mRNA
A/Residues: 1-288 <DAM>
A/Cross-references: EMBL:X68782; NID:G56442; PID:G1334294
A/Experimental source: strain D2B
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
P:12-95/Domain: immunoglobulin homology <IMM>

```

```

Db      123  VLPVSCSPUSDENLVAMGLARDFLPSSISFSWNVQNNTTEVMQGVTFPTFLRTGDKYT 182
Qy      180  ATSQVLLPSPKDVMOQGTDEHVV 200
        ||||| :|:|:|:|:|:|
Db      183  ATSQVLLSAKNVLEGSDEYLV 203

RESULT 12
S31512
Ig heavy chain - human
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S31512
R/Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A/Description: Dominance of clonotypic patterns and variable gene usage of ant
A/Reference number: S31509
A/Accession: S31512
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-155 <CHA>
A/Cross-references: EMBL:X69860; NID:G33082; PIDN:CAA49494.1; PID:G33083
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IMW>

```

RESULT 13

S31511
Ig heavy chain - human

C:Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S31511

R:Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992

A:Description: Dominance of clonotypic patterns and variable gene usage of ant
A:Reference number: S31509

A:Accession: S31511

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 <CHA>

A:Cross-references: EMBL:X69866; NID:G33094; PIDN:CAA49500.1; PID:G33095

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:47-129/Domain: immunoglobulin homology <IMM>

RESULT 14
JL0047

Ig heavy chain V region precursor (clone cr18) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C:Accession: J10047
R:Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.
J. Exp. Med. 167, 2011-2016, 1988
A:Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new S
A:Reference number: J10047; MUID:88258392; PMID:3133445
A:Accession: J10047
A:Molecule type: mRNA
A:Residues: 1-122 <BAE>
A:Experimental source: T-cell line RPMI 8402
A:Note: the authors translated the reading frame which extends to the stop codon; the se
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:23-105/Domain: immunoglobulin homology <IMM>

Query Match 44.3%; Score 480; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 5.6e-31;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLLKPESETLSLCAVYGGSFSGYVSWIRQPPGKGLWIGSGSTNNPFLKSRVTI 60
DB 18 GLLKPESETLSLCAVYGGSFSGYVSWIRQPPGKGLWIGSGSTNNPFLKSRVTI 77

QY 61 SVDTSKNQFSLKLSVTAADTAVYICARGT 90
DB 78 SVDTSKNQFSLKLSVTAADTAVYICARGT 107

RESULT 15
S31676
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31676
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31676
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-137 <CUI>
A:Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 44.1%; Score 478; DB 2; Length 137;
Best Local Similarity 83.2%; Pred. No. 9.1e-31;
Matches 94; Conservative 2; Mismatches 13; Indels 4; Gaps 1;

QY 1 GLLKPESETLSLCAVYGGSFSGYVSWIRQPPGKGLWIGSGSTNNPFLKSRVTI 60
DB 29 GLVKPESETLSLCTVSGGSISSYVSWIRQPPGKGLWIGRIYTSNSTNNPFLKSRVTM 88

QY 61 SVDTSKNQFSLKLSVTAADTAVYICARGTTEYYYYYGMVWGQGTVTVSS 113
DB 89 SVDTSKNQFSLKLSVTAADTAVYICARDAP----LMYGMVWGQGTVTVSS 137

Search completed: March 8, 2005, 06:39:20
Job time : 15.6192 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 76.5572 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083

Sequence: 1 GLLKPSETLSITCAVYGSF.....LPKDNVQGTDEHVVTGSGE 205

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	965.5	89.2	595	2	Q8WUX4	Q8WUX4 homo sapien
2	965.5	89.2	597	2	Q6GMX5	Q6GMX5 homo sapien
3	965.5	89.2	597	2	Q9BU10	Q9BU10 homo sapien
4	965.5	89.2	625	2	Q96AA6	Q96AA6 homo sapien
5	959.5	88.6	597	2	Q9BQ88	Q9BQ88 homo sapien
6	890	82.2	620	2	Q96EY0	Q96EY0 homo sapien
7	818	75.5	606	2	Q6GMX2	Q6GMX2 homo sapien
8	734	67.8	613	2	Q8WUK1	Q8WUK1 homo sapien
9	732.5	67.6	597	2	Q6GBB9	Q6GBB9 homo sapien
10	595	54.9	465	2	Q6GMX6	Q6GMX6 homo sapien
11	584.5	54.0	576	2	Q6P4I8	Q6P4I8 homo sapien
12	554.5	51.2	613	2	Q8VCX7	Q8VCX7 mus musculus
13	553.5	51.1	476	2	Q6GMX1	Q6GMX1 homo sapien
14	543.5	50.2	477	2	Q6GMX7	Q6GMX7 homo sapien
15	524	48.4	146	1	HV21 HUMAN	P06331 homo sapien
16	512	47.3	614	2	Q7TMT6	Q7TMT6 mus musculus
17	499	46.1	116	2	Q7Z3Y6	Q7Z3Y6 homo sapien
18	498.5	46.0	478	2	Q7Z379	Q7Z379 homo sapien
19	498	46.0	473	2	Q8TC63	Q8TC63 homo sapien
20	498	46.0	492	2	Q7Z374	Q7Z374 homo sapien
21	497	45.9	478	2	Q6NYH3	Q6NYH3 homo sapien
22	496.5	45.8	496	2	Q96KX8	Q96KX8 homo sapien
23	479.5	44.3	476	2	Q6MZX7	Q6MZX7 homo sapien
24	473.5	43.7	479	2	Q99M22	Q99M22 mus musculus
25	466	43.0	150	2	Q95973	Q95973 homo sapien
26	451.5	41.7	472	2	Q6N089	Q6N089 homo sapien
27	450	41.6	454	1	MUC HUMAN	P01871 homo sapien
28	446.5	41.2	478	2	Q6P181	Q6P181 homo sapien
29	444.5	41.0	119	2	Q9UL73	Q9UL73 homo sapien
30	439.5	40.6	573	2	Q8WU38	Q8WU38 homo sapien
31	431	39.8	482	2	Q91X92	Q91X92 mus musculus

Query Match

89.2% ; Score 965.5; DB 2; Length 595;

32	427.5	39.5	605	2	Q6GN83	Q6GN83 xenopus lae
33	424	39.2	139	2	Q86SX2	Q86SX2 homo sapien
34	423.5	39.1	470	2	Q6PJA4	Q6PJA4 homo sapien
35	418.5	38.6	129	1	HV2F HUMAN	P01824 homo sapien
36	417	38.5	593	2	Q6INM5	Q6INM5 xenopus lae
37	416.5	38.5	464	2	Q6MZU6	Q6MZU6 homo sapien
38	416	38.4	225	2	Q6PAF5	Q6PAF5 xenopus lae
39	415.5	38.4	482	2	Q7Z351	Q7Z351 homo sapien
40	413	38.1	465	2	Q6P6C4	Q6P6C4 homo sapien
41	413	38.1	470	2	Q7TMM1	Q7TMM1 mus musculus
42	405.5	37.4	466	2	Q6IN78	Q6IN78 homo sapien
43	403.5	37.3	480	2	Q91XE1	Q91XE1 mus musculus
44	403	37.2	499	2	Q8N5K4	Q8N5K4 homo sapien
45	402	37.1	475	2	Q6MZQ6	Q6MZQ6 homo sapien

ALIGNMENTS

RESULT 1

Q8WUX4	Q8WUX4	PRELIMINARY;	PRT;	595 AA.
AC	Q8WUX4;			
DT	01-MAR-2002 (Tremblrel. 20, Created)			
DT	01-MAR-2004 (Tremblrel. 26, Last sequence update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Lymph;			
EX	MEDLINE=23386257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RA	TISSUE=Lymph;			
RA	Strausberg R.;			
RL	Submitted (DSC-2001) to the ENBL/GenBank/DBJ databases.			
DR	EMBL; BC019235; AAH19235.2; -			
DR	PIR; G34964; G34964.			
DR	HSSP; P01861; 1ADQ.			
DR	Pfam; PF07654; C1-set; 4.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGc1; 4.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00835; IG LIKE; 5.			
DR	PROSITE; PS00290; IG MHC; UNKNOWN_3.			
KW	Hypothetical protein.			
SQ	SEQUENCE 595 AA; 65290 MW; 0D4B5076545714E CRC64;			

Best Local Similarity 87.6%; Pred. No. 1.3e-77;
Matches 191; Conservative 2; Mismatches 8; Indels 17; Gaps 3;

QY 1 GLLKPSSETLSITCAVYGGSGFYGYSWIRQPPGKLEWIGEINHSNSTYNNPSLSKSRVTI 60
Db 36 GLLKPSSETLSITCAVYGGSGFYGYSWIRQPPGKLEWIGEINHSNSTYNNPSLSKSRVTI 95
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGMVWGQGTIVTVSS 113
Db 96 SVDTSKKQLSLKLSVNAADTAIVYCARVITRASPGETG-----RYGMDVWGQGTIVTVSS 151
QY 114 GSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDXITTFWSKYKNNSDISSTRGFPSVL 173
Db 152 GSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITTFWSKYKNNSDISSTRGFPSVL 211
QY 174 RGGKYAATSOVLPSKDVMOGTDEHV-----TGSKE 205
Db 212 RGGKYAATSOVLPSKDVMOGTDEHVCKVQHPNGNKE 249

RESULT 2
Q6GMX5 PRELIMINARY; PRT; 597 AA.

ID Q6GMX5 AC Q6GMX5
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.ci.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF07654; CI-set; 4.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 89.2%; Score 965.5; DB 2; Length 597;
Best Local Similarity 87.6%; Pred. No. 1.3e-77;
Matches 191; Conservative 2; Mismatches 8; Indels 17; Gaps 3;

QY 1 GLLKPSSETLSITCAVYGGSGFYGYSWIRQPPGKLEWIGEINHSNSTYNNPSLSKSRVTI 60
Db 29 GLLKPSSETLSITCAVYGGSGFYGYSWIRQPPGKLEWIGEINHSNSTYNNPSLSKSRVTI 88
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGMVWGQGTIVTVSS 113
Db 89 SVDTSKKQLSLKLSVNAADTAIVYCARVITRASPGETG-----RYGMDVWGQGTIVTVSS 144
QY 114 GSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDXITTFWSKYKNNSDISSTRGFPSVL 173
Db 145 GSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITTFWSKYKNNSDISSTRGFPSVL 204
QY 174 RGGKYAATSOVLPSKDVMOGTDEHV-----TGSKE 205
Db 205 RGGKYAATSOVLPSKDVMOGTDEHVCKVQHPNGNKE 242

RESULT 3
Q9BU10 PRELIMINARY; PRT; 597 AA.

ID Q9BU10 AC Q9BU10
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.ci.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF07654; CI-set; 4.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA9FB7E055851 CRC64;

Query Match      89.2%; Score 965.5; DB 2; Length 597;
Best Local Similarity 87.6%; Pred. No. 1.3e-77;
Matches 191; Conservative 2; Mismatches 8; Indels 17; Gaps 3;

QY 1 GLLKPESETLSLTCAVYGGFSGYGWSWIRQPPGKLEWIGEHSGSTNYPNPSLSKRVTI 60
DB 29 GLLKPESETLSLTCAVYGGFSGYGWSWIRQPPGKLEWIGEHSGSTNYPNPSLSKRVTI 88
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGMVWGQTTVTVSS 113
DB 89 SVDTSKNQFSLKLSVTAADTAIVYCARITRASPGTDG---RYGMDVWGQTTVTVSS 144
QY 114 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDPLDPXITFMSWKYKNNSDISSTRGPPSVL 173
DB 145 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDPLDPXITFMSWKYKNNSDISSTRGPPSVL 204
QY 174 RGGKYAATSQVLLPSKDVWGQTDHVV-----TGSKE 205
DB 205 RGGKYAATSQVLLPSKDVWGQTDHVVCKVQHPNGNKE 242

RESULT 4
ID Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahay J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; RAH17356.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01861; IADO.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
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DR HSSP; P01861; 1ADQ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAPAD50A6375851 CRC64;

Query Match 88.6%; Score 959.5; DB 2; Length 597;
Best Local Similarity 87.2%; Pred. No. 4.6e-77;
Matches 190; Conservative 2; Mismatches 9; Indels 17; Gaps 3;

QY 1 GLLKPSETLSITCAVYGSGPSGYWWSWIRQPPGKLEWIGINHSNSTNYPNLSKSRVTI 60
DB 29 GLLKPSETLSITCGVYGSGPSGYWWSWIRQPPGKLEWIGINHSNSTNYPNLSKSRVTI 88
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCAR-----GTTEYYYYYGMVWGQTTVTVSS 113
DB 89 SVDTSKKQLSKLSVNAADTAIVYCARVITRASPDTG-----RYGMDVWGQTTVTVSS 144
QY 114 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSSL 173
DB 145 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSSL 204
QY 174 RGGKYAATSOVLLPSKDVMOGTDEHV-----TGSK 205
DB 205 RGGKYAATSOVLLPSKDVMOGTDEHVCKVQHPNGNKE 242

RESULT 6
Q96EY0 ID Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.J., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences;"
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 82.2%; Score 890; DB 2; Length 620;
Best Local Similarity 83.9%; Pred. No. 7.7e-71;
Matches 177; Conservative 7; Mismatches 19; Indels 8; Gaps 2;

QY 1 GLLKPSETLSITCAVYGSGPSGYWWSWIRQPPGKLEWIGINHSNSTNYPNLSKSRVTI 60
DB 36 GLVPSSETLSITCTVSGGSISSYWSWIRQPPGKLEWIGIRIYTSGTNYPNLSKSRVTM 95
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCARGTTEYYYYYGMVWGQTTVTVSSGSASAPT 120
DB 96 SVDTSKNQFSLKLSVTAADTAIVYCA--SQPWELPTVGLFWGQGLTVTVSSGSASAPT 153
QY 121 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSSLRGGKYAA 180
DB 154 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSSLRGGKYAA 213
QY 181 TSQVLLPSKDVMOGTDEHV-----TGSK 205
DB 214 TSQVLLPSKDVMOGTDEHVCKVQHPNGNKE 244

RESULT 7
Q6GMV2 ID Q6GMV2 PRELIMINARY; PRT; 606 AA.
AC Q6GMV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
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RA Blakesley R.W., Touchman J.W., Green E.J., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences;"
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAH15760.1; -;
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 67.6%; Score 732.5; DB 2; Length 597;
Best Local Similarity 69.6%; Pred. No. 8.7e-57;
Matches 149; Conservative 18; Mismatches 38; Indels 9; Gaps 3;
QY 1 GLLKPESETLSLTCVAVYGGFSGYVSWIRQPPGKLEWIGINHS-GSTNYPNPSLKSRTV 59
DB 29 GLLVQGGSLRLSCAASGFSFSSYANVRQAPGKLEWISALISGGSTYYADSVKGRPT 88
QY 60 ISVDTSKNQFSLKLSVTAADTAATVAVYCARGTTEYYY--YYTGMDVWGQGTITVTVSSGSAS 117
DB 89 ISRDNSRDTLYLQNNLSRAEDTAATVAVYCAKDRGYSGASGNYTREDVWGQGTITVTVSSGSAS 148
QY 118 APTLPPLVSCENSPSDTSSVAVGCLAQDFLDXITTFWSKYKNNSDISSTRGFPSPVLRGCK 177
DB 149 APTLPPLVSCENSPSDTSSVAVGCLAQDFLDXITTFWSKYKNNSDISSTRGFPSPVLRGCK 208
QY 178 YAATSOVLPLPSKDVWGQGTITVTVSSGSAS 205
DB 209 YAATSOVLPLPSKDVWGQGTITVTVSSGSAS 242

RESULT 10
Q6GMX6 PRELIMINARY; PRT; 465 AA.
ID Q6GMX6
AC Q6GMX6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00407; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;
Query Match 54.9%; Score 595; DB 2; Length 465;
Best Local Similarity 60.5%; Pred. No. 1.2e-44;
Matches 121; Conservative 22; Mismatches 45; Indels 12; Gaps 5;
QY 1 GLLKPESETLSLTCVAVYGGFSGYVSWIRQPPGKLEWIGINHSGSTNYPNPSLKSRTV 60
DB 29 GLLVQGGSLRLSCVAVYGGFSGYVSWIRQPPGKLEWIGIRIYSGTNYNPSLKSRTV 88
QY 61 SVDTSKNQFSLKLSVTAADTAATVAVYCARGTTEYYYGYGMDVWGQGTITVTVSSGSASAPT 120
DB 89 SVDTSKNQFSLKLSVTAADTAATVAVYCARGTTFY-----DYWGQGTITVTVSSASTKGPS 142
QY 121 LFPPLVSCENSPSDTSSVAVGCLAQDFLDXITTFWSKYKNNSDISSTRGFPSPVLR-GGKYA 179
DB 143 VFLAPSSKTSKG-GTAALGCLVDFPEPPTVSW--NSGALTSGVHTFPFVAVLQSSGLYS 199
QY 180 ATSOVLPLPSKDVWGQGTITVTVSS 199
DB 200 LSSVTVTPSSSL--GTQTYI 217
RESULT 11
Q6P4I8 PRELIMINARY; PRT; 576 AA.
ID Q6P4I8
AC Q6P4I8;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE IGHD protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]

149 TKGPSVPLAPSSKSTSG-GTAAAGCLVVKDYFPPEVTVSW--NSGALTSGVHTTPAVLQS 205

RESULT 13

O6GMX1
ID Q6GMX1 PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kryzyski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 51.1%; Score 553.5; DB 2; Length 476;
Best Local Similarity 55.6%; Pred. No. 6.4e-41;
Matches 114; Conservative 30; Mismatches 50; Indels 11; Gaps 6;
QY 1 GLLKPSFSLTCAVYGSFSG--YYWSWIROPKGLWIGEINHSGSTNNPPLSKSRV 58
DB 29 GLVPSQTLSTCTCTVSGGSISSGDYWSWIROPKGLWIGIYIYSGSTNNPPLSKSRV 88
QY 59 TISVDTSKNPSLKLSSVTAADTAVYCYARGTTEYYYYY---GNDVNGQGTVTVTSSGS 115
DB 89 TISLDTSKNPSLKLSSVTAADTAVYFCARAGVWSFRSWAIDGNFNGQGTVTVTSSAS 148
QY 116 ASAPTFLPLVSCENSPSDTSSVAVGCLAQDFLPDXITTFWSKYKNNSDISSTRGFPPLVR- 174
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

Db

175 GKYAATSQVLLPSKDVWQGTDEHV 199

206 SGLISLSSVTVTPSSSL--GTQTYI 228

RESULT 14

O6GMX7
ID Q6GMX7 PRELIMINARY; PRT; 477 AA.
AC Q6GMX7;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kryzyski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;

Query Match 50.2%; Score 543.5; DB 2; Length 477;
Best Local Similarity 56.3%; Pred. No. 5e-40;
Matches 111; Conservative 27; Mismatches 48; Indels 11; Gaps 6;
QY 1 GLLKPSFSLTCAVYGSFSGYWSWIROPKGLWIGEINHSGSTNNPPLSKSRVTI 60
DB 29 GLVPSFSLTCTCTVSGGSISSYWSWIROPKGLWIGIYIYSGSTNNPPLSKSRVTI 88
QY 61 SVDTSKNQPSLKLSSVTAADTAVVYCYARGTTEYYYYYGMVDVWQGTVTVTSSGSASAPT 120
| : : : : | : : : : | : : : : | : : : : | : : : : | : : : : | : : : : |

Db 89 SLDTSKNQFSLRLNSVTADTAATVYCAHGSS-----WDFADYWGQGLTLVTSSASPTSPK 144
QY 121 LFPLVSCNSPDSSTSVAVGCLAQDFLP-DXITFSWKYKNSDISSTRGFP--SVLRGGK 177
Db 145 VFPL-SLDTSPQD-GNVVAVCLVQGFPPQEPPLSVTWSESGQN--VTARNFPSPQDASGDL 200
QY 178 YAATSQVLLPSKDVMMQG 194
Db 201 YTTSSQLTLPATQCPDG 217

RESULT 15
HV2I_HUMAN
ID HV2I_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR PIR; A02101; GIHUH2.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.
FT DOMAIN 20 117 V segment.
FT DOMAIN 118 127 D segment.
FT DOMAIN 128 146 J segment.
FT DISULFID 42 115 By similarity.
FT NON_TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;

Query Match 48.4%; Score 524; DB 1; Length 146;
Best Local Similarity 85.5%; Pred. No. 6.5e-39;
Matches 100; Conservative 5; Mismatches 8; Indels 4; Gaps 1;
QY 1 GLLKPESETLSLTCVAVGSGFSGYYSWIRQPPGKGLEWIGEINHSNSTYNPSLKSRTVI 60
Db 30 GLVKESETLSLTCVAVGSGFSGYYSWIRQPPGKGLEWIGEINHSNSTYNPSLKSRTVI 89
QY 61 SVDTSKNQFSLRLNSVTADTAATVYCAHGTTEYYY-----YYGMDVWGQGLTLVTSS 113
Db 90 SLDTSKNQFSLRLNSVTADTAATVYCAHGLRGGWMDVYYGMDVWGQGLTLVTSS 146

Search completed: March 8, 2005, 06:35:44
Job time : 78.5572 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 95.0436 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083

Sequence: 1 GLLKPSFTLSLTCAVGGSP.....LPKDVMMQGTDEHVVTSKSE 205

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1083	100.0	205	2 AAY34299	Aay34299 Igm antib
2	1030	95.1	202	2 AAY34303	Aay34303 Igm antib
3	930	85.9	190	2 AAY34304	Aay34304 Igm antib
4	900.5	83.1	197	2 AAY34300	Aay34300 Igm antib
5	749.5	69.2	627	7 ADP97370	Adp97370 Human imm
6	747	68.0	595	7 ADM05427	Adm05427 Human pro
7	739.5	68.3	203	2 AAY34301	Aay34301 Igm antib
8	738	68.1	596	4 AAM23324	Aam23324 Human EST
9	735	67.9	223	2 AAY08598	Aay08598 Anti-huma
10	729	67.3	223	8 ADL70773	Adl70773 Anti-TNFA
11	727	67.1	588	2 AAW71880	Aaw71880 Anti-huma
12	727	67.1	588	3 AAB12917	Aab12917 Anti-TNFA
13	726.5	67.1	228	8 ADL70776	Adl70776 Anti-TNFA
14	725.5	67.0	266	8 ADF69305	Adf69305 Human lun
15	718.5	66.3	199	2 AAY34302	Aay34302 Igm antib
16	713	65.8	588	2 AAW71881	Aaw71881 Anti-huma
17	713	65.8	588	3 AAB12918	Aab12918 Anti-huma
18	705	65.1	533	7 ADB65070	Adb65070 Human pro
19	703	64.9	569	8 ADR19330	Adr19330 Chimeric
20	702.5	64.9	570	8 ADR19329	Adr19329 Chimeric
21	690	63.7	571	6 ADP84970	Adp84970 Chimeric
22	680.5	62.8	450	6 ABP96294	Abp96294 4A5-3.1.1
23	667.5	61.6	453	6 ABP96295	Abp96295 4A5-3.1.1
24	652.5	60.2	472	2 AAR93166	Aar93166 Anti-rhes
25	650	60.0	229	7 ADJ32128	Adj32128 Human int

26	643	59.4	223	7 ADJ32112	Adj32112 Human int
27	636.5	58.8	230	7 ADJ32118	Adj32118 Human int
28	635	58.6	537	3 AAY96290	Aay96290 Human IGF
29	623.5	57.6	462	3 AAB26884	Aab26884 Human imm
30	613.5	56.6	464	7 ADE28411	Ade28411 Human ant
31	598	55.2	473	4 AAB36206	Aab36206 Human imm
32	596	55.0	251	5 ABG80712	Abg80712 Amyloid p
33	596	55.0	254	5 ABG80713	Abg80713 Amyloid p
34	596	55.0	263	5 ABG80714	Abg80714 Human IGG
35	595.5	55.0	466	7 ADE28479	Ade28479 Human ant
36	593.5	54.8	580	6 AAO30915	Aao30915 di-NHS76
37	592.5	54.7	466	7 ADE28471	Ade28471 Human ant
38	589	54.4	580	6 AAO30913	Aao30913 di-NHS76
39	586.5	54.2	466	7 ADE28419	Ade28419 Human ant
40	583	53.8	221	7 ADJ32126	Adj32126 Human int
41	579	53.5	229	3 AAB30593	Aab30593 Variable
42	572.5	52.9	154	6 ABP96293	Abp96293 Human ant
43	571.5	52.8	172	3 AAY93713	Aay93713 The heavy
44	571.5	52.8	172	6 AAB35892	Aab35892 Human 2.1
45	571	52.7	241	8 ADS84467	Ad884467 Human ant

ALIGNMENTS

RESULT 1
AAY34299
ID AAY34299 standard; protein; 205 AA.
XX
AC AAY34299;
XX
DT 19-NOV-1999 (first entry)
XX
DE Igm antibody CEM 10.1 C3 heavy chain sequence.
XX
KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 150
FT /label= unknown
FT /note= "encoded by TVC"
XX
XX
FN WO9945031-A2.
XX
XX
PD 10-SEP-1999.
XX
XX
PF 03-MAR-1999; 99WO-US004583.
XX
XX
PR 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
XX
PA (ABGE-) ABGENIX INC.
XX
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
XX
DR WPI; 1999-540816/45.
XX
XX
N-PSDB; AAZ20400.
XX
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
XX
PS Claim 60; Fig 24; 245pp; English.
XX
XX
CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (mAb) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the Igm mAb ABX-CBL, providing that the antibody is not CBL1. The mAb

CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 205 AA;

Query Match 100.0%; Score 1083; DB 2; Length 205;
Best Local Similarity 100.0%; Pred. No. 8.5e-67;
Matches 205; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLLKPSLTLTCAVYGGSGFYWIRQPPGKLEWIGEHSGSTNYPNPSLKSRVTI 60
DB 1 GLLKPSLTLTCAVYGGSGFYWIRQPPGKLEWIGEHSGSTNYPNPSLKSRVTI 60
QY 61 SVDTSKNQFSLKLSSTAAADTAIVYTCARGTTEYYYYYGMVDMVWGQTTVTSSGSASAPT 120
DB 61 SVDTSKNQFSLKLSSTAAADTAIVYTCARGTTEYYYYYGMVDMVWGQTTVTSSGSASAPT 120
QY 121 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFWSKYKNNSDISSTRGFPVSLRGKYAA 180
DB 121 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFWSKYKNNSDISSTRGFPVSLRGKYAA 180
QY 181 TSQVLLPSKDVMOGQTDHVVVTGSKE 205
DB 181 TSQVLLPSKDVMOGQTDHVVVTGSKE 205

RESULT 2
AA34303
ID AAY34303 standard; protein; 202 AA.

XX AC AAY34303;
XX DT 19-NOV-1999 (first entry)
XX DE IgM antibody CEM 13.12 heavy chain sequence.

XX KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.
XX FH Key Location/Qualifiers
FT Misc-difference 147 /label= unknown
FT /note= "encoded by TYC"
FT Misc-difference 151 /label= unknown
FT /note= "encoded by TYC"

XX PN WO9945031-A2.
XX PD 10-SEP-1999.
XX PF 03-MAR-1999; 99WO-US004583.
XX PR 03-MAR-1998; 98US-00034607.
XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.
XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX DR WPI; 1999-540816/45.
XX DR N-PSDB; AAZ20404.

PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 60; Fig 28; 245pp; English.

XX This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX

SQ Sequence 202 AA;

Query Match 95.1%; Score 1030; DB 2; Length 202;
Best Local Similarity 97.5%; Pred. No. 3.7e-63;
Matches 197; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 4 KPSETLSLTCAVYGGSGFYWIRQPPGKLEWIGEHSGSTNYPNPSLKSRVTISVD 63
DB 1 KLPETLSLTCAVYGGSGFYWIRQPPGKLEWIGEHSGSTNYPNPSLKSRVTISVD 60
QY 64 TSKNQFSLKLSSTAAADTAIVYTCARGTTEYYYYYGMVDMVWGQTTVTSSGSASAPTLP 123
DB 61 TSKNQFSLKLSSTAAADTAIVYTCARGTTEYYYYYGMVDMVWGQTTVTSSGSASAPTLP 120
QY 124 LVSCNSPDSSTSSVAVGCLAQDFLPDXITFWSKYKNNSDISSTRGFPVSLRGKYAATSQ 183
DB 121 LVSCNSPDSSTSSVAVGCLAQDFLPDXITFWSKYKNNSDISSTRGFPVSLRGKYAATSQ 180
QY 184 VLLPSKDVMOGQTDHVVVTGSKE 205
DB 181 VLLPSKDVMOGQTDHVVVTGSKE 202

RESULT 3
AAY34304
ID AAY34304 standard; protein; 190 AA.

XX AC AAY34304;
XX DT 19-NOV-1999 (first entry)
XX DE IgM antibody CEM 13.5 heavy chain sequence.

XX KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.
XX PN WO9945031-A2.
XX PD 10-SEP-1999.
XX PF 03-MAR-1999; 99WO-US004583.
XX PR 03-MAR-1998; 98US-00034607.
XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.
XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX DR WPI; 1999-540816/45.
XX DR N-PSDB; AAZ20405.

XX New immunoadhesin, useful for treating anthrax and rhinovirus, comprises
PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and
PT J chain and secretory component associated with the chimeric toxin
PT receptor protein.
XX
XX Disclosure; SEQ ID NO 47; 288pp; English.
XX
XX The invention relates to a novel immunoadhesin comprising a chimeric
CC toxin receptor protein consisting of a toxin receptor protein linked to
CC at least a portion of an immunoglobulin heavy chain with a J (joining)
CC chain and secretory component (SC) associated with the chimeric toxin
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or
CC viral toxin receptor protein and the immunoadhesin has plant-specific
CC glycosylation. The immunoadhesin of the invention demonstrates virucide
CC and antibacterial activities and may be useful for reducing the binding
CC of a viral or bacterial antigen to a host cell and thus for treating or
CC preventing anthrax, as well as human rhinovirus infection which results
CC in the common cold. The current sequence is that of the human
CC immunoadhesin-related protein of the invention.
XX
SQ Sequence 627 AA;

Query Match 69.2%; Score 749.5; DB 7; Length 627;
Best Local Similarity 68.0%; Pred. No. 2.3e-43;
Matches 149; Conservative 22; Mismatches 31; Indels 17; Gaps 4;
QY 4 KPSETLSLTCAVYGGSPGYWIRQPPGKLEWIGB-INHSGSTYNPGLKSRVTISV 62
DB 32 KPGSSVKYCKRSGAGTTFSSAISWVRQAPGGQLEWMMGGIIPFGTANYAQKFGQRTIITA 91
QY 63 DTSKNQPSLKLSSVTAADTAVVYCARG-----TTEYY----YYYGMDVWGQGTITVTS 112
DB 92 DESTSTAYMELLSLRSEDTAVVYCAKTIILGPYSGGWTPNSDYIYYGMDVWGQGTITVTS 151
QY 113 SGSASAPTLFLPVCNSPSPDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVS 172
DB 152 SGSASAPTLFLPVCNSPSPDTSSVAVGCLAQDFLPDSDITFSWKYKNNSDISSTRGFPVS 211
QY 173 LRGGKYAATSOVLLPSKDVMOGTDEHVV-----TGSKE 205
DB 212 LRGGKYAATSOVLLPSKDVMOGTDEHVVCKVQHPNGNKE 250

RESULT 6
ADM05427
ID ADM05427 standard; protein; 595 AA.
XX
XX ADM05427;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human protein of the invention SEQ ID NO:4112.
XX
XX human; gene therapy; diagnostic marker; pharmaceutical.
XX
XX Homo sapiens.
XX
XX EP1347046-A1.
XX
XX 24-SEP-2003.
XX
XX 12-APR-2002; 2002EP-00008400.
XX
XX 22-MAR-2002; 2002JP-00137785.
XX
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX WPI; 2003-723558/69.

DR N-PSDB; ADM02984.
XX
XX New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.
XX
XX Claim 1; SEQ ID NO 4112; 305pp; English.
XX
XX The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
XX protein sequence of the invention.
XX
SQ Sequence 595 AA;

Query Match 69.0%; Score 747; DB 7; Length 595;
Best Local Similarity 70.3%; Pred. No. 3.2e-43;
Matches 149; Conservative 21; Mismatches 34; Indels 8; Gaps 3;
QY 1 GLLKPSSTLSLTCAVYGGSPGYWIRQPPGKLEWIGB-INHSGSTN-YNPSLKSRVT 59
DB 30 GLVOPGSLRLSCAASGTFSTFNPAHWVRQAPGKLEYVSTISSNQKYYGESVKGRFT 89
QY 60 ISVDTSKNQPSLKLSSVTAADTAVVYCARGTTEYYYYYGMVWGQGTITVSSGSASAP 119
DB 90 ISRDSSKNTLFLQMSLRDEDDTAVVYCARGHS-IDNYHYGVDVWGQGTITVSSGSASAP 148
QY 120 TLFLPVCNSPSPDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVSRLGGKYA 179
DB 149 TLFLPVCNSPSPDTSSVAVGCLAQDFLPDSDITFSWKYKNNSDISSTRGFPVSRLGGKYA 208
QY 180 ATSOVLLPSKDVMOGTDEHVV-----TGSKE 205
DB 209 ATSOVLLPSKDVMOGTDEHVVCKVQHPNGNKE 240

RESULT 7
AAY34301
ID AAY34301 standard; protein; 203 AA.
XX
XX AAY34301;
XX
XX 19-NOV-1999 (first entry)
XX
XX IgM antibody CEM 10.12 F3 heavy chain sequence.
XX
XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
XX Homo sapiens.
XX
XX WO9945031-A2.
XX
XX 10-SEP-1999.
XX
XX 03-MAR-1999; 99WO-US0004583.
XX
XX 03-MAR-1998; 98US-00034607.
XX
XX 03-FEB-1999; 99US-00244253.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;
XX

DR WPI; 1999-540816/45.
 DR N-PSDB; AAZ20402.
 XX
 PT New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.
 XX
 PS Claim 60; Fig 26; 245pp; English.
 XX
 CC This sequence represents the heavy chain of an antibody of the invention.
 CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
 CC complement and a variable region that binds to the epitope on CD147 bound
 CC by the IGM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
 CC can selectively kill activated T-cells, activated B-cells or resting or
 CC activated monocytes. The products and methods can be used for treating
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. Graft
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
 CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
 XX
 SQ Sequence 203 AA;
 Query Match 68.3%; Score 739.5; DB 2; Length 203;
 Best Local Similarity 71.5%; Pred. No. 3.4e-43; Indels 3; Gaps 2;
 Matches 143; Conservative 24; Mismatches 30; Indels 3; Gaps 2;
 Qy 4 KPSETLSITCAVYGGSGFYWIRQPPGKLEWIGEBIN-HSGSTNYPNLSKSRVTISV 62
 Db 2 KPGASVKVCKASGVTFTSYDINVRQATGQGLEWGMWGNFNSGNTGYAQKFGQRTVMNR 61
 Qy 63 DTSKNQPSLKLSSTVTAADTAVYICARG--TTEYYYYYYGMDVWGQGTITVTVSSGSASAPT 120
 Db 62 NTSISTAYMELSLRSEDATVYICARGGHGGSFYFYGGMDVWGQGTITVTVSSGSASAPT 121
 Qy 121 LFPVLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSPVLGGKYAA 180
 Db 122 LFPVLVSCNSPDSSTSSVAVGCLAQDFLPDITFSWKYKNNSDISSTRGFPSPVLGGKYAA 181
 Qy 181 TSQVLLPSKDVWGQGTDEHVV 200
 Db 182 TSQVLLPSKDVWGQGTDEHVV 201
 RESULT 8
 AAM23924
 ID AAM23924 standard; protein; 596 AA.
 XX
 AC AAM23924;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Human EST encoded protein SEQ ID NO: 1449.
 XX
 KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
 KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
 KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
 KW gene therapy; nutrition.
 XX
 OS Homo sapiens.
 XX
 PN WO200154477-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 25-JAN-2001; 2001WO-US002687.
 XX
 PR 25-JAN-2000; 2000US-00491404.
 PR 17-JUL-2000; 2000US-00617746.
 PR 03-AUG-2000; 2000US-00631451.
 PR 15-SEP-2000; 2000US-00663870.
 XX
 PA (HYSE-) HYSEQ INC.
 XX

PI Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Aoundi V;
 PI Cao Y, Drmanac RA, Zhang J, Werhman T;
 XX WPI; 2001-476164/51.
 DR N-PSDB; AAH98583.
 XX
 PT Isolated polypeptide for treatment of diseases, diagnostics, raising
 PT antibodies and research use.
 XX
 PS Claim 20; Page 1011-1012; 1275pp; English.
 XX
 CC The present invention provides the protein and coding sequences of novel
 CC proteins from a variety of organisms, including human, dog, cat, horse,
 CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
 CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
 CC from the organism of interest. They can be used in diagnostics,
 CC forensics, gene mapping, identification of mutations, to assess
 CC biodiversity and for nutritional purposes. The present sequence is a
 CC protein of the invention
 XX
 SQ Sequence 596 AA;
 Query Match 68.1%; Score 738; DB 4; Length 596;
 Best Local Similarity 69.0%; Pred. No. 1.3e-42;
 Matches 149; Conservative 19; Mismatches 34; Indels 14; Gaps 4;
 Qy 1 GLKXPSETLSITCAVYGGSGFYWIRQPPGKLEWIGEBIN-HSGSTNYPNLSKSRVT 59
 Db 29 GLVQPGSGLRLSCAASGFTFTSYWMMHVRQAPGKLVWVSRINTDGSSTSYADSVKGRFT 88
 Qy 60 ISVDTSKNQPSLKLSSTVTAADTAVYICAR----GTTEYYYYGMDVWGQGTITVTVSSGS 115
 Db 89 ISRDNAKNTLYLQWNSLRAEDTAVYICARADNCSTSCYKCF---DYWGQGTITVTVSSGS 145
 Qy 116 ASAPTLPVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSPVLRG 175
 Db 146 ASAPTLPVSCNSPDSSTSSVAVGCLAQDFLPDITFSWKYKNNSDISSTRGFPSPVLRG 205
 Qy 176 GKYAATSOVLLPSKDVWGQGTDEHVV-----TGSKE 205
 Db 206 GKYAATSOVLLPSKDVWGQGTDEHVVCKVQHPNGNKE 241
 RESULT 9
 AAY08598
 ID AAY08598 standard; protein; 223 AA.
 XX
 AC AAY08598;
 XX
 DT 05-AUG-1999 (first entry)
 XX
 DE Anti-human TNF-alpha monoclonal antibody H-chain protein.
 XX
 KW Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;
 KW tumour necrosis factor; light chain; L chain.
 XX
 OS Homo sapiens.
 XX
 PN JP11127855-A.
 XX
 PD 18-MAY-1999.
 XX
 PF 27-OCT-1997; 97JP-00293994.
 XX
 PR 27-OCT-1997; 97JP-00293994.
 XX
 PA (NIHA) JAPAN ENERGY CORP.
 XX
 DR WPI; 1999-350318/30.
 DR N-PSDB; AAX77407.
 XX
 PT Recombinant anti-human TNF-alpha human monoclonal antibody - produced
 PT stably with a high purity, and in large amounts.

XX Claim 3; Page 12-13; 22pp; Japanese.

XX This invention describes novel recombinant anti-human TNF-alpha human

CC monoclonal antibody consisting of a heavy (H) chain and a light (L)

CC chain. The recombinant anti-human TNF-alpha human monoclonal antibody can

CC be produced stably in a high purity and in a large amount

XX Sequence 223 AA;

Query Match 67.9%; Score 735; DB 2; Length 223;

Best Local Similarity 68.4%; Pred. No. 7.6e-43;

Matches 145; Conservative 22; Mismatches 33; Indels 12; Gaps 3;

Qy 1 GLKPSFTLSITCAVYGSFGSYWMIROPPGKGLWEIGINHSGSTN-YNPCLKSRVT 59

Db 10 GVQPGRLSLSCAASGFTSSYGMHWVRQAPGKGLWEVAVISYDGNKYVADSVKGRFT 69

Qy 60 ISVDTSKNQFSLKLSVTAADTAVYYCARGTTEYYYYYGMVWGQGTVTVTSSGSASAP 119

Db 70 ISRDNSKNTLYLQWNSLRAEDTAVYYCAKDSGLAF-----DIWGQGTMTVTSSGSASAP 124

Qy 120 TLPLVSCNSPDSSTSSVAVGCLAQDFLPDXITPSWKYKNSDISSTRGPPSVLRGGKYA 179

Db 125 TLPLVSCNSPDSSTSSVAVGCLAQDFLPDSITPSWKYKNSDISSTRGPPSVLRGGKYA 184

Qy 180 ATSOVLLPSKDVMOGTDEHVV-----TGSKE 205

Db 185 ATSOVLLPSKDVMOGTDEHVVCKVQHPNGNKE 216

RESULT 10

ADL70773

ID ADL70773 standard; protein; 223 AA.

XX AC ADL70773;

XX 03-JUN-2004 (first entry)

XX DE Anti-TNFalpha antibody VH region, SEQ ID 46.

XX Immunosuppressive; Haemostatic; Antiallergic; Antiaesthetic;

KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;

KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnary;

KW Antiparkinsonian; Nootropic; Cardiant; Antianemic; Antiatherosclerotic;

KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;

KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFalpha;

XX antibody; VH region.

OS Unidentified.

XX WO2004020588-A2.

PN 11-MAR-2004.

XX 28-AUG-2003; 2003WO-US026779.

XX 30-AUG-2002; 2002US-0406977P.

PR 10-MAR-2003; 2003US-00384060.

PR 09-JUL-2003; 2003US-0485404P.

XX (BIOR-) BIOREXIS PHARM CORP.

XX Prior CP, Turner AJ, Sadeghi H;

XX WPI; 2004-239175/22.

XX Novel library containing several fusion proteins each of which comprises

PT first transferrin polypeptide fused to at least one second peptide,

PT useful for screening for transferrin fusion protein having the particular

PT activity.

XX Example 8; SEQ ID NO 46; 243pp; English.

XX The present invention relates to a library (I) of modified fusion

CC proteins of transferrin (Tf) and therapeutic proteins with increased

CC serum half-life or serum stability. Preferred fusion proteins include

CC those modified so that the Tf moiety exhibits no or reduced

CC glycosylation, iron binding and/or Tf receptor binding. The transferrin

CC fusion proteins are useful for treating, preventing or ameliorating

CC disorders or diseases of endocrine system, nervous system, immune system,

CC respiratory system, cardiovascular system, diseases and/or disorders

CC relating to cell proliferation, and/or diseases or disorders relating to

CC blood. The modified fusion proteins are useful in diagnosis, prognosis,

CC prevention and/or treatment of autoimmune disorders; diseases and

CC disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia

CC and thrombocytopenia); allergic reactions such as allergic asthma,

CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and

CC eczema; inflammatory conditions e.g., inflammation associated with

CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,

CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders

CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel

CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders

CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative

CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The

CC fusion protein is also useful as an adjuvant to enhance antibacterial or

CC antifungal immune responses, antiparasitic immune responses, etc. The

CC fusion protein is also useful for treating monoclonal gammopathy of

CC undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,

CC adult respiratory distress syndrome, for stimulating wound repair, for

CC preventing or treating infections of joints, bones, skin, etc. The fusion

CC protein is also useful for treating or preventing thrombosis, myocardial

CC infarction, cancers, thrombocytopenia, sickle cell anaemia,

CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,

CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf

CC and a specific example of a SCA that can be fused to Tf is anti-tumour

CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence

CC from an anti-TNFalpha antibody.

XX SQ Sequence 223 AA;

Query Match 67.3%; Score 729; DB 8; Length 223;

Best Local Similarity 67.9%; Pred. No. 2e-42;

Matches 144; Conservative 22; Mismatches 34; Indels 12; Gaps 3;

Qy 1 GLKPSFTLSITCAVYGSFGSYWMIROPPGKGLWEIGINHSGSTN-YNPCLKSRVT 59

Db 10 GVQPGRLSLSCAASGFTSSYGMHWVRQAPGKGLWEVAVISYDGNKYVADSVKGRFT 69

Qy 60 ISVDTSKNQFSLKLSVTAADTAVYYCARGTTEYYYYYGMVWGQGTVTVTSSGSASAP 119

Db 70 ISRDNSKNTLYLQWNSLRAEDTAVYYCAKDSGLAF-----DIWGQGTMTVTSSGSASAP 124

Qy 120 TLPLVSCNSPDSSTSSVAVGCLAQDFLPDXITPSWKYKNSDISSTRGPPSVLRGGKYA 179

Db 125 TLPLVSCNSPDSSTSSVAVGCLAQDFLPDSITPSWKYKNSDISSTRGPPSVLRGGKYA 184

Qy 180 ATSOVLLPSKDVMOGTDEHVV-----TGSKE 205

Db 185 ATSOVLLPSKDVMOGTDEHVVCKVQHPNGNKE 216

RESULT 11

AAW71880

ID AAW71880 standard; protein; 588 AA.

XX AC AAW71880;

XX 18-JAN-1999 (first entry)

XX Anti-human Fas humanised antibody CH11 heavy chain HmuH.

XX Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;

KW autoimmune disease; rheumatoid arthritis; therapy; human;

XX antibody engineering.

Db 92 DNSASTAYMELSLRSBDTAVVYCARS-----YYAMDYWGQGLTVTVSSGSASAPTLF 144
QY 123 PLVSCENSPDTSVAVGCLAQDFLPDXITFSWKYKNSDISSTRGPPSVLRGGKYAATS 182
Db 145 PLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATS 204
QY 183 QVLLPSKDVMOGTDHVV-----TGSKE 205
Db 205 QVLLPSKDVMOGTDHVVCKVQHPNGNKE 233

RESULT 13

ADL70776

ID ADL70776 standard; protein; 228 AA.

XX

AC ADL70776;

XX

DT 03-JUN-2004 (first entry)

XX

XX Anti-TNFalpha antibody VH region, SEQ ID 49.

DE

XX Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;

KW Dermatologic; Antiinflammatory; Antibacterial; Vasotropic;

KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnerary;

KW Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antiatherosclerotic;

KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;

KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFalpha;

KW antibody; VH region.

XX

OS Unidentified.

XX

XX W02004020588-A2.

PN

XX 11-MAR-2004.

PD

XX 28-AUG-2003; 2003WO-US026779.

XX

XX 30-AUG-2002; 2002US-0406977P.

PR

XX 10-MAR-2003; 2003US-00384060.

PR

XX 09-JUL-2003; 2003US-0485404P.

XX

XX (BIOR-) BIOREXIS PHARM CORP.

PA

XX

XX Prior CP, Turner AJ, Sadeghi H;

PI

XX

XX WPI; 2004-239175/22.

DR

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XX

CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The
CC fusion protein is also useful as an adjuvant to enhance antibacterial or
CC antifungal immune responses, antiparasitic immune responses, etc. The
CC fusion protein is also useful for treating monoclonal gammopathy of
CC undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,
CC adult respiratory distress syndrome, for stimulating wound repair, for
CC preventing or treating infections of joints, bones, skin, etc. The fusion
CC protein is also useful for treating or preventing thrombosis, myocardial
CC infarction, cancers, thrombocytopenia, sickle cell anaemia,
CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf
CC and a specific example of a SCA that can be fused to Tf is anti-tumour
CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence
CC from an anti-TNFalpha antibody.
XX

SQ Sequence 228 AA;

Query Match 67.1%; Score 726.5; DB 8; Length 228;

Best Local Similarity 68.9%; Pred. No. 3e-42;

Matches 146; Conservative 19; Mismatches 40; Indels 7; Gaps 2;

QY 1 GLLPKSETSLTCAVYGGSPGYWIRQPPGKLEWIGEIN-HSGSTNYPNLSKSRVT 59

Db 10 GLVQPGGSLRLSCAASGFTSTVYMNWVRQAPGKLEWVSGISGGGTYVADSVKGRFT 69

QY 60 ISVDTKNQPSLKLSSVTADTAVYICARTGTTYYYYYGMVDVWGQGTTVTVSSGSASAP 119

Db 70 ISRDNSMNTLYLQWNSLRABDTAVYICAKDLSNLSGGGTFDIWGQGTMTVTVSSGSASAP 129

QY 120 TLPPLVSCENSPDTSVAVGCLAQDFLPDXITFSWKYKNSDISSTRGPPSVLRGGKYA 179

Db 130 TLPPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYA 189

QY 180 ATSQVLLPSKDVMOGTDHVV-----TGSKE 205

Db 190 ATSQVLLPSKDVMOGTDHVVCKVQHPNGNKE 221

RESULT 14

ID ADF69305

XX ADF69305 standard; protein; 266 AA.

XX

XX ADF69305;

XX

XX 26-FEB-2004 (first entry)

XX

XX Human lung specific protein sequence SEQ ID NO:62.

XX

XX human; lung specific nucleic acid; lung specific protein; lung cancer;

XX cytostatic; gene therapy.

XX

XX Homo sapiens.

XX

XX W02003102137-A2.

XX

XX 11-DEC-2003.

XX

XX 30-MAY-2003; 2003WO-US016810.

XX

XX 31-MAY-2002; 2002US-0385301P.

XX

XX (DIAD-) DIADEXUS INC.

XX

XX Chen S, Macina RA, Sun Y, Liu C, Turner LR;

XX WPI; 2004-053457/05.

XX

XX New human lung specific nucleic acid, useful for preparing a composition

XX for diagnosing or treating lung cancer.

XX

XX Claim 11; SEQ ID NO 62; 221pp; English.

XX

XX

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XX

XX The present invention describes a human lung specific nucleic acid
 CC molecule. Also described: (1) a method for determining the presence of a
 CC lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising
 CC the nucleic acid molecule; (3) a host cell comprising the vector; (4) a
 CC method for producing a polypeptide encoded by the nucleic acid molecule;
 CC (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody
 CC or its fragment that specifically binds to the polypeptide; (7) a method
 CC for determining the presence of a lung specific protein in a sample; (8)
 CC a method for diagnosing and monitoring the presence and metastases of
 CC lung cancer in a patient; (9) a kit for detecting a risk of cancer or
 CC presence of cancer in a patient comprising a means for determining the
 CC presence the nucleic acid molecule or polypeptide in a sample of a
 CC patient; (10) a method of treating a patient with lung cancer; and (11) a
 CC vaccine comprising the polypeptide or the nucleic acid encoding the
 CC polypeptide. Human LSNA molecules and related proteins have cytostatic
 CC activity, and can be used in gene therapy. They are useful for preparing
 CC a composition for diagnosing or treating lung cancer. The present
 CC sequence represents a human lung specific protein, which is used in the
 CC exemplification of the present invention.

XX
 SQ Sequence 266 AA;

Query Match 67.0%; Score 725.5; DB 8; Length 266;
 Best Local Similarity 69.9%; Pred. No. 4.1e-42;
 Matches 146; Conservative 19; Mismatches 35; Indels 9; Gaps 3;

QY 4 KPSETLSLTCAVYGGSGFYGWSMTROPKGLWIGINSGS-TNYNPSLKSRTVTSV 62
 DB 24 KPESLKTICKSGSYFTSYIGWTRQMPKGLWGLIYPCDSITRYSPFGQVTTISA 83
 QY 63 DTSKNQFSLKLSSTVTAADTAVVYVCARGTTEYYYYYGMVDMVGQGTTVTVSSGSASAPTLF 122
 DB 84 DKSISTAYLQWSSLKASDTAMYCARPIAVAGHYF--DYWGQGTLTAVTVSSGSASAPTLF 141
 QY 123 PLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPFSLRGKGYAATS 182
 DB 142 PLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFSLRGKGYAATS 201
 QY 183 QVLLPSKDVMOGTDHVV-----TGSKE 205
 DB 202 QVLLPSKDVMOGTDHVVCKVQHFNKNE 230

RESULT 15
 AAY34302
 ID AAY34302 standard; protein; 199 AA.
 XX
 AC AAY34302;
 XX
 DT 19-NOV-1999 (first entry)
 XX
 DE IGM antibody CEM 10.12 G5 heavy chain sequence.
 XX
 KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.
 XX
 OS Homo sapiens.
 XX
 PN WO9945031-A2.
 XX
 PD 10-SEP-1999.
 XX
 PF 03-MAR-1999; 99WO-US004583.
 XX
 PR 03-MAR-1998; 98US-00034607.
 PR 03-FEB-1999; 99US-00244253.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
 XX
 DR WPI; 1999-540816/45.
 DR N-PSDB; AAZ20403.
 XX
 PT New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.
 XX
 PS Claim 60; Fig 27; 245pp; English.
 XX
 CC This sequence represents the heavy chain of an antibody of the invention.
 CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
 CC complement and a variable region that binds to the epitope on CD147 bound
 CC by the IGM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
 CC can selectively kill activated T-cells, activated B-cells or rearing or
 CC activated monocytes. The products and methods can be used for treating
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
 CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

XX
 SQ Sequence 199 AA;

Query Match 66.3%; Score 718.5; DB 2; Length 199;
 Best Local Similarity 70.7%; Pred. No. 9.1e-42;
 Matches 140; Conservative 24; Mismatches 31; Indels 3; Gaps 2;

QY 4 KPSETLSLTCAVYGGSGFYGWSMTROPKGLWIGIN-HSGSTNYNPSLKSRTVTSV 62
 DB 4 KPGASVKVSKCAGSYFTSYDINWRQATGQGLEWGMWNPNSGNIGYAKFGQRTVMTTR 63
 QY 63 DTSKNQFSLKLSSTVTAADTAVVYVCARGTTEYYYYYGMVDMVGQGTTVTVSSGSASAPTLF 122
 DB 64 NTSISTAYMELSLRSEDVAVYCAR--EEMLVRYYGMDVMGQGTTVTVSSGSASAPTLF 121
 QY 123 PLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPFSLRGKGYAATS 182
 DB 122 PLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFSLRGKGYAATS 181
 QY 183 QVLLPSKDVMOGTDHVV 200
 DB 182 QVLLPSKDVMOGTDHVKV 199

Search completed: March 8, 2005, 06:17:04
 Job time : 98.0436 secs

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 108.788 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083

Sequence: 1 GLLKPSFSLTCAVYGGSF.....LPKDVMOGTDEHVVVTSKE 205

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	749.5	69.2	627	13	US-10-047-542-47
2	747	69.0	595	15	Sequence 47, Appl
3	705	65.1	533	15	Sequence 4112, Ap
4	650	60.0	229	10	Sequence 3224, Ap
5	643	59.4	223	10	Sequence 82, Appl
6	639.5	59.0	179	15	Sequence 66, Appl
7	636.5	58.8	230	10	Sequence 171, App
8	613.5	56.6	464	15	Sequence 72, Appl
9	595.5	55.0	466	15	Sequence 72, Appl
10	593.5	54.8	580	14	Sequence 86, Appl
11	592.5	54.7	466	15	Sequence 37, Appl
12	589	54.4	580	14	Sequence 70, Appl
13	586.5	54.2	466	15	Sequence 35, Appl
					Sequence 30, Appl

14	583	53.8	221	10	US-09-972-656-80
15	579	53.5	229	9	US-09-974-449-37
16	571.5	52.8	172	14	US-10-153-382-21
17	571	52.7	241	16	US-10-684-109-106
18	568	52.4	241	16	US-10-684-109-71
19	561	51.8	239	16	US-10-684-109-100
20	560	51.7	241	16	US-10-684-109-88
21	554	51.2	118	15	US-10-371-942-90
22	553	51.1	152	9	US-09-187-693-68
23	552	51.0	253	10	US-09-880-748-954
24	552	51.0	253	15	US-10-293-418-954
25	545	50.3	250	14	US-10-194-975-110
26	543.5	50.2	193	15	US-10-264-049-4331
27	543.5	50.2	254	10	US-09-880-748-1659
28	543.5	50.2	254	15	US-10-293-418-1659
29	542	50.0	429	14	US-10-194-801C-6
30	541	50.0	255	10	US-09-880-748-1642
31	541	50.0	255	15	US-10-293-418-1642
32	535.5	49.4	252	10	US-09-880-748-1326
33	535.5	49.4	252	15	US-10-293-418-1326
34	535	49.4	173	15	US-10-309-762-173
35	534.5	49.4	250	10	US-09-880-748-993
36	534.5	49.4	250	10	US-09-880-748-1413
37	534.5	49.4	250	15	US-10-293-418-993
38	534.5	49.4	250	15	US-10-293-418-1413
39	534	49.3	249	10	US-09-880-748-957
40	534	49.3	249	15	US-10-293-418-957
41	534	49.3	447	14	US-10-194-801C-2
42	533.5	49.3	467	14	US-10-211-357-8
43	533.5	49.3	467	14	US-10-211-357-10
44	533.5	49.3	467	14	US-10-211-357-12
45	533	49.2	249	10	US-09-880-748-1321

ALIGNMENTS

RESULT 1

US-10-047-542-47
; Sequence 47, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 47
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-47

Query Match 69.2%; Score 749.5; DB 13; Length 627;
Best Local Similarity 68.0%; Pred. No. 5e+46;
Matches 149; Conservative 22; Mismatches 31; Indels 17; Gaps 4;
QY 4 KPSETLSLTCAVYGSGPSGYWISWTRQPPGKLEWIGR-INHSGSTNTPSLKSRVTISV 62
Db 32 KFGSSVKVYSCKASGTFSSYAISWVRQAPGOGLEWGGIPIFGTANYAKFQGRVTITA 91
QY 63 DTSKNQFSLKLSSTVAADTAVVYCARG-----TTEYV-----YYYGMDVWGQTTVTYS 112
Db 92 DEBTSTAYMELSSLRSEDTAVVYCAKTGLPGYSSGWYPSNDDYYGYGMDVWGQTTVTYS 151

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QY 113 SGSASAPTLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVS 172
Db 152 SGSASAPTLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVS 211
QY 173 LRGGKYAATSOVLPLSKDVMQGTDEHVV-----TGSKE 205
Db 212 LRGGKYAATSOVLPLSKDVMQGTDEHVVCKVQHPNGNKE 250

RESULT 2
US-10-108-260A-4112
; Sequence 4112, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4112
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4112

Query Match 69.0%; Score 747; DB 15; Length 595;
Best Local Similarity 70.3%; Pred. No. 7.1e-46;
Matches 149; Conservative 21; Mismatches 34; Indels 8; Gaps 3;

QY 1 GLLKPSETLSLTCAVYGGSFSGYWSWIRQPPGKLEWIGEHSGSTN-YNPSLKSRVT 59
Db 30 GLVQPGGSLRLSCAASGTFNFAHWVRQAPGKLEWVSTISSNGRQKYGESVKGRFT 89
QY 60 ISVDTSKNQFSLKLSSTAAADTAVYVCARGTTEYYYYYGMVWGQGTTVTVSSGSASAP 119
Db 90 ISRDSSKNTLFLWGLSREDDTAVYVCARGHS-IDNYHYGVDVWGQGTTVTVSSGSASAP 148
QY 120 TLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVSLRGKGYA 179
Db 149 TLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVSLRGKGYA 208
QY 180 ATSOVLPLSKDVMQGTDEHVV-----TGSKE 205
Db 209 ATSOVLPLSKDVMQGTDEHVVCKVQHPNGNKE 240

RESULT 3
US-10-104-047-3224
; Sequence 3224, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3224
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3224

Query Match 65.1%; Score 705; DB 15; Length 533;
Best Local Similarity 67.9%; Pred. No. 6.8e-43;
Matches 144; Conservative 16; Mismatches 44; Indels 8; Gaps 3;

QY 1 GLLKPSETLSLTCAVYGGSFSGYWSWIRQPPGKLEWIGEHSGSTNYPNLSKSRVTI 60
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Db 29 GLVQPGGSLRLSCAASGFDVSSNTYMSWVRQSPGKPEWATMYGGNTYYAESVKGRFTV 88
QY 61 SVDTSKNQFSLKLSSTAAADTAVYVCARGTTEYY-YYYYGMDVWGQGTTVTVSSGSASAP 119
Db 89 SRDGSQNTLYLESSLRPDDTAVYVCVRDHRNYADTSPYGRK-WGQGTTLTVTVSSGSASAP 147
QY 120 TLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVSLRGKGYA 179
Db 148 TLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVSLRGKGYA 207
QY 180 ATSOVLPLSKDVMQGTDEHVV-----TGSKE 205
Db 208 ATSOVLPLSKDVMQGTDEHVVCKVQHPNGNKE 239

RESULT 4
US-09-972-656-82
; Sequence 82, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-82

Query Match 60.0%; Score 650; DB 10; Length 229;
Best Local Similarity 64.2%; Pred. No. 2.7e-39;
Matches 131; Conservative 20; Mismatches 43; Indels 10; Gaps 5;

QY 1 GLLKPSETLSLTCAVYGGSFSGYWSWIRQPPGKLEWIGEHSGSTNYPNLSKSRVTI 60
Db 10 GLLKPSETLSLTCAVYGGSFSGYWSWIRQPPGKLEWIGEHSGSTNYPNLSKSRVTI 69
QY 61 SVDTSKNQFSLKLSSTAAADTAVYVCARGTTEYYYYYGMVWGQGTTVTVSSGSASAP 116
Db 70 SVDTSKNQFSLKLSSTAAADTAVYVCARGTTEYYYYYGMVWGQGTTVTVSSAST 129
QY 117 SAPTLFPLVSCNSPSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVSLR-G 175
Db 130 KGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSS 186
QY 176 KYAATSOVLPLSKDVMQGTDEHV 199
Db 187 GLYSLSSVTVTPSSSL--GTQTYI 208

RESULT 5
US-09-972-656-66
; Sequence 66, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 223
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GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
FILE REFERENCE: LEX-020
CURRENT APPLICATION NUMBER: US/10/310,719
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,113
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/371,966
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 580
TYPE: PRT
ORGANISM: Artificial Sequence

OTHER INFORMATION: di-NHS76 (gamma2h) (FN>AQ)-ala-IL2 (D20T) heavy chain fused to IL2

US-10-310-719-35

Query Match 54.4%; Score 589; DB 14; Length 580;

Best Local Similarity 63.2%; Pred. No. 1.7e-34;

Matches 122; Conservative 20; Mismatches 39; Indels 12; Gaps 6;

Qy 1 GLLKPSETLSLTCVAVGGSF-SGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRVT 59

Db 10 GLVKPSETLSLTCVAVGGSF-SGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRVT 69

Qy 60 ISVDTSKNQFSLKSLSSVTAADTAVYVCARGTEYYYGGYVMDVWGQGTFTVSSG-SASA 118

Db 70 ISVDTSKNQFSLKSLSSVTAADTAVYVCARGKWSKF-----DYMGGQGLTVTVSSGASTKG 123

Qy 119 PTLPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNSDISSTRGPPSVLR-GGK 177

Db 124 PSVFLAPCSRSTSE-STAALGCLVKDYFPFPTVSW--NSGALTSGVHTTTPAVLQSSGL 180

Qy 178 YAATSQVLLPSKD 190

Db 181 YLSLSSVTVTPSSN 193

RESULT 13

US-10-292-088-30

Sequence 30, Application US/10292088

Publication No. US2003021100A1

GENERAL INFORMATION:

APPLICANT: BEDIAN, VAHE

APPLICANT: GLADUE, RONALD P.

APPLICANT: CORVALAN, JOSE

APPLICANT: JIA, XIAO-CHI

APPLICANT: FENG, XIAO

TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFERENCE: ABX-PF/3 US

CURRENT APPLICATION NUMBER: US/10/292,088

CURRENT FILING DATE: 2003-03-14

PRIOR APPLICATION NUMBER: 60/348,980

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 30

LENGTH: 466

TYPE: PRT

ORGANISM: Homo sapiens

US-10-292-088-30

Query Match 54.2%; Score 586.5; DB 15; Length 466;

Best Local Similarity 60.2%; Pred. No. 2.1e-34;

Matches 118; Conservative 23; Mismatches 40; Indels 15; Gaps 5;

Qy 1 GLLKPSETLSLTCVAVGGSFSGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRVTI 60

Db 29 GLVKPSETLSLTCVAVGGSFSGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRVTI 88

GENERAL INFORMATION:
APPLICANT: Gillies, Stephen
TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
FILE REFERENCE: LEX-020
CURRENT APPLICATION NUMBER: US/10/310,719
CURRENT FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 60/337,113
PRIOR FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 60/371,966
PRIOR FILING DATE: 2002-04-12
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.1
SEQ ID NO 35
LENGTH: 580
TYPE: PRT
ORGANISM: Artificial Sequence

OTHER INFORMATION: di-NHS76 (gamma2h) (FN>AQ)-ala-IL2 (D20T) heavy chain fused to IL2

US-10-310-719-35

Query Match 54.4%; Score 589; DB 14; Length 580;

Best Local Similarity 63.2%; Pred. No. 1.7e-34;

Matches 122; Conservative 20; Mismatches 39; Indels 12; Gaps 6;

Qy 1 GLLKPSETLSLTCVAVGGSF-SGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRVT 59

Db 10 GLVKPSETLSLTCVAVGGSF-SGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRVT 69

Qy 60 ISVDTSKNQFSLKSLSSVTAADTAVYVCARGTEYYYGGYVMDVWGQGTFTVSSG-SASA 118

Db 70 ISVDTSKNQFSLKSLSSVTAADTAVYVCARGKWSKF-----DYMGGQGLTVTVSSGASTKG 123

Qy 119 PTLPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNSDISSTRGPPSVLR-GGK 177

Db 124 PSVFLAPCSRSTSE-STAALGCLVKDYFPFPTVSW--NSGALTSGVHTTTPAVLQSSGL 180

Qy 178 YAATSQVLLPSKD 190

Db 181 YLSLSSVTVTPSSN 193

RESULT 13

US-10-292-088-30

Sequence 30, Application US/10292088

Publication No. US2003021100A1

GENERAL INFORMATION:

APPLICANT: BEDIAN, VAHE

APPLICANT: GLADUE, RONALD P.

APPLICANT: CORVALAN, JOSE

APPLICANT: JIA, XIAO-CHI

APPLICANT: FENG, XIAO

TITLE OF INVENTION: ANTIBODIES TO CD40

FILE REFERENCE: ABX-PF/3 US

CURRENT APPLICATION NUMBER: US/10/292,088

CURRENT FILING DATE: 2003-03-14

PRIOR APPLICATION NUMBER: 60/348,980

PRIOR FILING DATE: 2001-11-09

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 30

LENGTH: 466

TYPE: PRT

ORGANISM: Homo sapiens

US-10-292-088-30

Query Match 54.2%; Score 586.5; DB 15; Length 466;

Best Local Similarity 60.2%; Pred. No. 2.1e-34;

Matches 118; Conservative 23; Mismatches 40; Indels 15; Gaps 5;

Qy 1 GLLKPSETLSLTCVAVGGSFSGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRVTI 60

Db 29 GLVKPSETLSLTCVAVGGSFSGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRVTI 88

Qy 61 SVDTSKNQFSLKSLSSVTAADTAVYVCAR-----GTTEYYYYYGMVMDVWGQGTFTVSSGS 115

Db 89 SVDMSKNQFSLKSLSSVTAADTAVYVCARKGDYGGNFYFHQ-----WGQGLTVTVSSAS 142

Qy 116 ASAPTLPVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNSDISSTRGPPSVLR- 174

Db 143 TKGPSVPLAPCSRSTSE-STAALGCLVKDYFPFPTVSW--NSGALTSGVHTTTPAVLQSS 199

Qy 175 GGYAATSQVLLPSKD 190

Db 200 SGLYSLSSVTVTPSSN 215

RESULT 14

US-09-972-656-80

Sequence 80, Application US/09972656

Publication No. US20030099647A1

GENERAL INFORMATION:

APPLICANT: Deshpande, Rajendra

APPLICANT: Tsai, Mei-Mei

TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

TITLE OF INVENTION: Neutralizing Activity

FILE REFERENCE: A-799

CURRENT APPLICATION NUMBER: US/09/972,656

CURRENT FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PatentIn version 3.0

SEQ ID NO 80

LENGTH: 221

TYPE: PRT

ORGANISM: Homo sapiens

US-09-972-656-80

Query Match 53.8%; Score 583; DB 10; Length 221;

Best Local Similarity 60.4%; Pred. No. 1.8e-34;

Matches 122; Conservative 21; Mismatches 45; Indels 14; Gaps 6;

Qy 1 GLLKPSETLSLTCVAVGGSF-SGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRV 58

Db 10 GLVKPSETLSLTCVAVGGSF-SGYYSWIRQPPGKLEWIGEHNSGSTNPNLSKSRV 69

Qy 59 TISVDTSKNQFSLKSLSSVTAADTAVYVCARGTEYYYGGYVMDVWGQGTFTVSSGSASA 118

Db 70 TISVDRSKNQFSLKSLSSVTAADTAVYVCARGDWYF-----DYMGGQGLTVTVSSASTKG 123

Qy 119 PTLPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNSDISSTRGPPSVLR-CGK 177

Db 124 PSVFLAPSSKSTSG-GTAALGCLVKDYFPFPTVSW--NSGALTSGVHTTTPAVLQSSGL 180

Qy 178 YAATSQVLLPSKDVMQGTDEHV 199

Db 181 YLSLSSVTVTPSSSL--GTQTYI 200

RESULT 15

US-09-974-449-37

Sequence 37, Application US/09974449

Patent No. US20020141989A1

GENERAL INFORMATION:

APPLICANT: Krichek, Franz

APPLICANT: Stadler, Beda

APPLICANT: Vogel, Monique

TITLE OF INVENTION: ANTI-IDIOTYPIC ANTIBODIES AGAINST

TITLE OF INVENTION: ANTIBODIES WHICH INHIBIT THE BINDING OF IMMUNOGLOBULIN E TO

TITLE OF INVENTION: ITS HIGH AFFINITY RECEPTOR

FILE REFERENCE: 4-30888A

CURRENT APPLICATION NUMBER: US/09/974,449

CURRENT FILING DATE: 2001-10-10

PRIOR APPLICATION NUMBER: PCT/EP00/03288

PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 62

SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 37
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-449-37

Query Match      53.5%; Score 579; DB 9; Length 229;
Best Local Similarity 59.3%; Pred. No. 3.6e-34;
Matches 121; Conservative 26; Mismatches 47; Indels 10; Gaps 6;

Qy 1 GLLKPSETLSLTCAVYGGSFs--GYVWSWIRQPEKGLEWIGENHSGSTNYPNPKSRV 58
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 10 GLVXPSETLSLTCTVSGGSISGGGYTWWIRQPEKGLEWIGYIYSGSTYNPKSRV 69
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 59 TISVDTSKNQPSLKLSSVTAADTAVYCA--RGTEVYVYVYVYVYVYVYVYVYVYV 116
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 70 TMSVDTSKNQPSLRLTSVTAADTAVYCARERGETGLYPYIYIDVWGTGTTVTVSAST 129
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 117 SAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFWSKYKNNSDISSTRGFPSPVLR-G 175
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 130 KGPSVFFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTFPAVLQSS 186
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 176 GKYAATSOVLLPSKDVNQGTDEHV 199
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 187 GLYSLSVSVTVPSSSL--GTQTYI 208
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
```

Search completed: March 8, 2005, 07:05:47
Job time : 109.788 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 22.5411 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-23

Perfect score: 1083

Sequence: 1 GLLRPELTLSTCAVGGSF.....LPKDVMOGTDEHVTGSK 205

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	652.5	60.2	472	3	US-08-793-450-8
2	598	55.2	473	3	US-09-049-672A-4
3	571.5	52.8	172	4	US-09-472-087-7
4	571.5	52.8	172	4	US-09-472-087-86
5	556	51.3	832	3	US-08-630-820-7
6	556	51.3	832	4	US-09-273-453-7
7	542	50.0	429	4	US-09-372-425A-6
8	534	49.3	447	4	US-09-372-425A-2
9	533.5	49.3	467	3	US-08-523-894-8
10	533.5	49.3	467	3	US-08-523-894-10
11	533.5	49.3	467	3	US-08-523-894-12
12	527.5	48.7	123	3	US-08-793-450-4
13	526.5	48.6	487	4	US-09-800-729-145
14	525.5	48.5	476	3	US-08-487-550-12
15	525.5	48.5	476	4	US-09-526-098-12
16	525.5	48.5	476	4	US-09-383-916-12
17	517.5	47.8	476	3	US-08-487-550-4
18	517.5	47.8	476	4	US-09-526-098-4
19	517.5	47.8	476	4	US-09-383-916-4
20	517	47.7	139	4	US-09-203-768A-2
21	512.5	47.3	219	3	US-09-460-384-37
22	497	45.9	122	1	US-08-360-125-11
23	497	45.9	122	2	US-08-450-578-11
24	497	45.9	122	2	US-09-017-628-11
25	497	45.9	122	2	US-09-014-880-11
26	497	45.9	122	2	US-08-450-363-11
27	497	45.9	122	4	US-09-467-903-11

28 491 45.3 467 4 US-08-030-175-42 Sequence 42, Appl
29 488 45.1 467 4 US-08-030-175-41 Sequence 41, Appl
30 486.5 44.9 229 2 US-08-887-352B-20 Sequence 20, Appl
31 486.5 44.9 229 3 US-09-109-207C-20 Sequence 20, Appl
32 486.5 44.9 229 3 US-09-296-005-20 Sequence 20, Appl
33 486.5 44.9 229 4 US-09-920-171-20 Sequence 20, Appl
34 486.5 44.9 229 4 US-09-716-028-20 Sequence 20, Appl
35 486.5 44.9 229 4 US-10-113-996-20 Sequence 20, Appl
36 486.5 44.9 233 2 US-08-887-352B-25 Sequence 25, Appl
37 486.5 44.9 233 3 US-09-109-207C-25 Sequence 25, Appl
38 486.5 44.9 233 3 US-09-296-005-25 Sequence 25, Appl
39 486.5 44.9 233 4 US-09-920-171-25 Sequence 25, Appl
40 486.5 44.9 233 4 US-09-716-028-25 Sequence 25, Appl
41 486.5 44.9 233 4 US-10-113-996-25 Sequence 25, Appl
42 486.5 44.9 451 2 US-08-887-352B-14 Sequence 14, Appl
43 486.5 44.9 451 2 US-08-887-352B-16 Sequence 16, Appl
44 486.5 44.9 451 3 US-08-466-151-65 Sequence 65, Appl
45 486.5 44.9 451 3 US-09-109-207C-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABRIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-793-450-8

Query Match 60.2%; Score 652.5; DB 3; Length 472;
Best Local Similarity 64.9%; Pred. No. 1.9e-51;
Matches 131; Conservative 22; Mismatches 40; Indels 9; Gaps 6;

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QY 1 GLLKPSETLSLTCAVYGGSFSGYYWSWIRQPPGKLEWIGEHSGSTNYPNPSLKSRTVI 60
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Db 29 GLLKPSETLSLTCTVYGGSFSGYYWSWIRQPPGKLEWIGEHSGSTNYPNPSLKSRTVI 88
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SVDTSKNQFSLKLSVTAADTAIVYCARGTTEYYYYY--MDVMGQGTTVTVSSGSASA 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 SVDTSKNQFSLKLSVTAADTAIVYCAR-APEYKWKYHGDWFDPMGQGTTVTVSSASTKG 147
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 PTLFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSVLR-CGK 177
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 148 PSVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPPAVLQSSGL 204
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 YAATSOVLLPSKDVMOGTDEHV 199
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 YLSVSVTVTPSSSL--GTQTYI 224
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 2

```
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
```

GENERAL INFORMATION:

```
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
```

```
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
```

```
; NUMBER OF SEQUENCES: 28
```

```
; CORRESPONDENCE ADDRESS:
```

```
; ADDRESS: Incyte Pharmaceuticals, Inc.
```

```
; STREET: 3174 Porter Drive
```

```
; CITY: Palo Alto
```

```
; STATE: CA
```

```
; COUNTRY: USA
```

```
; ZIP: 94304
```

```
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Diskette
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; COMPUTER: IBM Compatible
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; OPERATING SYSTEM: DOS
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; SOFTWARE: FastSeq for Windows Version 2.0
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```
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/09/049,672A
```

```
; FILING DATE: HEREWITH
```

```
; CLASSIFICATION: 536
```

```
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER:
```

```
; FILING DATE:
```

```
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Cerrone, Michael C
```

```
; REGISTRATION NUMBER: 39,132
```

```
; REFERENCE/DOCKET NUMBER: PF-0497 US
```

```
; TELECOMMUNICATION INFORMATION:
```

```
; TELEPHONE: 650-855-0555
```

```
; TELEFAX: 650-845-4166
```

```
; TELEX:
```

```
; INFORMATION FOR SEQ ID NO: 4:
```

```
; SEQUENCE CHARACTERISTICS:
```

```
; LENGTH: 473 amino acids
```

```
; TYPE: amino acid
```

```
; STRANDEDNESS: single
```

```
; TOPOLOGY: linear
```

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; IMMEDIATE SOURCE:
```

```
; LIBRARY: PANCUT01
```

```
; CLONE: 1513264
```

```
US-09-049-672A-4
```

```
Query Match
```

```
Best Local Similarity 55.2%; Score 598; DB 3; Length 473;
```

```
61.4%; Pred. No. 1.8e-46;
```

```
Matches 124; Conservative 22; Mismatches 48; Indels 8; Gaps 5;
QY 1 GLLKPSETLSLTCAVYGGSPS--GYVWSWIRQPPGKLEWIGEHSGSTNYPNPSLKSRTV 58
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Db 29 GLVVPSETLSLTCAVSGSITSGGYVWSWIRQPPGKLEWIGIYYIGSTLYNPSLKSRTV 88
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 TISVDTSKNQFSLKLSVTAADTAIVYCARGTTEYYYYY--YVMDVMGQGTTVTVSSGSASA 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 TISVDTSKNQFSLKLSVTAADTAIVYCARDDVGLRGNGYGMVDMGQGTTVTVSSASTKG 148
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 PTLFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSVLR-CGK 177
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Db 149 PSVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPPAVLQSSGL 205
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 178 YAATSOVLLPSKDVMOGTDEHV 199
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 206 YLSVSVTVTPSSSL--GTQTYI 225
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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RESULT 3

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US-09-472-087-7
```

```
; Sequence 7, Application US/09472087
```

```
; Patent No. 6682736
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: HANSON, DOUGLAS C.
```

```
; APPLICANT: NEVEU, MARK J.
```

```
; APPLICANT: MUELLER, EILLEN E.
```

```
; APPLICANT: HANKE, JEFFREY H.
```

```
; APPLICANT: GILMAN, STEVEN C.
```

```
; APPLICANT: DAVIS, C. GEOFFREY
```

```
; APPLICANT: CORVALAN, JOSE R.
```

```
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
```

```
; FILE REFERENCE: AEX-PF1
```

```
; CURRENT APPLICATION NUMBER: US/09/472,087
```

```
; CURRENT FILING DATE: 1999-12-23
```

```
; PRIOR APPLICATION NUMBER: 60/113,647
```

```
; PRIOR FILING DATE: 1998-12-23
```

```
; NUMBER OF SEQ ID NOS: 147
```

```
; SOFTWARE: PatentIn Ver. 2.1
```

```
; SEQ ID NO 7
```

```
; LENGTH: 172
```

```
; TYPE: PRT
```

```
; ORGANISM: Homo sapiens
```

```
US-09-472-087-7
```

```
Query Match 52.8%; Score 571.5; DB 4; Length 172;
```

```
Best Local Similarity 64.2%; Pred. No. 1.2e-44;
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```
Matches 113; Conservative 22; Mismatches 32; Indels 9; Gaps 4;
```

```
QY 1 GLLKPSETLSLTCAVYGGSPS--GYVWSWIRQPPGKLEWIGEHSGSTNYPNPSLKSRTV 58
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Db 4 GLVVPSETLSLTCTVSGSISGGHYSWIRQHPGKLEWIGIYYIGNTYINPSLKSRTV 63
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 59 TISVDTSKNQFSLKLSVTAADTAIVYCARGTTEYYYYY--YVMDVMGQGTTVTVSSGSASA 118
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 64 TISVDTSKNQFSLKLSVTAADTAIVYCARDSG----YYGIDVMGQGTTVTVSSASTKG 119
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 119 PTLFPLVSCENSPSDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGPPSVLR 174
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 120 PSVFPPLAPCSRSTSE-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPPAVLQ 172
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

RESULT 4

```
US-09-472-087-86
```

```
; Sequence 86, Application US/09472087
```

```
; Patent No. 6682736
```

```
; GENERAL INFORMATION:
```

```
; APPLICANT: HANSON, DOUGLAS C.
```

```
; APPLICANT: NEVEU, MARK J.
```

```
; APPLICANT: MUELLER, EILLEN E.
```

```
; APPLICANT: HANKE, JEFFREY H.
```

```
; APPLICANT: GILMAN, STEVEN C.
```

```
; APPLICANT: DAVIS, C. GEOFFREY
```


APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-86

Query Match 52.8%; Score 571.5; DB 4; Length 172;
Best Local Similarity 64.2%; Pred. No. 1.2e-44;
Matches 113; Conservative 22; Mismatches 32; Indels 9; Gaps 4;
QY 1 GLLKPSETLSLTCAVYGGFS--GYVWSWIRPPGKLEWIGEIHNHSGSTNPNLSKRV 58
DB 4 GLVKPSQLSLCTVSGGSISSGHHWSWIRHPKLEWIGIYIYIGNTYNPNLSKRV 63
QY 59 TISVDTSKNQFSKLSSVTAADTAVYYCARGTEYYYGGMDVWGQGTITVTVSSGSASA 118
DB 64 TISVDTSKNQFSKLSSVTAADTAVYYCARDSDG---YYGIDVWGQGTITVTVSSASTKG 119
QY 119 PTLFPLVCENSPDTSVAVGCLAQDFLPDITFSWKYKKNDSISSTRGPPSVLR 174
DB 120 PSVFFPLAPCSRSTSE--STAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQ 172

RESULT 5
US-08-630-820-7
Sequence 7, Application US/08630820
Patent No. 6008023
GENERAL INFORMATION:
APPLICANT: OPPER, Martin
APPLICANT: BOSSLET, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,820
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19513676.4
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7;
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-820-7
Query Match 51.3%; Score 556; DB 3; Length 832;
Best Local Similarity 55.9%; Pred. No. 2.6e-42;
Matches 113; Conservative 32; Mismatches 45; Indels 12; Gaps 7;
QY 1 GLLKPSETLSLTCAVYGGSF--SGYYWSWIRPPGKLEWIGEIHNHSGSTNPNLSKRV 59
DB 11 GLVRSQTLSTCTVSGFTISSGYSHWVRPPGKLEWIGIYIOYSGITNPNLSKRV 70
QY 60 ISVDTSKNQFSKLSSVTAADTAVYYCARGTEYYYGGMDVWGQGT--TVTVSSGSAS 117
DB 71 MLVDTSKNQFSKLSSVTAADTAVYYCAREDYDHYWF---DVMQGGSLVTVTVSSASTK 127
QY 118 APTLFPLVCENSPDTSVAVGCLAQDFLPDITFSWKYKKNDSISSTRGPPSVLR-GG 176
DB 128 GPSVFFPLAPCSRSTSG--GTAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSSG 184
QY 177 KYAATSOVLLPSKDVMOGTDEH 198
DB 185 LYSLSVTVTFSSSL--GTQTY 204

RESULT 6
US-09-273-453-7
Sequence 7, Application US/09273453
Patent No. 6602688
GENERAL INFORMATION:
APPLICANT: OPPER, Martin
APPLICANT: BOSSLET, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,453
FILING DATE: 22-Mar-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,820
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7;
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7;
US-09-273-453-7

Query Match	51.3%	Score	556;	DB	4;	Length	932;
Best Local Similarity	55.9%;	Pred. No.	2.6e-42;				
Matches	113;	Conservative	32;	Mismatches	45;	Indels	12;
Gaps	7;						
QY	1	GLLKPSFTLSLTCATVYGGSF--SGYYWSWIRPPGKGLEWIGEINHSGSTNNPSLKSRVT	59				
Db	11	GLVRPSQTLSLTCTVSGFTISSGYSMHWVRPPGKGLEWIGIYQSGITNNPSLKSRVT	70				
QY	60	ISVDTSKNQSFLKUSSVTAADTAIVYVCARGTTEIYYIYGMVWGQGT--TVTVSSSGAS	117				
Db	71	MLVDTSKNQSFLRSLSSVTAADTAIVYVCAREDYHWTYF--DVRGQGSVLTVTVSSASTK	127				
QY	118	APTLFPLVLCENSPPDSTSSVAVGCLAODFLPDXITFSWKYKNNSDISSTRGFPSVLR--GG	176				
Db	128	GPSVFPLAPCSRSTSG--GTAALGCLVXDYFPEPVTVSW--NSGALTSGVHTFPFVQLQSG	184				
QY	177	KYAATSQVLLPFSKDVMOGTDEH	198				
Db	185	LYSLSSVTVTPSSSL--GTQTY	204				

RESULT 7

```

US-09-372-425A-6
; Sequence 6, Application US/09372425A
; Patent No. 6475749
;
; GENERAL INFORMATION:
;
; APPLICANT: Sherie L. Morrison
; APPLICANT: Ramon Montano
; TITLE OF INVENTION: Improved Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: MS Word
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,425A
; FILING DATE: August 11, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:

```

Query Match 50.0%; Score 542; DB 4; Length 429;
Best Local Similarity 57.1%; Pred. NO. 2.1e-41;
Matches 120; Conservative 11; Mismatches 35; Indels 44; Gaps 6;

Qy	61	SVDTSKNOFSLKLSSTVAADTAVYCAR-----GITEYV-YYYGMDVWGCGTTTVT	111
Db	89	SVDTSKNOFSLKLSSTVAADTAVYCARSHCTSIISCFYLYGYYYVMDVWGKGTITV	148
Qy	112	SS-----GSASAPTLFPLV-----SCENSP-----STSSVA	138
Db	149	SSELKPLGDTHTPCRCPEPKSCDTPPCPCRCPEPKSCDTPPCPCRCPEPKSCDTPPC	208
Qy	139	VGCLAQDFL--PDXITFSWKYKNNSDISST	166
Db	209	PRCPAPELLGGPSVFLFPKPKDTLMISRT	238

RESULT 8

US-09-372-425A-2
; Sequence 2, Application US/09372425A
; Patent No. 6475749
; GENERAL INFORMATION:
; APPLICANT: Sherie L. Morrison
; APPLICANT: Ramon Montano
; TITLE OF INVENTION: Improved Rh Antibody
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Oppenheimer Wolff & Donnelly LLP
; STREET: 209 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 98
; SOFTWARE: MS Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/372,425A
; FILING DATE: August 11, 1999
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenakmp, David J.
; REGISTRATION NUMBER: 29,421
; REFERENCE/DOCKET NUMBER: 510015-223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 788-5100
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Heavy chain with Tailpiece - A
US-09-372-425A-2

Query Match 49.3%; Score 534; DB 4; Length 447;
Best Local Similarity 56.7%; Pred. No. 1.2e-40;
Matches 119; Conservative 11; Mismatches 36; Indels 44; Gaps 6;

Qy	61	SVDTSKNQFSLKLSVTAADTAIVYCAR	-----GTTEYY-YYYGHVDVWGQGVTTVV	111
		: : : : :		
Db	89	SVDTSKNQFVKLTSVTAADTAIVYCAR	SHCTSI SCFQYXLYGYYYVNDWVGKGVTTVV	148
		: : : : :		
Qy	112	SS-----GSASAPTLFLV-----SCNSP-----SDTSSVA	138	
		: : : : :		
Db	149	SSELKPLGDTHTCRCPPEKSCDTPPCPRCPPEKSCDTPPCPRCPPEKSCDTPPC	208	
		: : : : :		

QY 172 VLGGKYAATSOVLPLSKDVMQ 194
DB 205 DASGLYTTSQLTUPATQCPDG 227

RESULT 14

US-08-487-550-12

; Sequence 12, Application US/08487550

; Patent No. 6113898

; GENERAL INFORMATION:

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF, AND USE THEREOF AS

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,550

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-487-550-12

Query Match

Best Local Similarity 48.5%; Score 525.5; DB 3; Length 476;

Matches 113; Conservative 27; Mismatches 51; Indels 17; Gaps 8;

QY 1 GLKPSSETLSLTCVAVGGSFS-GYVWSWIRQPPGKLEWIGEI-NHSGSTNYPNLSKSRV 58

DB 29 GLVKESETLSLTCVAVGGSISGGYGVGWIRQPPGKLEWIGSFYSSGNTYNNPSLKSOV 88

QY 59 TISVDTSKNQFSLKLSVTAADTAVYVCARGTTEYYYYYGM-----DVMGQGTVTVS 112

DB 89 TISTDTSKNQFSLKLSNMTAADTAVYVCV---DRLFSVGVGVNNWFDVWPGVLVTVS 145

QY 113 SGASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPV 172

DB 146 SASTKGPSVFPLAPSSKSTSG-GTAAAGCLVKDYFPEPTVSW--NSGALTSGVHTFPAV 202

QY 173 LR-GGKYAATSOVLPLSKDVMQGTDEHV 199

DB 203 LQSSGLYSLSSVTVVPSSSL--GTQTYI 228

RESULT 15

US-09-526-098-12

; Sequence 12, Application US/09526098

; Patent No. 6492134

; GENERAL INFORMATION:

;

; APPLICANT: Anderson, Darrell R.

; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC

; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,

; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"

; NUMBER OF SEQUENCES: 12

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS

; STREET: 699 Prince Street

; CITY: Alexandria

; STATE: VA

; COUNTRY: USA

; ZIP: 22314

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/526,098

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/383,916

; FILING DATE:

; APPLICATION NUMBER: US 08/487,550

; FILING DATE: 07-JUN-1995

; ATTORNEY/AGENT INFORMATION:

; NAME: Teskin, Robin L.

; REGISTRATION NUMBER: 35,030

; REFERENCE/DOCKET NUMBER: 012712-131

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 703-836-6620

; TELEFAX: 703-836-2021

; INFORMATION FOR SEQ ID NO: 12:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 476 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-09-526-098-12

Query Match

Best Local Similarity 48.5%; Score 525.5; DB 4; Length 476;

Matches 113; Conservative 27; Mismatches 51; Indels 17; Gaps 8;

QY 1 GLKPSSETLSLTCVAVGGSFS-GYVWSWIRQPPGKLEWIGEI-NHSGSTNYPNLSKSRV 58

DB 29 GLVKESETLSLTCVAVGGSISGGYGVGWIRQPPGKLEWIGSFYSSGNTYNNPSLKSOV 88

QY 59 TISVDTSKNQFSLKLSVTAADTAVYVCARGTTEYYYYYGM-----DVMGQGTVTVS 112

DB 89 TISTDTSKNQFSLKLSNMTAADTAVYVCV---DRLFSVGVGVNNWFDVWPGVLVTVS 145

QY 113 SGASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPV 172

DB 146 SASTKGPSVFPLAPSSKSTSG-GTAAAGCLVKDYFPEPTVSW--NSGALTSGVHTFPAV 202

QY 173 LR-GGKYAATSOVLPLSKDVMQGTDEHV 199

DB 203 LQSSGLYSLSSVTVVPSSSL--GTQTYI 228

Search completed: March 8, 2005, 05:53:51

Job time : 24.5411 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.5183 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-24

Perfect score: 776

Sequence: 1 LSLPVTGPSPASISCRSSQS.....VVCLLNFFYPREAKEHQSP 148

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567	73.1	135	2 S40342	Ig kappa chain - h
2	562	72.4	219	2 PC4203	Ig kappa chain (mo
3	561	72.3	121	2 S40371	Ig kappa chain - h
4	553	71.3	219	2 S52028	Ig kappa chain - m
5	551	71.0	197	2 S29593	Ig kappa chain (WM
6	544	70.1	136	2 S40357	Ig kappa chain V-J
7	541	69.7	219	2 S16112	Ig kappa chain V r
8	539	69.5	217	2 S42772	Ig kappa chain - m
9	539	69.5	219	2 S38865	Ig kappa chain - m
10	533	68.7	215	2 JE0242	Ig kappa chain NIG
11	530	68.3	132	2 S26882	Ig kappa chain V r
12	529	68.2	125	2 S40356	Ig kappa chain - h
13	529	68.2	225	2 JL0029	Ig kappa chain pre
14	528	68.0	124	2 S03876	Ig kappa chain V-I
15	526	67.8	112	2 S58207	Ig light chain V r
16	525	67.7	112	2 K2HUGM	Ig kappa chain pre
17	516	66.5	112	2 S58206	Ig light chain V r
18	507	65.3	215	2 JE0241	Ig kappa chain NIG
19	501.5	64.6	126	2 S40339	Ig kappa chain - h
20	497	64.0	215	2 A23746	Ig kappa chain V-I
21	490.5	63.2	240	2 S06084	Ig kappa chain pre
22	489	63.0	131	2 S40372	Ig kappa chain V-J
23	488	62.9	215	2 JE0243	Ig kappa chain NIG
24	484.5	62.4	216	2 JE0241	Ig kappa chain An3
25	482	62.1	113	1 K2HUTW	Ig kappa chain V-I
26	472.5	60.9	214	2 S68212	Ig kappa chain (Ma
27	469	60.4	123	2 S40319	Ig kappa chain V r
28	468.5	60.4	112	1 K2HUMU	Ig kappa chain V-I
29	465.5	60.0	220	2 A31790	Ig kappa chain V r

ALIGNMENTS

RESULT 1

S40342
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40342
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40342
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-135 <KLE>
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X72452; NID:G441372; PID:G441373
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:29-108/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 567; DB 2; Length 135;
Best Local Similarity 97.3%; Pred. No. 1.7e-42;
Matches 108; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY	1	LSLPVTGPSPASISCRSSQSLHNSGYNLYDLWYLOKPGQSPOLLYLGSNRRASGVDPDRFS	60
DB	22	LSLPVTGPSPASISCRSSQSLHNSGYNLYDLWYLOKPGQSPOLLYLGSNRRASGVDPDRFS	81
QY	61	SGSGTDTFTLKISRVEADVGVIYCMQTRQTPRTFGQGTKEIKRTVAAPS	111
DB	82	SGSGTDTFTLKISRVEADVGVIYCMQALQTPRTFGQGTKEIKRTVAAPS	132

RESULT 2

PC4203
Ig kappa chain (monoclonal antibody MABA34) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A>Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mor
A:Reference number: PC4202; MUID:97082978; PMID:8964510
A:Accession: PC4203
A:Molecule type: mRNA
A:Residues: 1-219 <KWA>
A:Cross-references: GB:U99147; NID:G1594225; PIDN:AA52821.1; PID:G1594226
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density l
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-112/Domain: V region #status predicted <VRG>
F:113-219/Domain: C region #status predicted <CRG>

Query Match 72.4%; Score 562; DB 2; Length 219;

```
Best Local Similarity 76.4%; Pred. No. 7.9e-42;
Matches 107; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 1 LSLPVTPEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSRASGVDPDRFS 60
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 9 LSLPVLGDQASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYKVSNRFSGVDPDRFS 68
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GSGSGTDFTLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVAAPSVEIFPPSDE 120
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 GSGSGTDFTLKISRVEADVGIYCFQGSHPVPTFGGTKEIKRADAAPTIVSIFPPSSE 128
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 QKSGTASVVCLLNNFYPRE 140
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 QLTSGGASVVCFLNNFYPKD 148
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
S40371
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40371
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40371
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-121 <KLE>
A:Cross-references: EMBL:X72481; NID:G441430; PIDN:CAA51149.1; PID:G441431
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:13-92/Domain: immunoglobulin homology <IMM>

Query Match 72.3%; Score 561; DB 2; Length 121;
Best Local Similarity 92.2%; Pred. No. 5.1e-42;
Matches 107; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 LSLPVTPEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSRASGVDPDRFS 60
Db 6 LSLPVTPEPASISCRSSQSLYSTGYLDWYLOKPGSQPLLIIYLGSKRASGVDPDRFS 65
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GSGSGTDFTLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVAAPSVEIFPP 116
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 66 GSGSGTDFTLKISRVEADVGIYCMQGLQPTTFGGQTKLEIKRTVAAPSVEIFPP 121
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
S52028
Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C:Accession: S52028
R:van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schote, A.;
submitted to the EMBL Data Library, August 1994
A:Description: Coordinate expression of antibody subunit genes yields high levels of fur
A:Reference number: S52028
A:Accession: S52028
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <VAN>
A:Cross-references: EMBL:L35138; NID:G522336; PIDN:AAA67525.1; PID:G522337
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 71.3%; Score 553; DB 2; Length 219;
Best Local Similarity 75.7%; Pred. No. 4.8e-41;
Matches 106; Conservative 12; Mismatches 22; Indels 0; Gaps 0;

QY 1 LSLPVTPEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSRASGVDPDRFS 60
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
Db 9 LSLPVLGDQASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYKVSNRFSGVDPDRFS 68
QY 61 GSGSGTDFTLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVAAPSVEIFPPSDE 120
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 69 GSGSGTDFTLKISRVEADVGIYCFQGSHPVPTFGGTKEIKRADAAPTIVSIFPPSSE 128
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 QKSGTASVVCLLNNFYPRE 140
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 129 QLTSGGASVVCFLNNFYPKD 148
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S29593
Ig kappa chain (NM65) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S29593
R:Seymour, R.
submitted to the EMBL Data Library, February 1991
A:Reference number: S29593
A:Accession: S29593
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-197 <SEY>
A:Cross-references: EMBL:X57856; NID:G52588; PIDN:CAA40991.1; PID:G52589
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 71.0%; Score 551; DB 2; Length 197;
Best Local Similarity 77.0%; Pred. No. 6.4e-41;
Matches 107; Conservative 11; Mismatches 21; Indels 0; Gaps 0;

QY 2 SLPVTPEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSRASGVDPDRFSG 61
Db 25 SIPVTGESASISCRSSKSLHNSGDTLYLWFLORPGSQPLLIIYRNSNLASGVDPDRFSG 84
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 62 GSGSGTDFTLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVAAPSVEIFPPSDEQ 121
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 GSGSGTDFTLKISRVEADVGFYFCMQHLEYPTFGGTKEIKRADAAPTIVSIFPPSSEQ 144
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 122 LKSGTASVVCLLNNFYPRE 140
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 LTSGGASVVCFLNNFYPKD 163
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S40357
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C:Accession: S40357
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40357
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-136 <KLE>
A:Cross-references: UNIPROT:Q8NEK0; EMBL:X72467
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-115/Domain: immunoglobulin homology <IMM>

Query Match 70.1%; Score 544; DB 2; Length 136;
Best Local Similarity 96.3%; Pred. No. 1.8e-40;
Matches 104; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSLPVTPEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSRASGVDPDRFS 60
Db 29 LSLPVTPEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSRASGVDPDRFS 88
    |||||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 GSGSGTDFTLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVA 108
```


C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C:Accession: S26882
R:Weichhold, G.M.; Klobeck, H.G.; Ohnheiser, R.; Combrinato, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A:Title: Megabase inversions in the human genome as physiological events.
A:Reference number: S26882, MUID:90370099, PMID:2118596
A:Accession: S26882
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 1-132 <WEI>
A:Cross-references: EMBL:X54248; NID:g37626; PIDN:CAA38149.1; PID:g1335367
C:Genetics:
A:Introns: 17/1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:136-115/Domain: immunoglobulin homology <IMM>

Query Match 68.3%; Score 530; DB 2; Length 132;
Best Local Similarity 96.2%; Pred. No. 2.8e-39;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFS 60
Db 29 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFS 88
QY 61 GSGSGTDTFLKISRVEADVGIYCMQTRQTPRTFGQGTKEIK 104
Db 89 GSGSGTDTFLKISRVEADVGIYCMQALQTPQTGQGTKEIK 132

RESULT 12
S40356
Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40356
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40356
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLP>
A:Cross-references: EMBL:X72466; NID:g441400; PIDN:CAA51134.1; PID:g441401
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:125-104/Domain: immunoglobulin homology <IMM>

Query Match 68.2%; Score 529; DB 2; Length 125;
Best Local Similarity 93.5%; Pred. No. 3.2e-39;
Matches 101; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFS 60
Db 18 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFS 77
QY 61 GSGSGTDTFLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVA 108
Db 78 GSGSGTDTFLKISRVEADVGIYCMQVLIQPLTFGGGTKEIKRTVA 125

RESULT 13
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphospho
A:Reference number: JL0029; MUID:86171315; PMID:3127529

A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Cross-references: UNIPROT:Q99W37
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <JLR>
F:120-225/Domain: C region #status predicted <COR>

Query Match 68.2%; Score 529; DB 2; Length 225;
Best Local Similarity 72.1%; Pred. No. 6e-39;
Matches 101; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFS 60
Db 15 LSLPVSGLGDQASISCRSSQNVHSTGNTYLEWYLQKPGQSPNLLIYKISNRFSGVDPDRFS 74
QY 61 GSGSGTDTFLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVAAPSVFPPPSDE 120
Db 75 GSGSGTDTFLKISRVEADVGIYCFQSSHVWTFGGGTKEIKRAADAAPTVISFPPTSE 134
QY 121 QKSGTASVCLLNFPYRE 140
Db 135 QLTSGASVWCFLNFPKD 154

RESULT 14
S03876
Ig kappa chain V-II region (Inc) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S03876
R:Ferri, G.; Stoppini, M.; Iadarola, P.; Bellotti, V.; Merlini, G.
Biochim. Biophys. Acta 995, 103-108, 1989
A:Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.
A:Reference number: S03876; MUID:89194238; PMID:2495028
A:Accession: S03876
A:Molecule type: protein
A:Residues: 1-124 <FER>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <IMM>

Query Match 68.0%; Score 528; DB 2; Length 124;
Best Local Similarity 87.1%; Pred. No. 3.9e-39;
Matches 101; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFS 60
Db 9 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQIVYLGNSRAGVDPDRFS 68
QY 61 GSGSGTDTFLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVAAPSVFIPP 116
Db 69 GSGSGTDTFLISSVGADVGVYCMQALQTPWTFGGGTKEIKRTVAAPSVFIPP 124

RESULT 15
S58207
Ig light chain V region anti-F(ab')2 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1996 #sequence_revision 19-Apr-1996 #text_change 21-Jan-2000
C:Accession: S58207
R:Weischof, M.; Terness, P.; Stanescu, D.; Zewe, M.; Hain, C.H.; Doebe, S.; Breitling, I.
submitted to the EMBL Data Library, July 1995
A:Description: Characterization of heavy and light chain immunoglobulin variable region
A:Reference number: S58206

A:Accession: S58207
 A:Status: Preliminary
 A:Molecule type: mRNA
 A:Residues: 1-112 <WEL>
 A:Cross-references: EMBL:X89056; NID:g929642; PIDN:CAA61443.1; PID:g929643
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:16-95/Domain: immunoglobulin homology <IMM>

 Query Match 67.8%; Score 526; DB 2; Length 112;
 Best Local Similarity 96.2%; Pred. No. 5.3e-39;
 Matches 100; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

 QY 1 LSLPTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGOSPOLLTYLGSNRASGVDPDRFS 60
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 9 LSLPTPGEPASISCRSSQSLHSHNGYNYLDWYLOKPGOSPOLLTYLGSNRASGVDPDRFS 68
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 GSGSGTDFTLKISRVEAEDVGIIYCMQTQTPRTFGQTKVEIK 104
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 69 GSGSGTDFTLKISRVEAEDVGIIYCMQTQTPRTFGQTKVEIK 112
 Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

 Search completed: March 8, 2005, 06:39:21
 Job time : 11.5683 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 55.2705 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-24

Perfect score: 776

Sequence: 1 LSLPTGPSPASISCRSSQS.....VVCLLNFPYPRAEKHQKSP 148

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt 03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	ID	Description
1	717	92.4	Q8NEK0	Q8nek0 homo sapien
2	691.5	89.1	Q6PIH6	Q6pih6 homo sapien
3	621	80.0	Q6P491	Q6p491 homo sapien
4	607	78.2	Q8TCD0	Q8tcd0 homo sapien
5	541	69.7	Q65ZC0	Q65zc0 mus musculus
6	526	67.8	Q6GMV9	Q6gmv9 homo sapien
7	525	67.7	Q62E HUMAN	P06309 homo sapien
8	522.5	67.3	Q6PIL8	Q6pil8 homo sapien
9	511	65.9	Q6PJF2	Q6pjf2 homo sapien
10	505.5	65.1	Q6P5S8	Q6p5s8 homo sapien
11	490.5	63.2	Q6GMW1	Q6gmw1 homo sapien
12	490	63.1	Q6GMW0	Q6gmw0 homo sapien
13	488.5	63.0	Q72473	Q72473 homo sapien
14	482	62.1	Q72473	Q72473 homo sapien
15	481.5	62.0	Q6PIH7	Q6pih7 homo sapien
16	480.5	61.9	Q6GMX0	Q6gmx0 homo sapien
17	478.5	61.7	Q6GMX8	Q6gmx8 homo sapien
18	474.5	61.1	Q723Y4	Q723y4 homo sapien
19	473.5	61.0	Q6PIT5	Q6pit5 homo sapien
20	468.5	60.4	Q72473	Q72473 homo sapien
21	459.5	59.2	Q6GMX9	Q6gmx9 homo sapien
22	449.5	57.9	Q6PIH4	Q6pih4 homo sapien
23	437.5	56.4	Q72473	Q72473 homo sapien
24	435.5	55.1	Q66J57	Q66j57 mus musculus
25	432	55.7	Q72473	Q72473 homo sapien
26	432	55.7	Q6NTU5	Q6ntu5 homo sapien
27	426.5	55.0	Q75236	Q75236 xenopus lae
28	425	54.8	Q72G MOUSE	P01631 mus musculus
29	419	54.0	Q72F HUMAN	P06310 homo sapien
30	419	54.0	Q65ZQ7	Q65zq7 mus sp. b3(
31	416.5	53.7	Q7T598	Q7t598 mus musculus

RESULT 1

ID	Q8NEK0	PRELIMINARY;	PRT;	239 AA.
AC	Q8NEK0;			
DT	01-OCT-2002 (Tremblrel. 22, Created)			
DT	01-OCT-2002 (Tremblrel. 22, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh F., Hopkins R.F., Jordan H., Moore K., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K., Statchenko M., Bonaldo M.P., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McSwain P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.			
DR	EMBL; BC030814; AAH30814.1; -.			
DR	PIR; S23638; S23638.			
DR	PIR; S34091; S34091.			
DR	PIR; S40342; S40342.			
DR	PIR; S40357; S40357.			
DR	HSSP; P01834; I17Z.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig.c1.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig v.			
DR	Pfam; PF07654; C1-set; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; P550835; IG_LIKE; 2.			

ALIGNMENTS

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DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match          92.4%; Score 717; DB 2; Length 239;
Best Local Similarity 94.5%; Pred. No. 1.7e-64;
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGSQPOLLYLGSNRASGVDPDRFS 60
Db 29 LSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGSQPOLLYLGSNRASGVDPDRFS 88
QY 61 GSGSGTDFTLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVAAPSVFIFFPSDE 120
Db 89 GSGSGTDFTLKISRVEADVGIYCMQGLQTPQTFGQGTKEIKRTVAAPSVFIFFPSDE 148
QY 121 QLKSGTASVCLLNPNFYPREAKHQK 146
Db 149 QLKSGTASVCLLNPNFYPREAKVQWK 174

RESULT 2
Q6PIH6 PRELIMINARY; PRT; 240 AA.
ID Q6PIH6
AC Q6PIH6;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; -.
DR HSSP; P01837; IKB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
```

```
DR PROSITE; PS0835; IG LIKE; 2.
KW PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8B8781EC4 CRC64;

Query Match          89.1%; Score 691.5; DB 2; Length 240;
Best Local Similarity 91.8%; Pred. No. 6.7e-62;
Matches 135; Conservative 2; Mismatches 9; Indels 1; Gaps 1;

QY 1 LSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGSQPOLLYLGSNRASGVDPDRFS 60
Db 29 LSLPVTGPEPASISCRSSQSLHSHNGYNYLDWYLOKPGSQPOLLYLGSNRASGVDPDRFS 88
QY 61 GSGSGTDFTLKISRVEADVGIYCMQTRQTPRTFGQGTKEIKRTVAAPSVFIFFPSD 119
Db 89 GSGSGTDFTLKISRVEADVGIYCMQALQTPPTFGQGTKEIKRTVAAPSVFIFFPSD 148
QY 120 EQLKSGTASVCLLNPNFYPREAKHQK 146
Db 149 EQLKSGTASVCLLNPNFYPREAKVQWK 175

RESULT 3
Q6P491 PRELIMINARY; PRT; 239 AA.
ID Q6P491
AC Q6P491;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063599; AAH63599.1; -.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD7313DDFFD358B3 CRC64;

Query Match
Best Local Similarity 80.0%; Score 621; DB 2; Length 239;
Matches 121; Conservative 7; Mismatches 18; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGOSPOLLIYLGNSRAGVDPDRFS 60
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 29 LSSPVTLGOPASISCRSSQSLHNSGNYLDWYLOKPGOSPOLLIYKISNRFSGVDPDRFS 88
QY 61 GSGSGTDFTLKISRVEADVGIYCMQTRQTRPTFGQGTKEIKRTVAAPSFIIPPDSDE 120
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 89 GSGAGTDFTLKISRVEADVGIYCMQVSHFPRTFGQGTKEIKRTVAAPSFIIPPDSDE 148
QY 121 OLKSGTASVVCLLNNFYPREAKEHOK 146
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 149 QLKSGTASVVCLLNNFYPREAKVQWK 174

RESULT 4
Q8TCD0 PRELIMINARY; PRT; 239 AA.
AC Q8TCD0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSP; P01834; I172.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match
Best Local Similarity 78.2%; Score 607; DB 2; Length 239;
Matches 117; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGOSPOLLIYLGNSRAGVDPDRFS 60
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 29 LSLPVTLGOPASISCRSSQSLHNSGNYLDWYLOKPGOSPOLLIYKISNRFSGVDPDRFS 88
QY 61 GSGSGTDFTLKISRVEADVGIYCMQTRQTRPTFGQGTKEIKRTVAAPSFIIPPDSDE 120
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 89 GSGAGTDFTLKISRVEADVGIYCMQVSHFPRTFGQGTKEIKRTVAAPSFIIPPDSDE 148
QY 121 OLKSGTASVVCLLNNFYPREAKEHOK 146
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 149 QLKSGTASVVCLLNNFYPREAKVQWK 174

RESULT 5
Q65ZC0 PRELIMINARY; PRT; 219 AA.
ID Q65ZC0
AC Q65ZC0;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chi t I."
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL; Z37499; CA85724.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1
FT NON_TER 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match
Best Local Similarity 69.7%; Score 541; DB 2; Length 219;
Matches 104; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 1 LSLPVTGPEPASISCRSSQSLHNSGNYLDWYLOKPGOSPOLLIYLGNSRAGVDPDRFS 60
DQ |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 9 LSLSVSLGDAQSISCRSSQSLVHTNGTYLHWYLOKPGSLPKLLIYIVNRFSGVDPDRFS 68

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Db 87 SSGGDTFTLTKISRVAEADVGIIYCMOTRQ-TPTFTGQGTKEIKRTVAAPSVFIIPPSDEQ 146
122 LKSGTASVVCLNNFYPREAKEHQK 146
147 LKSGTASVVCLNNFYPREAKVQWK 171

RESULT 12
Q6GMW0 PRELIMINARY; PRT; 235 AA.
ID Q6GMW0
AC Q6GMW0
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IgC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 63.1%; Score 490; DB 2; Length 235;
Best Local Similarity 66.4%; Pred. No. 1.9e-41;
Matches 97; Conservative 19; Mismatches 24; Indels 6; Gaps 2;

QY 2 SLVPTGPBPASISCRSSQSLHNSNGYNDWYLPKQGPQLLIYLGNSRAGVDPFRSG 61
Db 30 TLVSFGERATLSCRASQSI-----SNLAWYQQRPGQAPRLIYICASRVITGIFRFSQ 84

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QY 62 SSGGDTFTLTKISRVAEADVGIIYCMOTRQ-TPTFTGQGTKEIKRTVAAPSVFIIPPSDE 120
Db 85 SSGGTEFTLSISLQSDFAVYFCQYNDWLLYTFGQGTKEIKRTVAAPSVFIIPPSDE 144
QY 121 QKSGTASVVCLNNFYPREAKEHQK 146
Db 145 QKSGTASVVCLNNFYPREAKVQWK 170

RESULT 13
Q7Z473 PRELIMINARY; PRT; 234 AA.
ID Q7Z473
AC Q7Z473
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 63.0%; Score 488.5; DB 2; Length 234;
Best Local Similarity 67.6%; Pred. No. 2.7e-41;
Matches 98; Conservative 12; Mismatches 30; Indels 5; Gaps 1;

QY 2 SLVPTGPBPASISCRSSQSLHNSNGYNDWYLPKQGPQLLIYLGNSRAGVDPFRSG 61
Db 30 SPSASTGDRVTITCRASQSI-----GSYLAWYQQRPGAPQLLIYAAASTLQSGVPSRFSQ 84
QY 62 SSGGDTFTLTKISRVAEADVGIIYCMOTRQ-TPTFTGQGTKEIKRTVAAPSVFIIPPSDEQ 121

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Db      85 SASGTDFTLSICLQSEDFATYYCQYYTYPTWFGQTKVEIKRTVAAPSVFIFPPSDEQ 144
Qy      122 LKSGTASVCLNNFYPREAKEHQK 146
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Db      145 LKSGTASVCLNNFYPREAKVQWK 169
          |||||

RESULT 14
KV2D_HUMAN
ID      KV2D_HUMAN          STANDARD;          PRT;          113 AA.
AC      P01617;
DT      21-JUN-1986 (Rel. 01, Created)
DT      21-JUL-1986 (Rel. 01, Last sequence update)
DE      05-JUL-2004 (Rel. 44, Last annotation update)
ID      IG kappa chain V-II region TEW.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
RN      SEQUENCE (BENCE-JONES PROTEIN TEW).
RX      MEDLINE=741148480; PubMed=4596149;
RA      Putnam F.W., Whitley E.J. Jr., Paul C., Davidson J.N.;
RT      "Amino acid sequence of a kappa Bence Jones protein from a case of
RL      primary amyloidosis."
RL      Biochemistry 12:3763-3780(1973).
[2]
RX      SEQUENCE OF 1-27 (AMYLOID PROTEIN TEW).
RA      MEDLINE=73166638; PubMed=4700495;
RA      Terry W.D., Page D.L., Kimura S., Isobe T., Osseerman E.F.,
RA      Glenner G.G.;
RT      "Structural identity of Bence Jones and amyloid fibril proteins in a
RL      patient with plasma cell dyscrasia and amyloidosis."
RL      J. Clin. Invest. 52:1276-1281(1973).
CC      -1- MISCELLANEOUS: The major amyloid protein appears to be identical
CC      with the Bence Jones protein isolated from the same patient.
CC      -1- MISCELLANEOUS: This protein was isolated from the urine of a
CC      patient with plasma cell dyscrasia and amyloidosis.
CC      -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC      marker.
DR      PR; A90370; K2HUTW.
DR      HSP; Q99M37; I191.
DR      GO; GO:0005576; C:extracellular; NAS.
DR      GO; GO:0003823; F:antigen binding; NAS.
DR      GO; GO:0006955; P:immune response; NAS.
DR      InterPro; IPR007110; IG-like.
DR      InterPro; IPR003596; IG_v.
DR      Pfam; PF00047; Ig; 1.
DR      SMART; SM00406; IGV; 1.
DR      PROSITE; PS50835; IG LIKE; 1.
KW      Amyloid; Bence-Jones protein; Direct protein sequencing;
KW      Immunoglobulin V region.
FT      DOMAIN 1 23
FT      DOMAIN 24 39
FT      DOMAIN 40 54
FT      DOMAIN 55 61
FT      DOMAIN 62 93
FT      DOMAIN 94 102
FT      DOMAIN 103 112
FT      DISULFID 23 93
FT      NON TER 113 113
SQ      SEQUENCE 113 AA; 12316 MW; 0C3C38F81F1843CA CRC64;

Query March 62.1%; Score 482; DB 1; Length 113;
Best Local Similarity 85.7%; Prid. No. 4.9e-41;
Matches 90; Conservative 9; Mismatches 6; Indels 0; Gaps 0

Qy      1 LSLPVTGPEPASISCRSSQLHSGNYLDWYLOKPGOSPOLLIYLGSRASGVDPDRS 60
Db      9 LSLPVTGPEPASISCRSSQLHSGDFYLDWYLOKPGOSPZLLIYALSNRASGVDPDRS 68
Qy      61 GSGSGTDFTLTKISRVEAEDVGIVYCMQTRQTPRTFGQTKVEIKR 105

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Db 148 KSGTASVVCLLNNEYBREAKVOMK 171

Search completed: March 8, 2005, 06:35:45
Job time : 56.2705 secs

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	776	100.0	148	2	AAy34309	Aay34309	Igm antiB
2	723	93.2	238	8	ADL93653	Adl93653	Human CD4
3	722	93.0	238	8	ADL93654	Adl93654	Human CD4
4	720	92.8	239	7	ADe28405	Ade28405	Human ant
5	719	92.7	238	8	ADL93650	Adl93650	Human CD4
6	719	92.7	239	7	ADe28465	Ade28465	Human ant
7	717	92.4	239	7	ADe28521	Human ant	Human ant
8	717	92.4	239	7	ADe28397	Human ant	Human ant
9	716	92.3	238	8	ADL93649	Adl93649	Human CD4
10	716	92.3	239	7	ADe28477	Human ant	Human ant
11	713	91.9	219	8	ADr16817	Adr16817	Human bre
12	709	91.4	239	3	AAy82616	Aay82616	Human PTH
13	709	91.4	239	7	ADe28421	Human ant	Human ant
14	707.5	91.2	237	8	ADL93657	Human CD4	Human CD4
15	707	91.1	219	8	ADH34590	Adh34590	O21 light
16	707	91.1	239	3	AAy82618	Aay82618	Human PTH
17	705	90.9	219	7	ADJ321150	Human int	Human PTH
18	704	90.7	238	8	ADL93652	Human CD4	Human CD4
19	704	90.7	239	7	ADe28461	Human ant	Human ant
20	702	90.5	239	7	ADe28469	Human ant	Human ant
21	697.5	89.9	237	8	ADL93658	Human CD4	Human CD4
22	697.5	89.9	237	8	ADL93651	Human CD4	Human CD4
23	695	89.6	143	2	AAy34313	Igm antiB	Igm antiB
24	692	89.2	239	3	AAy82617	Human PTH	Human PTH
25	691	89.0	239	3	AAy82615	Human PTH	Human PTH

CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a human CD44-binding
CC antibody light chain.
XX
SQ Sequence 238 AA;

Query Match 93.0%; Score 722; DB 8; Length 238;
Best Local Similarity 95.2%; Pred. No. 5.8e-49;
Matches 139; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 LSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGSPOLLIYLGSNRAGVDPDRFS 60
DB 28 LSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGSPOLLIYLGSNRAGVDPDRFS 87
QY 61 GSGSGTDTFLKISRVEADVGIYCMQOTRPTRTGQGTKEIKRTVAAPSFIIPPSPDE 120
DB 88 GSGSGTDTFLKISRVEADVGIYCMQALQTPWTFGQGTKEIKRTVAAPSFIIPPSPDE 147
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146
DB 148 QLKSGTASVCLNNFYPREAKVQWK 173

RESULT 4
ADE28405
ID ADE28405 standard; protein; 239 AA.
XX
AC ADE28405;
XX

DT 29-JAN-2004 (first entry)
XX
DE Human anti-CD40 antibody 7-1-2 variable region light chain protein.
XX
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; variable region light chain; 7-1-2.
XX

OS Homo sapiens.
XX
PN WO2003040170-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036107.
XX
PR 09-NOV-2001; 2001US-0348980P.
XX
PA (PFIZ) PFIZER PROD INC.
PA (ABGE-) ABGENIX INC.
XX
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
DR WPI; 2003-441521/41.
DR N-PSDB; ADE28404.
XX

XX New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX

PS Claim 1; SEQ ID NO 12; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV

CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody variable region light chain protein of the invention.
XX
SQ Sequence 239 AA;

Query Match 92.8%; Score 720; DB 7; Length 239;
Best Local Similarity 94.5%; Pred. No. 8.3e-49;
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 LSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGSPOLLIYLGSNRAGVDPDRFS 60
DB 29 LSLPVTGEPASISCRSSQSLHNSGYNVLDWYLOKPGSPOLLIYLGSNRAGVDPDRFS 88
QY 61 GSGSGTDTFLKISRVEADVGIYCMQOTRPTRTGQGTKEIKRTVAAPSFIIPPSPDE 120
DB 89 GSGSGTDTFLKISRVEADVGIYCMQALQTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 148
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146
DB 149 QLKSGTASVCLNNFYPREAKVQWK 174

RESULT 5
ADL93650
ID ADL93650 standard; protein; 238 AA.
XX
AC ADL93650;
XX

DT 17-JUN-2004 (first entry)
XX
DE Human CD44-binding antibody light chain HAE-G2-kappa-light SEQ ID NO:145.
XX
KW heavy; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;
KW antinflammatory; immunosuppressive; antiarthritic; antineumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX

OS Homo sapiens.
XX
PN WO2004024750-A2.
XX
PD 25-MAR-2004.
XX

PF 15-SEP-2003; 2003WO-US029318.
XX
PR 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Rondon IJ, Edge A, Baribault Kent R;
XX
DR WPI; 2004-270003/25.
XX

XX New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX

PS Disclosure; SEQ ID NO 145; 128pp; English.
XX
CC The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CDR3 of the LC variable domain sequence. A protein of the invention has
CC cytostatic, antinflammatory, immunosuppressive, antiarthritic,
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity.

CC antibody mutant variable region light chain protein of the invention.
XX NOTE: this sequence appears to have an incorrect SEQ ID NO.
SQ Sequence 239 AA;
Query Match 92.4%; Score 717; DB 7; Length 239;
Best Local Similarity 95.2%; Pred. NO. 1.4e-48;
Matches 139; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLPKPGQSPQLLYLGSNRASGVDPDRFS 60
DB 29 LSLPVTGEPASISCRSSQSLPGNGYLDWYLPKPGQSPQLLYLGSNRASGVDPDRFS 88
QY 61 GSGSGTDTFTLKISRVEAEDVGIYYCMQTRPTFGQGTKEIKRTVAAPSFIIPPDSDE 120
DB 89 GSGSGTDTFTLKISRVEAEDVGIYYCMQALQTPRTFGQGTKEIKRTVAAPSFIIPPDSDE 148
QY 121 QLKSGTASVVCLLNNFYPREAKEHOK 146
DB 149 QLKSGTASVVCLLNNFYPREAKVQWK 174
RESULT 8
ADE28397
ID ADE28397 standard; protein; 239 AA.
XX
AC ADE28397;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human anti-CD40 antibody 3-1-1 variable region light chain protein.
XX
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; variable region light chain; 3-1-1.
XX
OS Homo sapiens.
XX
PN WO2003040170-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036107.
XX
PR 09-NOV-2001; 2001US-0348980P.
XX
PA (PRIZ) PRIZER PROD INC.
PA (ABGE-) ABGENIX INC.
XX
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
PI WPI; 2003-441521/41.
DR N-PSDB; ADE28396.
XX
PT New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX
PS Claim 1; SEQ ID NO 4; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody variable region light chain protein of the invention.

XX SQ Sequence 239 AA;
Query Match 92.4%; Score 717; DB 7; Length 239;
Best Local Similarity 93.8%; Pred. NO. 1.4e-48;
Matches 137; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLPKPGQSPQLLYLGSNRASGVDPDRFS 60
DB 29 LSLPVTGEPASISCRSSQSLLYSNGYNFLDWYLPKPGQSPQLLYLGSNRASGVDPDRFS 88
QY 61 GSGSGTDTFTLKISRVEAEDVGIYYCMQTRPTFGQGTKEIKRTVAAPSFIIPPDSDE 120
DB 89 GSGSGTDTFTLKISRLEAEDVGYYCMQALQTPRTFGQGTKEIKRTVAAPSFIIPPDSDE 148
QY 121 QLKSGTASVVCLLNNFYPREAKEHOK 146
DB 149 QLKSGTASVVCLLNNFYPREAKVQWK 174
RESULT 9
ADL93649
ID ADL93649 standard; protein; 238 AA.
XX
AC ADL93649;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CD44-binding antibody light chain HAB-A3-kappa-light SEQ ID NO:144.
XX
KW human; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;
KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX
OS Homo sapiens.
XX
PN WO2004024750-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029318.
XX
PR 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Rondon IJ, Edge A, Baribault Kent R;
XX
DR WPI; 2004-270003/25.
XX
PT New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX
PS Disclosure; SEQ ID NO 144; 128pp; English.
XX
CC The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CDR3 of the LC variable domain sequence. A protein of the invention has
CC cytostatic, antiinflammatory, immunosuppressive, antirheumatic,
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or

CC metastatic cancer. The present sequence represents a human CD44-binding
CC antibody light chain.
XX
SQ Sequence 238 AA;

Query Match 92.3%; Score 716; DB 8; Length 238;
Best Local Similarity 94.5%; Pred. No. 1.7e-48;
Matches 138; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

Qy 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 60
Db 28 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 87

Qy 61 GSGGTDFTLKISRVEADVGIIYCMQTRPTPTFGQGTKEIKRTVAAPSVFIIPPSDE 120
Db 88 GSGGTDFTLKISRVEADVGIIYCMQALQTPPTFGGTRKVEIKRTVAAPSVFIIPPSDE 147

Qy 121 QLKSGTASVCLNNFYPREAKHQK 146
Db 148 QLKSGTASVCLNNFYPREAKVQWK 173

RESULT 10
ADE28477
ID ADE28477 standard; protein; 239 AA.
XX
AC ADE28477;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human anti-CD40 antibody 24-2-1 variable region light chain protein.
XX
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; variable region light chain; 24-2-1.
XX
OS Homo sapiens.
XX
FN WO2003040170-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036107.
XX
PR 09-NOV-2001; 2001US-0348980P.
XX
PA (PFIZ) PFIZER PROD INC.
PA (ABGE-) ABGENIX INC.
XX
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
DR WPI; 2003-441521/41.
DR N-PSDB; ADE28476.
XX
PS New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX
PS Claim 1; SEQ ID NO 84; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody variable region light chain protein of the invention.

XX
SQ Sequence 239 AA;

Query Match 92.3%; Score 716; DB 7; Length 239;
Best Local Similarity 97.2%; Pred. No. 1.7e-48;
Matches 138; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 60
Db 29 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 88

Qy 61 GSGGTDFTLKISRVEADVGIIYCMQTRPTPTFGQGTKEIKRTVAAPSVFIIPPSDE 120
Db 89 GSGGTDFTLKISRVEADVGIIYCMQALQTPRTFGQGTKEIKRTVAAPSVFIIPPSDE 148

Qy 121 QLKSGTASVCLNNFYPREAK 142
Db 149 QLKSGTASVCLNNFYPREAK 170

RESULT 11
ADRI6817
ID ADRI6817 standard; protein; 219 AA.
XX
AC ADRI6817;
XX
DT 21-OCT-2004 (first entry)
XX
DE Human breast cancer-specific antibody Fab fragment, Fab14.6.19 #2.
XX
KW Breast cancer; diagnosis; therapy; human; antibody; Fab 14.6.19.
XX
OS Homo sapiens.
XX
FN US2004151724-A1.
XX
PD 05-AUG-2004.
XX
PF 30-OCT-2003; 2003US-00698041.
XX
PR 31-OCT-2002; 2002US-0423052P.
XX
PA (CORO/) CORONELLA-WOOD J.
XX
PI Coronella-Wood J;
XX
DR WPI; 2004-570704/55.
DR N-PSDB; ADRI6814.
XX
PT New isolated polynucleotides encoding breast cancer-specific antibody Fab
PT fragments 14.6.19 and 14.6.20, useful as clinical reagents for diagnosing
PT or treating breast cancer.
XX
PS Claim 8; SEQ ID NO 4; 36pp; English.
XX
CC The invention provides a breast cancer-specific antibody fragment
CC polynucleotide and its corresponding polypeptide. The invention is useful
CC as clinical reagents for the diagnosis and therapy of breast cancer. The
CC present sequence is human breast cancer-specific antibody Fab fragment,
CC Fab14.6.19.
XX
SQ Sequence 219 AA;

Query Match 91.9%; Score 713; DB 8; Length 219;
Best Local Similarity 93.2%; Pred. No. 2.7e-48;
Matches 136; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 60
Db 9 LSLPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 68

Qy 61 GSGGTDFTLKISRVEADVGIIYCMQTRPTPTFGQGTKEIKRTVAAPSVFIIPPSDE 120

	Query Match	91.4%; Score 709; DB 3; Length 239;
	Best Local Similarity	93.2%; Pred. No. 6.le-48;
	Matches 136; Conservative	3; Mismatches 7; Indels 0; Gaps 0;
QY	1 LSLPVTGPGEPASISCRSSOSLLHSNGVNYLDWYLKPGSGQLLIYLGSNRASGVDPDRFS	60
DB	LSLPVTGPGEPASISCRSSOSLLHSNGVNYLDWFLKPGGSQPLLIIYLGSNRASGVDPDRFS	88
QY	61 GSGSGTDFTLKISRVEAEDVGIYYCMTQTPTFGGTKEIKRTVAAPSVFIFPPSDE	120
DB	GSGSGTDFTLKISRVEAEDGVVYYCMQALQTPTTFGGTKVDIKRTVAAPSFIIPPSDE	148
QY	121 QLKSGETASVVCLLNFPYREAKHOK	146
DB	QLKSGETASVVCLLNFPYREAKVQWK	174
RESULT 13		
ADE28421	ID ADE28421 standard; protein; 239 AA.	
XX AC	ADB28421;	
XX XX	29-JAN-2004 (first entry)	
DT XX	Human anti-CD40 antibody 15-1-1 variable region light chain protein.	
DE XX	anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;	
KW KW	immunostimulant; anti-HIV; hyperproliferative; cancer; viral;	
KW KW	bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;	
KW KW	human; variable region light chain; 15-1-1.	
XX OS	Homo sapiens.	
XX XX	WO2003040170-A2.	
PN XX	15-MAY-2003.	
PD XX	08-NOV-2002; 2002WO-US036107.	
PX XX	09-NOV-2001; 2001US-0348980P.	
PR XX	(PFIZ) PFIZER PROD INC.	
PA PA	(ABGE-) ABGENIX INC.	
XX PI	Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;	
XX DR	WPI; 2003-441521/41.	
XX N-	PSDE; ADE28420.	
PT PT	New chimeric or human monoclonal antibody or its antigen-binding portion	
PT PT	that specifically binds to and activates human CD40, useful for enhancing	
PT PT	an immune response in a human, or treating cancer, HIV, neutropenia or	
XX XX	viral infections.	
PS PS	Claim 1; SEQ ID NO 28; 177pp; English.	
XX CC	The invention relates to a novel chimeric or human monoclonal antibody or	
CC CC	its antigen-binding portion that specifically binds to and activates	
CC CC	human CD40. The anti-CD40 antibody of the invention demonstrates	
CC CC	cytostatic, virucide, antibacterial, immunostimulant and anti-HIV	
CC CC	activities and may be useful for treating a hyperproliferative disorder	
CC CC	such as cancer, viral and bacterial infection or genetic, primary or	
CC CC	combined immunodeficiency conditions including neutropenia or HIV	
CC CC	infection. The anti-CD40 antibodies may also be useful for detecting CD40	
CC CC	in a biological sample in vitro or in vivo, as well as during gene	
CC CC	therapy procedures. The current sequence is that of the human anti-CD40	
XX XX	antibody variable region light chain protein of the invention.	
SQ	Sequence 239 AA;	
Query Match	91.4%; Score 709; DB 7; Length 239;	
Best Local Similarity	92.5%; Pred. No. 6.le-48;	

CC disorder or disease such as leukaemias, neoplasm, bile duct carcinoma,
CC bladder carcinoma, viral disorder or disease associated with severe acute
CC respiratory syndrome (SARS), herpes simplex virus (HSV), hepatitis B
CC virus (HBV), HIV and bacterial disorder or disease associated with
CC Mycobacterium tuberculosis, Pseudomonas aeruginosa and Vibrio cholerae.
XX
SQ Sequence 219 AA;

Query Match 91.1%; Score 707; DB 8; Length 219;
Best Local Similarity 92.5%; Pred. No. 8e-48;
Matches 135; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
Qy 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPOLLIYLGNSRAGVPPDRFS 60
Db :|||||
Qy 9 VSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPOLLIYLGNSRAGVPPDRFS 68
Db :|||||
Qy 61 GSGSGTDTLTKISRVEADVGIIYCMQTRQTPRTFGQTKVEIKRTVAAPSVFIPPPSDE 120
Db :|||||
Qy 69 GSGSGTDTLTKISRVEADVGIIYCMQTRQTPRTFGQTKVEIKRTVAAPSVFIPPPSDE 128
Db :|||||
Qy 121 QLKSGTASVVCLLNNFYPREAKEHOK 146
Db :|||||
Qy 129 QLKSGTASVVCLLNNFYPREAKVQWK 154
Db :|||||

Search completed: March 8, 2005, 06:17:05
Job time : 69.6168 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 78.5397 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-24

Perfect score: 776

Sequence: 1 LSLPVTGEPASISCRSSQS.....VVCLLNFPYRAKHQKSP 148

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	723	93.2	238	16	US-10-663-244-148 Sequence 148, Appl
2	722	93.0	238	15	US-10-663-244-149 Sequence 149, Appl
3	720	92.8	239	15	US-10-292-088-16 Sequence 16, Appl
4	719	92.7	238	16	US-10-663-244-145 Sequence 145, Appl
5	719	92.7	239	15	US-10-292-088-56 Sequence 56, Appl
6	717	92.4	239	15	US-10-292-088-8 Sequence 8, Appl
7	717	92.4	239	15	US-10-292-088-102 Sequence 102, Appl
8	716	92.3	238	16	US-10-663-244-144 Sequence 144, Appl
9	716	92.3	239	15	US-10-292-088-80 Sequence 80, Appl
10	713	91.9	219	16	US-10-698-041-4 Sequence 4, Appl
11	709	91.4	239	15	US-10-292-088-32 Sequence 32, Appl
12	707.5	91.2	239	16	US-10-663-244-152 Sequence 152, Appl
13	705	90.9	237	10	US-09-972-656-104 Sequence 104, Appl

14	704	90.7	238	16	US-10-663-244-147 Sequence 147, Appl
15	704	90.7	239	15	US-10-292-088-40 Sequence 40, Appl
16	702	90.5	239	15	US-10-292-088-64 Sequence 64, Appl
17	697.5	89.9	237	16	US-10-663-244-146 Sequence 146, Appl
18	697.5	89.9	237	16	US-10-663-244-153 Sequence 153, Appl
19	686	88.4	239	15	US-10-108-260A-4028 Sequence 4028, Appl
20	676	87.1	239	10	US-09-922-600A-8 Sequence 8, Appl
21	676	87.1	239	10	US-09-924-340-8 Sequence 8, Appl
22	676	87.1	239	10	US-09-992-095B-8 Sequence 8, Appl
23	676	87.1	239	10	US-09-999-570-8 Sequence 8, Appl
24	676	87.1	239	14	US-10-000-489-8 Sequence 8, Appl
25	676	87.1	239	14	US-10-000-986-8 Sequence 8, Appl
26	676	87.1	239	14	US-10-154-678-8 Sequence 8, Appl
27	676	87.1	239	17	US-10-838-854-8 Sequence 8, Appl
28	675	87.0	247	15	US-10-466-164-69 Sequence 69, Appl
29	671	86.5	133	14	US-10-153-382-39 Sequence 39, Appl
30	667.5	86.0	220	9	US-09-822-698A-24 Sequence 24, Appl
31	666	85.8	219	10	US-09-972-656-106 Sequence 106, Appl
32	660	85.1	219	10	US-09-972-656-94 Sequence 94, Appl
33	657	84.7	239	15	US-10-404-724-12 Sequence 12, Appl
34	657	84.7	239	17	US-10-816-276-8 Sequence 8, Appl
35	650	83.8	239	15	US-10-404-724-49 Sequence 49, Appl
36	650	83.8	239	17	US-10-816-276-45 Sequence 45, Appl
37	642	82.7	239	15	US-10-404-724-41 Sequence 41, Appl
38	642	82.7	239	15	US-10-404-724-45 Sequence 45, Appl
39	642	82.7	239	17	US-10-816-276-37 Sequence 37, Appl
40	642	82.7	239	17	US-10-816-276-41 Sequence 41, Appl
41	640	82.5	239	15	US-10-404-724-43 Sequence 43, Appl
42	640	82.5	239	15	US-10-404-724-47 Sequence 47, Appl
43	640	82.5	239	17	US-10-816-276-39 Sequence 39, Appl
44	640	82.5	239	17	US-10-816-276-43 Sequence 43, Appl
45	632	81.4	239	15	US-10-404-724-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-10-663-244-148
; Sequence 148, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-148

Query Match	93.2%	Score 723;	DB 16;	Length 238;
Best Local Similarity	95.2%	Pred. No. 1.1e-49;		
Matches 139;	Conservative 1;	Mismatches 6;	Indels 0;	Gaps 0;
Qy	1	LSLPVTGEPASISCRSSQSLHNSGNYLDWYKPGQSPOLLIYLGNSRAGVDPDRFS	60	
Db	28	LSLPVTGEPASISCRSSQSLHNSGNYLDWYKPGQSPOLLIYLGNSRAGVDPDRFS	87	
Qy	61	GGSGTDFTLKLSRVEADVGIIYCMQRTQRTTQCGTKVEIKRTVAAPSVFIIPPSDE	120	

Db 88 GSGSGTDFTLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 147
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146
Db 148 QLKSGTASVCLNNFYPREAKVQWK 173

RESULT 2

US-10-663-244-149
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149

Query Match 93.0%; Score 722; DB 16; Length 238;
Best Local Similarity 95.2%; Pred. No. 1.4e-49;
Matches 139; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRAGVDPDRFS 60
Db 28 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRAGVDPDRFS 87
QY 61 GSGSGTDFTLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 120
Db 88 GSGSGTDFTLKISRVEADVGVYCMQALQTPWTFTGGTKVEIKRTVAAPSVFIPPPSDE 147
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146
Db 148 QLKSGTASVCLNNFYPREAKVQWK 173

RESULT 3

US-10-292-088-16
; Sequence 16, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-16

Query Match 92.8%; Score 720; DB 15; Length 239;
Best Local Similarity 94.5%; Pred. No. 2e-49;
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRAGVDPDRFS 60
Db 29 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRAGVDPDRFS 88
QY 61 GSGSGTDFTLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 120
Db 89 GSGSGTDFTLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 148
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146
Db 149 QLKSGTASVCLNNFYPREAKVQWK 174

RESULT 4

US-10-663-244-145
; Sequence 145, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-145

Query Match 92.7%; Score 719; DB 16; Length 238;
Best Local Similarity 94.5%; Pred. No. 2.4e-49;
Matches 138; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 1 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRAGVDPDRFS 60
Db 28 LSLPVTGEPASISCRSSQSLHSGNYLDWYLOKPGQSPQLLIYLGSNRAGVDPDRFS 87
QY 61 GSGSGTDFTLKISRVEADVGVYCMQALQTPRTFTGGTKVEIKRTVAAPSVFIPPPSDE 120
Db 88 GSGSGTDFTLKISRVEADVGVYCMQALQTPWTFTGGTKVEIKRTVAAPSVFIPPPSDE 147
QY 121 QLKSGTASVCLNNFYPREAKEHOK 146
Db 148 QLKSGTASVCLNNFYPREAKVQWK 173

RESULT 5

US-10-292-088-56
; Sequence 56, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US

```

: CURRENT APPLICATION NUMBER: US/10/292,088
:
: CURRENT FILING DATE: 2003-03-14
:
: PRIOR APPLICATION NUMBER: 60/348,980
:
: PRIOR FILING DATE: 2001-11-09
:
: NUMBER OF SEQ ID NOS: 147
:
: SOFTWARE: Patentin Ver. 2.1
:
: SEQ ID NO 56
:
: LENGTH: 239
:
: TYPE: PRT
:
: ORGANISM: Homo sapiens
:
: US-10-292-088-56

```

Query Match	92.7%	Score 719;	DB 15;	Length 239;
Best Local Similarity	94.5%	Pred. NO. 2.4e-49;		
Matches 138; Conservative	2;	Mismatches 6;	Indels 0;	Gaps 0;

Qy	1	L	S	L	P	V	T	P	G	E	P	A	S	I	C	R	S	S	O	S	L	L	H	N	G	Y	N	L	D	W	Y	L	O	K	F	G	Q	S	P	O	L	L	I	Y	L	G	S	N	R	A	S	G	V	P	D	R	S	60	
Db	29	L	S	L	P	V	T	P	G	E	P	A	S	I	C	R	S	S	O	S	L	L	H	N	G	Y	N	L	D	W	Y	L	O	K	F	G	Q	S	P	H	L	L	I	Y	L	G	S	N	R	A	S	G	V	P	D	R	S	88	
Qy	61	G	S	G	S	G	T	D	F	T	L	K	S	R	V	E	A	E	D	V	G	I	Y	C	M	O	T	R	P	T	F	G	O	G	T	K	V	E	I	K	R	T	V	A	A	P	S	V	I	F	P	P	S	D	E	120			
Db	89	G	S	G	S	G	T	D	F	T	L	K	S	R	V	E	A	E	D	V	G	I	Y	C	M	O	A	L	O	T	P	R	T	F	G	O	G	T	K	V	E	I	K	R	T	V	A	A	P	S	V	I	F	P	P	S	D	E	148
Qy	121	Q	L	K	S	G	T	A	S	V	V	C	L	L	N	N	F	P	R	E	A	K	E	H	O	K	146																																
Db	149	Q	L	K	S	G	T	A	S	V	V	C	L	L	N	N	F	P	R	E	A	K	V	O	W	K	174																																

```

RESULT 6
US-10-292-088-8
/ Sequence 8, Application US/10292088
/ Publication No. US2003021100A1
/ GENERAL INFORMATION:
/ APPLICANT: BEDIAN, VAHE
/ APPLICANT: GLADUE, RONALD P.
/ APPLICANT: CORVALAN, JOSE
/ APPLICANT: JIA, XIAO-CHI
/ APPLICANT: FENG, XIAO
/ TITLE OF INVENTION: ANTIBODIES TO CD40
/ FILE REFERENCE: ABX-PP/3 US
/ CURRENT APPLICATION NUMBER: US/10/292,088
/ CURRENT FILING DATE: 2003-03-14
/ PRIOR APPLICATION NUMBER: 60/348,980
/ PRIOR FILING DATE: 2001-11-09
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 239
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-292-088-8

```

Query Match 92.4%; Score 717; DB 15; Length 239;
Best Local Similarity 93.8%; Pred. NO. 3.4e-49;
Matches 137; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

	QY	1 LSLPVTGPBPASISCRSSQSLLHNGNYNLDWYLQKPGQPQLLIYYLGSNRASGVDPDRS	60
	Dd	29 LSLPVTGPBPASISCRSSQSLLYSGYNFLNDWYLQKPGQPQLLIYYLGSNRASGVDPDRS	88
	QY	61 GSGGTDFTLKLSRVEAEDVGIYCMOTQTPRTFGGTKEIKRTVAAPSVFIPPPSD	120
	Dd	89 GSGGTDFTLKLSRLAEADVGYICMQALQPTPTFGGTKEIKRTVAAPSVFIPPPSD	148
	QY	121 QLKSGTASVVCLLNFFYPRAKEHQK	146
	Dd	149 QLKSGTASVVCLLNFFYPREAKVOWK	174

RESULT 7
US-10-292-088-102
: Sequence 102, Application US/10292088

```

; Publication No. US20030211100A1
;
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: CLAVIAN, RONALD P.
; APPLICANT: GRADUS, RONALD P.
; APPLICANT: COLARNE, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
;
; TITLE OF INVENTION: ANTIBODIES
;
; FILE REFERENCE: ABX-PF/3 US
;
; CURRENT APPLICATION NUMBER: US
;
; CURRENT FILING DATE: 2003-03-
;
; PRIOR APPLICATION NUMBER: 60/373
;
; PRIOR FILING DATE: 2001-11-09
;
; NUMBER OF SEQ IDS NOS: 147
;
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 102
;
; LENGTH: 239
;
; TYPE: PRT
;
; ORGANISM: Homo sapiens
;
; US-10-292-088-102

```

```
Query Match          92.4%; Score 717; DB 15; Length 239;
Best Local Similarity 95.2%; Pred. No. 3.4e-49;
Matches 139; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

[illegible]

```

RESULT 8
US-10-663-244-144
; Sequence 144, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE OF INVENTION: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated
US-10-663-244-144

```

```
Query Match          92.3%; Score 716; DB 16; Length 238;
Best Local Similarity 94.5%; Pred. NO. 4.1e-49;
Matches 138; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

[illegible]


```

; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-152

Query Match          91.2%; Score 707.5; DB 16; Length 237;
Best Local Similarity 94.5%; Pred. No. 1.9e-48;
Matches 137; Conservative 2; Mismatches 5; Indels 1; Gaps 1;

QY 2 SLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 61
Db 29 SLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 88

QY 62 GSGSGTDFTLKISRVEAEDVGIIYCMQTRPTFTFGQGTKEIKRTVAAPSVFIIPPSPDE 121
Db 89 GSGSGTDFTLKINRVEAEDVGIIYCMQALQTP-TFGQGTKEIKRTVAAPSVFIIPPSPDE 147

QY 122 LKSGTASVVCLLNNFYPREAKEHOK 146
Db 148 LKSGTASVVCLLNNFYPREAKVQWK 172

RESULT 13
US-09-972-656-104
; Sequence 104, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE OF INVENTION: Neutralizing Activity
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 104
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-104

Query Match          90.9%; Score 705; DB 10; Length 219;
Best Local Similarity 91.8%; Pred. No. 2.8e-48;
Matches 134; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 LSLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 60
Db 9 LSLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRAPGVDPDRFS 68

QY 61 GSGSGTDFTLKISRVEAEDVGIIYCMQTRPTFTFGQGTKEIKRTVAAPSVFIIPPSPDE 120
Db 69 GSGSGTDFTLKISRVEADVGIIYCMQALQTP-TFTFGQGTKEIKRTVAAPSVFIIPPSPDE 128

QY 121 QKSGTASVVCLLNNFYPREAKEHOK 146
Db 129 QKSGTASVVCLLNNFYPREAKVQWK 154

RESULT 14
US-10-663-244-147
; Sequence 147, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 Ligands
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
```

```

; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-147

Query Match          90.7%; Score 704; DB 16; Length 238;
Best Local Similarity 93.2%; Pred. No. 3.6e-48;
Matches 136; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 1 LSLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 60
Db 28 LSLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 87

QY 61 GSGSGTDFTLKISRVEAEDVGIIYCMQTRPTFTFGQGTKEIKRTVAAPSVFIIPPSPDE 120
Db 88 GSGSGTDFTLKISRVEAEDVGIIYCMQALQTP-TFTFGQGTKEIKRTVAAPSVFIIPPSPDE 147

QY 121 QKSGTASVVCLLNNFYPREAKEHOK 146
Db 148 QKSGTASVVCLLNNFYPREAKVQWK 173

RESULT 15
US-10-292-088-40
; Sequence 40, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 40
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-40

Query Match          90.7%; Score 704; DB 15; Length 239;
Best Local Similarity 92.5%; Pred. No. 3.7e-48;
Matches 135; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 1 LSLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 60
Db 29 LSLPTVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSNRASGVDPDRFS 88

QY 61 GSGSGTDFTLKISRVEAEDVGIIYCMQTRPTFTFGQGTKEIKRTVAAPSVFIIPPSPDE 120
Db 89 GSGSGTDFTLKISRVEAEDVGIIYCMQVLTQPTFTFGTGTVDIKRTVAAPSVFIIPPSPDE 148

QY 121 QKSGTASVVCLLNNFYPREAKEHOK 146
Db 149 QKSGTASVVCLLNNFYPREAKVQWK 174

Search completed: March 8, 2005, 07:05:48
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Job time : 79.5397 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.2736 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-24

Perfect score: 776

Sequence: 1 LSLPVTGPASISCRSSQS.....VVCLLNFPYREAKEHQSP 148

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/aaa/5A-COMB.pep.*
- 2: /cgn2_6/prodata/1/aaa/5B-COMB.pep.*
- 3: /cgn2_6/prodata/1/aaa/6A-COMB.pep.*
- 4: /cgn2_6/prodata/1/aaa/6B-COMB.pep.*
- 5: /cgn2_6/prodata/1/aaa/PCTUS-COMB.pep.*
- 6: /cgn2_6/prodata/1/aaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	676	87.1	239	US-10-000-489-8	Sequence 8, Appli
2	671	86.5	133	US-09-472-087-26	Sequence 26, Appl
3	671	86.5	133	US-09-472-087-116	Sequence 116, App
4	621	80.0	239	US-08-487-550-6	Sequence 6, Appli
5	621	80.0	239	US-09-526-098-6	Sequence 6, Appli
6	621	80.0	239	US-09-383-916-6	Sequence 6, Appli
7	609	78.5	238	US-09-698-705-10	Sequence 10, Appl
8	591	76.2	139	US-09-472-087-25	Sequence 25, Appl
9	591	76.2	139	US-09-472-087-114	Sequence 114, App
10	585	75.4	218	US-09-698-705-12	Sequence 12, Appl
11	585	75.4	242	US-08-398-613A-56	Sequence 56, Appl
12	585	75.4	242	US-08-398-612A-56	Sequence 56, Appl
13	585	75.4	242	US-08-398-611A-56	Sequence 56, Appl
14	585	75.4	242	US-08-491-334A-56	Sequence 56, Appl
15	585	75.4	242	US-09-027-449-42	Sequence 42, Appl
16	585	75.4	242	US-08-804-444A-42	Sequence 42, Appl
17	585	75.4	242	US-09-026-985-42	Sequence 42, Appl
18	585	75.4	242	US-09-121-952A-42	Sequence 42, Appl
19	585	75.4	242	US-09-234-340A-42	Sequence 42, Appl
20	557	71.8	238	US-09-192-545-4	Sequence 4, Appli
21	550	70.9	173	PCR-US91-02942-3	Sequence 3, Appli
22	550	70.9	173	PCR-US91-02946-3	Sequence 3, Appli
23	548	70.6	222	US-09-479-614-26	Sequence 26, Appl
24	548	70.6	242	US-09-479-614-20	Sequence 20, Appl
25	547	70.5	216	US-09-254-180C-182	Sequence 182, App
26	546	70.4	216	US-09-254-180C-132	Sequence 132, App
27	546	70.4	216	US-09-254-180C-183	Sequence 183, App

ALIGNMENTS

RESULT 1

US-10-000-489-8

; Sequence 8, Application US/10000489

; Patent No. 6794363

; GENERAL INFORMATION:

; APPLICANT: Benjanin, Stephane

; APPLICANT: Tanaka, Hiroaki

; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF

; FILE REFERENCE: 91.US6.DIV

; CURRENT APPLICATION NUMBER: US/10/000,489

; CURRENT FILING DATE: 2001-11-14

; PRIOR APPLICATION NUMBER: US 09/924,340

; PRIOR FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: PCT/IB01/01715

; PRIOR FILING DATE: 2001-08-06

; PRIOR APPLICATION NUMBER: US 60/305,456

; PRIOR FILING DATE: 2001-07-13

; PRIOR APPLICATION NUMBER: US 60/302,277

; PRIOR FILING DATE: 2001-06-29

; PRIOR APPLICATION NUMBER: US 60/298,698

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: US 60/293,574

; PRIOR FILING DATE: 2001-05-25

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: JPatent

; SEQ ID NO 8

; LENGTH: 239

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: SIGNAL

; LOCATION: 1..20

US-10-000-489-8

Query Match

Best Local Similarity 87.1%; Score 676; DB 4; Length 239;

Matches 131; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

28	545.5	70.3	240	4	US-09-301-593-36	Sequence 36, Appl
29	538.5	69.4	224	4	US-09-456-090A-82	Sequence 82, Appl
30	538.5	69.4	224	4	US-09-456-090A-88	Sequence 88, Appl
31	538.5	69.4	224	4	US-09-456-090A-90	Sequence 90, Appl
32	538.5	69.4	224	4	US-09-453-234-82	Sequence 82, Appl
33	538.5	69.4	224	4	US-09-453-234-88	Sequence 88, Appl
34	538.5	69.4	224	4	US-09-453-234-90	Sequence 90, Appl
35	538	69.3	219	3	US-09-027-449-72	Sequence 72, Appl
36	538	69.3	219	3	US-09-026-985-72	Sequence 72, Appl
37	538	69.3	219	4	US-09-121-952A-72	Sequence 72, Appl
38	538	69.3	219	4	US-09-234-340A-72	Sequence 72, Appl
39	538	69.3	239	4	US-09-627-898B-22	Sequence 22, Appl
40	538	69.3	242	3	US-09-027-449-51	Sequence 51, Appl
41	538	69.3	242	3	US-09-027-449-56	Sequence 56, Appl
42	538	69.3	242	3	US-09-027-449-62	Sequence 62, Appl
43	538	69.3	242	3	US-08-804-444A-51	Sequence 51, Appl
44	538	69.3	242	3	US-08-804-444A-56	Sequence 56, Appl
45	538	69.3	242	3	US-09-026-985-51	Sequence 51, Appl

	QY	7	PGEPAISCRSSQSLLHNSGNYNDWYLOKPGOSPOLLIYLGNRASGVDRFSGSGST	66
	Db	1	PGEPAISCRSSQSLLHNSGNYNDWYLOKPGOSPOLLIYLGNRASGVDRFSGSGST	60
	QY	67	DFTLKISRVEADVGIYYCMQTROTPTFTGGTKVEIKRTVAAPSVFIFFPSDEQLKSGT	126
	Db	61	DFTLKISRVEADVGVVYCMQALOTPLTFGGTKVEIKRTVAAPSVFIFFPSDEQLKSGT	120
	QY	127	ASVVCLLNFPYR 139	
	Db	121	ASVVCLLNFPYR 133	
			RESULT 4	
			US-08-487-550-6	
			; Sequence 6, Application US/08487550	
			; Patent No. 6113898	
			; GENERAL INFORMATION:	
			; APPLICANT: Anderson, Darrell R.	
			; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC	
			; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,	
			; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS	
			; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"	
			; NUMBER OF SEQUENCES: 12	
			; CORRESPONDENCE ADDRESS:	
			; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS	
			; STREET: 699 Prince Street	
			; CITY: Alexandria	
			; STATE: VA	
			; COUNTRY: USA	
			; ZIP: 22314	
			; COMPUTER READABLE FORM:	
			; MEDIUM TYPE: Floppy disk	
			; COMPUTER: IBM PC compatible	
			; OPERATING SYSTEM: PC-DOS/MS-DOS	
			; SOFTWARE: PatentIn Release #1.0, Version #1.30	
			; CURRENT APPLICATION DATA:	
			; APPLICATION NUMBER: US/08/487,550	
			; FILING DATE: 07-JUN-1995	
			; CLASSIFICATION: 435	
			; ATTORNEY/AGENT INFORMATION:	
			; NAME: Teskin, Robin L.	
			; REGISTRATION NUMBER: 35,030	
			; REFERENCE/DOCKET NUMBER: 012712-131	
			; TELECOMMUNICATION INFORMATION:	
			; TELEPHONE: 703-836-6620	
			; TELEFAX: 703-836-2021	
			; INFORMATION FOR SEQ ID NO: 6:	
			; SEQUENCE CHARACTERISTICS:	
			; LENGTH: 239 amino acids	
			; TYPE: amino acid	
			; TOPOLOGY: linear	
			; MOLECULE TYPE: protein	
			US-08-487-550-6	
			Query Match	80.0%; Score 621; DB 3; Length 239;
			Best Local Similarity	82.9%; Pred. No. 2.8e-53;
			Matches 121; Conservative	7; Mismatches 18; Indels 0; Gaps 0;
	QY	1	LSPVTGPEPASISCRSSQSLLHNSGNYNDWYLOKPGOSPOLLIYLGNRASGVDRFSGSGST	60
	Db	29	LSPVTGPEPASISCRSSQSLLHNSGNYNDWYLOKPGOSPOLLIYLGNRASGVDRFSGSGST	88
	QY	61	GSGGTDFTLKISRVEADVGIYYCMQTROTPTFTGGTKVEIKRTVAAPSVFIFFPSDE	120
	Db	89	GSGGTDFTLKISRVEADVGVVYCMQALOTPLTFGGTKVEIKRTVAAPSVFIFFPSDE	148
	QY	121	OLKSGTASVCLLNFPYRPREAKEHQK 146	
	Db	149	OLKSGTASVCLLNFPYRPREAKVQWK 174	

RESULT 6
US-09-383-916-6
; Sequence 6, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; THEREOF,

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RESULT 7
US-09-698-705-10
; Sequence 10, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 10
; LENGTH: 238

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; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-10

Query Match
Best Local Similarity 78.5%; Score 609; DB 4; Length 238;
Matches 118; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 2 LSLPVTGPEASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFS 61
Db 29 SVPVTGPEASISCRSSQSLHNSGNTLYLWFLQRPQSPQLLIYRMSNLASGVDPDRFS 88

Qy 62 GSGGTDFTLKISRVEAEDVGIYCMQTRQTRTFGGGTKEIKRTVAAPSVFIFPPSDEQ 121
Db 89 GSGGTAFTLRISRAEDVGVIYCLQHLEYPYTFGGGTKEIKRTVAAPSVFIFPPSDEQ 148

Qy 122 LKSGTASVVCLLNNFYPREAKEHQK 146
Db 149 LKSGTASVVCLLNNFYPREAKVQWK 173

RESULT 8
US-09-472-087-25
; Sequence 25, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; FILE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-472-087-25

Query Match
Best Local Similarity 76.2%; Score 591; DB 4; Length 139;
Matches 115; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 LSLPVTGPEASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFS 60
Db 2 LSLPVTGPEASISCRSSQSLVSDGNTYLNWFOQRPQSPRLIYKVSNWDSGVDPDRFS 61

Qy 61 GSGGTDFTLKISRVEAEDVGIYCMQTRQTRTFGGGTKEIKRTVAAPSVFIFPPSDE 120
Db 62 GSGGTDFTLKISRVEAEDVGIYCMQSHWPPPTFGGTKEIKRTVAAPSVFIFPPSDE 121

Qy 121 QKSGTASVVCLLNNFYP 138
Db 122 QKSGTASVVCLLNNFYP 139

RESULT 9
US-09-472-087-114
; Sequence 114, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
```

```
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; FILE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 114
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-472-087-114

Query Match
Best Local Similarity 76.2%; Score 591; DB 4; Length 139;
Matches 115; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

Qy 1 LSLPVTGPEASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFS 60
Db 2 LSLPVTGPEASISCRSSQSLVSDGNTYLNWFOQRPQSPRLIYKVSNWDSGVDPDRFS 61

Qy 61 GSGGTDFTLKISRVEAEDVGIYCMQTRQTRTFGGGTKEIKRTVAAPSVFIFPPSDE 120
Db 62 GSGGTDFTLKISRVEAEDVGIYCMQSHWPPPTFGGTKEIKRTVAAPSVFIFPPSDE 121

Qy 121 QKSGTASVVCLLNNFYP 138
Db 122 QKSGTASVVCLLNNFYP 139

RESULT 10
US-09-698-705-12
; Sequence 12, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; FILE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: PL777R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12

Query Match
Best Local Similarity 75.4%; Score 585; DB 4; Length 218;
Matches 115; Conservative 11; Mismatches 20; Indels 0; Gaps 0;

Qy 1 LSLPVTGPEASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFS 60
Db 9 LLSVTIGQPASISCKSSQSLSDGKTYLNWLLQRPQSPKRLIYLVSTLDSGVDPDRFT 68

Qy 61 GSGGTDFTLKISRVEAEDVGIYCMQTRQTRTFGGGTKEIKRTVAAPSVFIFPPSDE 120
Db 69 GSGGTDFTLKISRVEAEDLVGYICWQGHPTFRTFGGTKEIKRTVAAPSVFIFPPSDE 128
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QY 121 QLKSGTASVVCLLNNFYPREAKEHOK 146
      |||||||
Db 129 QLKSGTASVVCLLNNFYPREAKVQWK 154

RESULT 11
US-08-398-613A-56
; Sequence 56, Application US/08398613A
; Patent No. 5677426
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory
; DISORDERS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,613A
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 874P1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1489
; TELEFAX: 415/952-9881
; TOPOLOGY: linear
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-398-613A-56

Query Match 75.4%; Score 585; DB 1; Length 242;
Best Local Similarity 77.4%; Pred. No. 9.9e-50;
Matches 113; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 LSLPVTGPBPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFS 60
      |||||||
Db 32 LSLPVSGLDQASISCRSSQSLVHGIGNTYLLHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFS 91

QY 61 GSGSGTDFTLKISRVEAEDVGIIYCMQTRQTPRTFGQTKVEIKRTVAAPSFIIPPSDE 120
      |||||||
Db 92 GSGSGTDFTLRISRVEAEDGLGYFCQSTHVLFTFGAGTKLEKRAVAAPTFTIIPPSSE 151

QY 121 QLKSGTASVVCLLNNFYPREAKEHOK 146
      |||||||
Db 152 QLKSGTASVVCLLNNFYPREAKVQWK 177

RESULT 12
US-08-398-612A-56
; Sequence 56, Application US/08398612A
; Patent No. 5686070
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
; OF INFLAMMATORY DISORDERS
```

```
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
; TREATMENT OF INFLAMMATORY DISORDERS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,612A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-Mar-1995
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TOPOLOGY: linear
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-398-612A-56

Query Match 75.4%; Score 585; DB 1; Length 242;
Best Local Similarity 77.4%; Pred. No. 9.9e-50;
Matches 113; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 LSLPVTGPBPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFS 60
      |||||||
Db 32 LSLPVSGLDQASISCRSSQSLVHGIGNTYLLHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFS 91

QY 61 GSGSGTDFTLKISRVEAEDVGIIYCMQTRQTPRTFGQTKVEIKRTVAAPSFIIPPSDE 120
      |||||||
Db 92 GSGSGTDFTLRISRVEAEDGLGYFCQSTHVLFTFGAGTKLEKRAVAAPTFTIIPPSSE 151

QY 121 QLKSGTASVVCLLNNFYPREAKEHOK 146
      |||||||
Db 152 QLKSGTASVVCLLNNFYPREAKVQWK 177

RESULT 13
US-08-398-611A-56
; Sequence 56, Application US/08398611A
; Patent No. 5702946
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
; OF INFLAMMATORY DISORDERS
```



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;
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
US-09-027-449-42

Query Match 75.4%; Score 585; DB 3; Length 242;
Best Local Similarity 77.4%; Pred. No. 9.9e-50;
Matches 113; Conservative 12; Mismatches 21; Indels 0; Gaps 0;

QY 1 LSLPVTGPBPASTICRSSQSLHSHNGYNYLDWYLOKPGQSPOLLIYLGSNRASGVDPDRFS 60
   ||||:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||
Db 32 LSLPWSLGDQASICRSSQSLVHGIGNTYLNWYLOKPGQSPKLLIYKVSNRFSGVDPDRFS 91
   |||||:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||
QY 61 GSGSGTDFTLKISRVEAEDVGIIYCMQTRPTFGQGTKEIKRTVAAPSVEFIPPPSDE 120
   |||||:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||
Db 92 GSGSGTDFTLRISRVEAEDGLYFCSQSTHVPLTFGAGTKLELKRAVAAPTVEFIPPPSSE 151
   |||||:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||
QY 121 QLKSGTASVVCCLNNFYPREAKEHOK 146
   |||||:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||
Db 152 QLKSGTASVVCCLNNFYPREAKVQWK 177
   |||||:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||:|:|:|||||||
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Job time : 17.2736 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.0007 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039

Sequence: 1 LVKPSSETLSLTCTVSGGSIS.....SQVLLPSKDVMOGTDEHKVC 197

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	709	68.2	627	2 S14683	Ig mu chain precu
3	569	54.8	592	2 S25705	Ig mu chain - shee
4	544.5	52.4	220	2 A49444	Ig gamma-i heavy c
5	520	50.0	140	2 I37782	Ig variable region
6	520	50.0	143	2 B49028	Ig heavy chain V-I
7	515	49.6	288	2 S29690	Ig heavy chain VDJ
8	507	48.8	130	2 S31690	Ig heavy chain V r
9	491	47.3	155	2 S31511	Ig heavy chain - h
10	489	47.1	155	2 S31512	Ig heavy chain - h
11	486	46.8	147	2 S33519	Ig heavy chain V r
12	484.5	46.6	139	2 S31586	Ig heavy chain V r
13	481.5	46.3	137	2 S31676	Ig heavy chain V r
14	480.5	46.2	130	2 S30534	Ig heavy chain V r
15	479	46.1	140	2 A49045	Ig heavy chain V r
16	471	45.3	121	2 S44113	Ig heavy chain V r
17	471	45.3	139	2 S31696	Ig heavy chain V r
18	469.5	45.2	118	2 S20780	Ig heavy chain V r
19	469.5	45.2	140	2 S78052	Ig heavy chain pre
20	463.5	44.6	568	2 A34891	Ig heavy chain pre
21	463	44.6	116	2 S37456	Ig mu chain - huma
22	462.5	44.5	110	2 S44110	Ig heavy chain V-D
23	460.5	44.3	470	2 S22080	Ig heavy chain pre
24	460	44.3	135	2 S78051	Ig heavy chain pre
25	459.5	44.2	129	2 S44114	Ig heavy chain V r
26	458	44.1	134	2 S54906	Ig heavy chain V r
27	457	44.0	105	2 S44125	Ig lambda chain V
28	457	44.0	109	2 PH1673	Ig heavy chain V r
29	456	43.9	97	2 S26906	Ig heavy chain V r

30	455	43.8	116	2 B26340	Ig heavy chain pre
31	455	43.8	123	2 S30530	Ig heavy chain V r
32	454.5	43.7	126	2 S47010	Ig heavy chain V4.
33	453	43.6	97	2 S12416	Ig heavy chain V r
34	452	43.5	146	2 S09711	Ig heavy chain V r
35	452	43.5	452	1 MHU	Ig mu chain C regi
36	452	43.5	453	2 S37768	Ig mu chain C regi
37	452	43.5	473	1 MHUM	Ig mu chain C regi
38	452	43.5	474	2 S15590	Ig heavy chain - h
39	451.5	43.5	145	2 S78055	Ig heavy chain pre
40	445.5	42.9	118	2 S24443	Ig heavy chain V r
41	444	42.7	118	2 A26340	Ig heavy chain pre
42	441	42.4	146	2 S09710	Ig heavy chain V r
43	439.5	42.3	231	2 PC4155	Ig gamma-2b chain
44	438	42.2	99	2 S12412	Ig heavy chain V r
45	437	42.1	114	2 I72667	cold agglutinin FS

ALIGNMENTS

RESULT 1

B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: B23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: B23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-231 <LEO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F140-209/Domain: immunoglobulin homology <IMW>

Query Match 86.7%; Score 900.5; DB 2; Length 231;
Best Local Similarity 88.9%; Pred. No. 8e-62;
Matches 176; Conservative 5; Mismatches 16; Indels 1; Gaps 1;

Qy	1	LVKPSSETLSLTCTVSGGSIS	YWNWIROPKGLEWIGYIYVSGSTNPNPSLKSRVTIS	60
Db	10	LLKPSSETLSLTGAVYGGSF	SDYVSWIRPPKGLEWIGIHNHSGSTNPNPSLKSRVTIS	69
Qy	61	VDTSKNQPSLKLSSTVTAAD	TAVYVYCAR-DRGVGATGFDYWGQGLTVTVSSGSASAPTLP	119
Db	70	VDTSKNQPSLKLSSTVTAAD	TAVYVYCARPPHDTSGHYWYWGQGLTVTVSSGSASAPTLP	129
Qy	120	LVSCNSPDSSTSSVAVGCLA	QDFLPDSITTFWKYKNNSDISSTRGFPSVLRGGKYAATSQ	179
Db	130	LVSCNSPDSSTSSVAVGCLA	QDFLPDSITTFWKYKNNSDISSTRGFPSVLRGGKYAATSQ	189
Qy	180	VLLPSKDVMOGTDEHKVC	197	
Db	190	VLLPSKDVMOGTDEHVVC	207	

RESULT 2

S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzeig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-827 <PRI>
A:Cross-References: EMBL:X17115; NID:g33450; PIDN:CAA34971.1; PID:g33451


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Eur. J. Immunol. 21, 2355-2363, 1991
A:Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphob
A:Reference number: A49028; MUID:92008140; PMID:1915549
A:Accession: B49028
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-143 <IM>
A:Cross-references: GB:S64473; NID:9236906; PIDN:AAB20012.1; PID:9236907
A:Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines
A>Note: sequence extracted from NCBI backbone (NCBI:64473, NCBI:P:64472)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IM>

Query Match 50.0%; Score 520; DB 2; Length 143;
Best Local Similarity 78.9%; Pred. No. 5.6e-33;
Matches 105; Conservative 3; Mismatches 15; Indels 10; Gaps 2;

QY 1 LVKPBETSLTCTVSGGSISSYYWNIWIRPPGKLEWIGIYYSGSTNPNPSLKSRVTIS 60
DB 11 LVKPBETSLTCAVYGGSGFYWNIWIRPPGKLEWIGIYYSGSTNPNPSLKSRVTIS 70
QY 61 VDTSKNQFSLKSLSSVTAADTAVYICARD-----RGVG-ATGFDYWGQGLTVTVSSG 110
DB 71 VDTSKNQFSLKSLSSVTAADTAVYICARGPIVVVPAWRGRGNDYGMVWGQGLTVTVSSG 130
QY 111 SASAPTLPLVSC 123
DB 131 SRSAPTLPLVSC 143

RESULT 7
S29690
Ig heavy chain VDJ region - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C:Accession: S29690
R:Dammer, P.M.; Bos, N.A.; Kroese, F.G.M.
submitted to the EMBL Data Library, October 1992
A:Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.
A:Reference number: S29690
A:Accession: S29690
A:Molecule type: mRNA
A:Residues: 1-288 <DAM>
A:Cross-references: EMBL:X68782; NID:g56442; PID:g1334294
A:Experimental source: strain D2B
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:12-95/Domain: immunoglobulin homology <IM>

Query Match 49.6%; Score 515; DB 2; Length 289;
Best Local Similarity 49.3%; Pred. No. 2.9e-32;
Matches 99; Conservative 41; Mismatches 53; Indels 8; Gaps 4;

QY 1 LVKPBETSLTCTVSGGSISSYYWNIWIRPPGKLEWIGIYYSGSTNPNPSLKSRVTI 59
DB 8 LVKPGSVKISKASGYTFTDYIMHWVKQRPQGLWIGRIINPANGNTEYAEKFKSRATL 67
QY 60 SVDTSKNQFSLKSLSSVTAADTAVYICARDRGVAT--GFDYWGQGLTVTVSSGSASAPTL 117
DB 68 TADKSNATYMQULSSDTSATYFT-----TGTVPFDYWGQGVWTVSSGSQSPTV 123
QY 118 PFLVSCNSPSPDTSVAVAGLAQDFLPDSITFSWKYKNSDI--SSTRGFPSVLRGKYAA 176
DB 124 PFLVSCSPFLSDENLVAMGLARDFLPSSISFSWNYQNTEVMQGVRTPTTLRTGDKYTA 183
QY 177 TSQVLLPSKDVWGQTDDEHKVC 197
DB 184 TSQVLLSAKNVLEGSDEYLVC 204

RESULT 8
S31690
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31690
R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
A:Reference number: S31585
A:Accession: S31690
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-130 <CU>
A:Cross-references: EMBL:Z14199; NID:g30984; PIDN:CAA78568.1; PID:g30985
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:20-102/Domain: immunoglobulin homology <IM>

Query Match 48.8%; Score 507; DB 2; Length 130;
Best Local Similarity 87.8%; Pred. No. 5e-32;
Matches 101; Conservative 1; Mismatches 7; Indels 6; Gaps 2;

QY 1 LVKPBETSLTCTVSGGSISSYYWNIWIRPPGKLEWIGIYYSGSTNPNPSLKSRVTIS 60
DB 16 LVKPBETSLTCTVSGGSISSYYWNIWIRPPGKLEWIGIYYSGSTNPNPSLKSRVTIS 75
QY 61 VDTSKNQFSLKSLSSVTAADTAVYICARDGV----GAT--GFDYWGQGLTVTVSS 109
DB 76 VDTSKNQFSLKSLSSVTAADTAVYICARGSVLLWFGELLYYEDYWGQGLTVTVSS 130

RESULT 9
S31511
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31511
R:Chastagner, P.; Demaison, C.; These, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31511
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <CHA>
A:Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:47-129/Domain: immunoglobulin homology <IM>

Query Match 47.3%; Score 491; DB 2; Length 155;
Best Local Similarity 83.2%; Pred. No. 1e-30;
Matches 94; Conservative 5; Mismatches 10; Indels 4; Gaps 1;

QY 1 LVKPBETSLTCTVSGGSISSYYWNIWIRPPGKLEWIGIYYSGSTNPNPSLKSRVTIS 60
DB 43 LVKPBETSLTCTVSGGSISSYYWNIWIRPPGKLEWIGIYYSGSATNPNPSLKSRVTIS 102
QY 61 VDTSKNQFSLKSLSSVTAADTAVYICARDRGVCA---TGFDYWGQGLTVTVSS 109
DB 103 VDTSKNQFSLKSLSSVTAADTAVYICARGGSISSYDYDGMDYWGQGLTVTVSS 155

RESULT 10
S31512
Ig heavy chain - human
C:Species: Homo sapiens (man)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31512
R:Chastagner, P.; Demaison, C.; These, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A:Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A:Reference number: S31509
A:Accession: S31512
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CH>
A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 47.1%; Score 489; DB 2; Length 155;
Best Local Similarity 82.3%; Pred. No. 1.4e-30;
Matches 93; Conservative 6; Mismatches 10; Indels 4; Gaps 1;

Qy 1 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVTIS 60
Db 43 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVTIS 102
Qy 61 VDTSKNQFSLKLSVTAADTAVYICARDRGVGA----TGFDPWGGTTLVTSS 109
Db 103 VDTSKNQFSLKLSVTAADTAVYICARGGSISSVYVYGMVDWGGTTLVTSS 155

RESULT 11
S13519
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S13519
R;Mortari, F.; Ochs, H.D.; Wedgwood, R.J.P.; Schroeder Jr., H.W.
Nucleic Acids Res. 19, 673, 1991
A;Title: Immunoglobulin variable heavy chain cDNA sequence from a patient with X-linked
A;Reference number: S13519; MUID:91187691; PMID:2011536
A;Accession: S13519
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <MOR>
A;Cross-references: EMBL:X56158; NID:g37724; PIDN:CAA39626.1; PID:g37725
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;41-125/Domain: immunoglobulin homology <IMM>

Query Match 46.8%; Score 486; DB 2; Length 147;
Best Local Similarity 88.3%; Pred. No. 2.3e-30;
Matches 98; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

Qy 1 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVT 58
Db 37 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVT 96
Qy 59 ISVDTSKNQFSLKLSVTAADTAVYICARDRGVGAATGPDYWGQGLTIVTSS 109
Db 97 ISVDTSKNQFSLKLSVTAADTAVYICARPLLMFGEFDYWGQGLTIVTSS 147

RESULT 12
S1586
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S1586
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S1586
A;Accession: S1586
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-139 <CUI>
A;Cross-references: EMBL:Z14196; NID:g30978; PIDN:CAA78565.1; PID:g30979
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 46.6%; Score 484.5; DB 2; Length 139;

Best Local Similarity 86.4%; Pred. No. 2.8e-30;
Matches 95; Conservative 4; Mismatches 10; Indels 1; Gaps 1;

Qy 1 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVTIS 60
Db 30 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVTIS 89
Qy 61 VDTSKNQFSLKLSVTAADTAVYICAR--DRGVGATGFDYWGQGLTIVTSS 109
Db 90 VDTSKNQFSLKLSVTAADTAVYICARGGLIRGAFDINGQGTIVTSS 139

RESULT 13
S1676
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S1676
R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the
A;Reference number: S1585
A;Accession: S1676
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-137 <CUI>
A;Cross-references: EMBL:Z14182; NID:g31031; PIDN:CAA78551.1; PID:g31032
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-116/Domain: immunoglobulin homology <IMM>

Query Match 46.3%; Score 481.5; DB 2; Length 137;
Best Local Similarity 87.2%; Pred. No. 4.7e-30;
Matches 95; Conservative 3; Mismatches 10; Indels 1; Gaps 1;

Qy 1 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVTIS 60
Db 30 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVTIS 89
Qy 61 VDTSKNQFSLKLSVTAADTAVYICARDRGVGAATGFDYWGQGLTIVTSS 109
Db 90 VDTSKNQFSLKLSVTAADTAVYICARDAPL-MYGMVDWGGTIVTSS 137

RESULT 14
S30534
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30534
R;Mariette, X.
submitted to the EMBL Data Library, October 1992
A;Reference number: S30520
A;Accession: S30534
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <MAP>
A;Cross-references: EMBL:Z18320
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 46.2%; Score 480.5; DB 2; Length 130;
Best Local Similarity 80.8%; Pred. No. 5.3e-30;
Matches 97; Conservative 5; Mismatches 7; Indels 11; Gaps 2;

Qy 1 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVT 58
Db 11 LVKPSLTLCTCTVSGGSISSYYNNWIROPKGLWIGIYYSGSTNNPNSLKSRVT 70
Qy 59 ISVDTSKNQFSLKLSVTAADTAVYICARDRGVGAATG-----FDYWGQGLTIVTSS 109
Db 71 ISVDTSKNQFSLKLSVTAADTAVYICARDGGFWGYTRNSRAAFDINGQGTIVTSS 130

RESULT

P;34-116/Domain: immunoglobulin homology <IMM>

90 VDTSKNQFSLKLSSTADTAVYCYCARG-GFAATIVESFDYWGQGLTVTVSS 140

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 73.5696 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039

Sequence: 1 LVKPSSETLSLCTVSGSIS.....SQVLLPSKVMQGTDEHKVC 197

Scoring table: BLASTSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_prot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	925.5	89.1	620	2	Q96EY0	Q96EY0 homo sapien
2	892	85.9	595	2	Q8WUX4	Q8WUX4 homo sapien
3	892	85.9	597	2	Q6GMX5	Q6GMX5 homo sapien
4	892	85.9	597	2	Q9BU10	Q9BU10 homo sapien
5	892	85.9	625	2	Q96AA6	Q96AA6 homo sapien
6	886	85.3	597	2	Q9BQ88	Q9BQ88 homo sapien
7	760.5	73.2	613	2	Q8WUK1	Q8WUK1 homo sapien
8	760	73.1	597	2	Q96BB9	Q96BB9 homo sapien
9	759.5	73.1	606	2	Q6GMV2	Q6GMV2 homo sapien
10	614	59.1	465	2	Q6GMX6	Q6GMX6 homo sapien
11	596.5	57.4	476	2	Q6GMX1	Q6GMX1 homo sapien
12	562	54.1	477	2	Q6GMX7	Q6GMX7 homo sapien
13	554.5	53.4	614	2	Q7TWT6	Q7TWT6 mus musculus
14	554	53.3	576	2	Q6P4I8	Q6P4I8 homo sapien
15	553	53.2	478	2	Q7Z379	Q7Z379 homo sapien
16	542	52.2	613	2	Q8VCX7	Q8VCX7 mus musculus
17	541	52.1	496	2	Q96KX8	Q96KX8 homo sapien
18	526.5	50.7	492	2	Q7Z374	Q7Z374 homo sapien
19	518.5	49.9	478	2	Q6NYH3	Q6NYH3 homo sapien
20	512.5	49.3	473	2	Q8TC63	Q8TC63 homo sapien
21	500.5	48.2	150	2	Q95973	Q95973 homo sapien
22	498	47.9	119	2	Q9UL73	Q9UL73 homo sapien
23	494	47.5	479	2	Q9NM22	Q9NM22 mus musculus
24	492	47.4	476	2	Q6MZK7	Q6MZK7 homo sapien
25	462	44.5	139	2	Q86SX2	Q86SX2 homo sapien
26	462	44.5	605	2	Q6GN83	Q6GN83 xenopus lae
27	457.5	44.0	482	2	Q91X92	Q91X92 mus musculus
28	452	43.5	454	1	MUC_HUMAN	P01871 homo sapien
29	434.5	41.8	464	2	Q6MZU6	Q6MZU6 homo sapien
30	433.5	41.7	593	2	Q6INM5	Q6INM5 xenopus lae
31	431.5	41.5	146	1	HV21_HUMAN	P06331 homo sapien

RESULT 1

ID	Q96EY0	PRELIMINARY;	PRT;	620 AA.
AC	Q96EY0;			
DT	01-DEC-2001 (Tremblrel. 19, Created)			
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DE	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	IGHM protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RT	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RA	Strausberg R.;			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC011857; AAH1857.2; -.			
DR	PIR; S15590; S15590.			
DR	HSSP; P01820; 1G7J.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig.C1.			
DR	InterPro; IPR003006; Ig.MHC.			
DR	InterPro; IPR003596; Ig.V.			
DR	Pfam; PF07654; C1-set; 4.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGc1; 4.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 5.			

DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 89.1%; Score 925.5; DB 2; Length 620;
Best Local Similarity 91.4%; Pred. No. 1.2e-73;
Matches 181; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 1 LVKPSSETLSLCTVSGGSISSYWNWIRQPPKGLWIGYIYSGSTNNPNSLKSRTVIS 60
DB 37 LVKPSSETLSLCTVSGGSISSYWNWIRQPPKGLWIGYIYSGSTNNPNSLKSRTVIS 96
QY 61 VDTSKNQPSLKLSSVTAADTAVYYCA--RDRGVGATGFDYWGQGLTVTVSSGSASAPTLPF 119
DB 97 VDTSKNQPSLKLSSVTAADTAVYYCASQPELPTVGLFYWGQGLTVTVSSGSASAPTLPF 156
QY 120 LVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPFSLRGKYAATSQ 179
DB 157 LVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPFSLRGKYAATSQ 216
QY 180 VLLPSKDVMOGTDHVKV 197
DB 217 VLLPSKDVMOGTDHVKV 234

RESULT 2
Q8WUX4
ID Q8WUX4 PRELIMINARY; PRT; 595 AA.
AC Q8WUX4
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR FIP; G34964; G34964.
DR HSP; P01861; 1A0Q.
DR PFam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.

DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Query Match 85.9%; Score 892; DB 2; Length 595;
Best Local Similarity 86.7%; Pred. No. 1.1e-70;
Matches 176; Conservative 3; Mismatches 18; Indels 6; Gaps 2;

QY 1 LVKPSSETLSLCTVSGGSISSYWNWIRQPPKGLWIGYIYSGSTNNPNSLKSRTVIS 60
DB 37 LVKPSSETLSLCTVSGGSISSYWNWIRQPPKGLWIGYIYSGSTNNPNSLKSRTVIS 96
QY 61 VDTSKNQPSLKLSSVTAADTAVYYCA--RDRGVGATGFDYWGQGLTVTVSSGSASA 114
DB 97 VDTSKNQPSLKLSSVTAADTAVYYCA--RDRGVGATGFDYWGQGLTVTVSSGSASA 156
QY 115 PTLFPLVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPFSLRGKY 174
DB 157 PTLFPLVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPFSLRGKY 216
QY 175 AATSOVLLPSKDVMOGTDHVKV 197
DB 217 AATSOVLLPSKDVMOGTDHVKV 239

RESULT 3
Q6GMX5
ID Q6GMX5 PRELIMINARY; PRT; 597 AA.
AC Q6GMX5
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073767; AAH73767.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR PFam; PF07654; Cl-set; 4.

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DR Pfam; PF00047; ig; 4.
DR SMART; SM00409; ig; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR DR PROSITE; PS00835; IG LIKE; 5.
DR DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6ABD85230 CRC64;

Query Match      85.9%; Score 892; DB 2; Length 597;
Best Local Similarity 86.7%; Pred. No. 1.1e-70;
Matches 176; Conservative 3; Mismatches 18; Indels 6; Gaps 2;

QY 1 LVKPSSETLSLCTVSGGSISSYYWNIQPPKGLGWIGIYYISGSTNNPNSLKSRVTIS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 30 LKLPSETLSLTCGVYGGSPGYWNIQPPKGLGWIGIINHSSTNNPNSLKSRVTIS 89
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 VDTSKNQPSLKLSSVTAADTAVYYCAR-----DRGV-GATGPDYWGQGLTVTVSSGSASA 114
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 90 VDTSKKQLSLKLSSVNAADTAVYYCARVITRASPGTDGRYGMVMDVWGQGLTVTVSSGSASA 149
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 115 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGPFPSVLRGGKY 174
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 150 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGPFPSVLRGGKY 209
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 175 AATSOVLLPSKDVMDQGTDEHKVC 197
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 210 AATSOVLLPSKDVMDQGTDEHVVC 232
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
Q9BU10
ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002963; AAH02963.1; -.
DR HSSP; F01861; IADQ.
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DR PIR; S15590; S15590.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBFE CRC64;

Query Match 85.9%; Score 892; DB 2; Length 625;
Best Local Similarity 86.7%; Pred. No. 1.1e-70;
Matches 176; Conservative 3; Mismatches 18; Indels 6; Gaps 2;

QY 1 LVKPESETLSLTCTVSGGSISSYYNNWIROPKGLWIGYIYSGSTNNPNSLKSRVTIS 60
DB 37 LKPESETLSLTCTGVYSGSFGYYNSWIROPKGLWIGIENHSGSTNNPNSLKSRVTIS 96
QY 61 VDTSKNQPSLKLSSVTAADTAIVYCAR-----DRGV-GATGFDYWGQGLTVTVSSGSASA 114
DB 97 VDTSKKQLSLKLSSVNAADTAIVYCARVITRASPGTDGRYGMVWGQGLTVTVSSGSASA 156
QY 115 PTLPLVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSPVLRGKY 174
DB 157 PTLPLVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSPVLRGKY 216
QY 175 AATSOVLPLSKDVMOGTDEHKVC 197
DB 217 AATSOVLPLSKDVMOGTDEHVVC 239

RESULT 6

ID Q9BQ88 PRELIMINARY; PRT; 597 AA.
AC Q9BQ88;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AA06180.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;

Query Match 85.3%; Score 886; DB 2; Length 597;
Best Local Similarity 86.2%; Pred. No. 3.7e-70;
Matches 175; Conservative 3; Mismatches 19; Indels 6; Gaps 2;

QY 1 LVKPESETLSLTCTVSGGSISSYYNNWIROPKGLWIGYIYSGSTNNPNSLKSRVTIS 60
DB 30 LKPESETLSLTCTGVYSGSFGYYNSWIROPKGLWIGIENHSGITNNPNSLKSRVTIS 89
QY 61 VDTSKNQPSLKLSSVTAADTAIVYCAR-----DRGV-GATGFDYWGQGLTVTVSSGSASA 114
DB 90 VDTSKKQLSLKLSSVNAADTAIVYCARVITRASPGTDGRYGMVWGQGLTVTVSSGSASA 149
QY 115 PTLPLVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSPVLRGKY 174
DB 150 PTLPLVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSPVLRGKY 209
QY 175 AATSOVLPLSKDVMOGTDEHKVC 197
DB 210 AATSOVLPLSKDVMOGTDEHVVC 232

RESULT 7

ID Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]


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[2]
SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC020240; RAH20240.1; -.
DR PIR: F36005; F36005.
DR PIR: G36005; G36005.
DR PIR: PH1642; PH1642.
DR PIR: PH1643; PH1643.
DR PIR: PH1645; PH1645.
DR PIR: PH1646; PH1646.
DR PIR: PH0098; PH0098.
DR PIR: PH0120; PH0120.
DR PIR: S15590; S15590.
DR PIR: S31116; S31116.
DR PIR: S31119; S31119.
DR PIR: S70442; S70442.
DR HSP: F01861; LADQ.
DR Pfam: PF07654; Cl-set; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 3.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67295 MW; 60CFP5950671B315 CRC64;

Query Match 73.2%; Score 760.5; DB 2; Length 613;
Best Local Similarity 74.2%; Pred. No. 5.4e-59;
Matches 147; Conservative 15; Mismatches 35; Indels 1; Gaps 1;

QY 1 LVKPSSETLCTVSGGSISSYWNWIRQPGKGLWIGIYYSSTN-YNPSLKSRTVI 59
DB 30 VVQPGSLRLSCAASGFTSFSSYGMHWVRQAPGKGLWVAISYDGSNKYIADSVKGRFTI 89
QY 60 SVDTSKNPSLSSVTAADTAIVYICARDRGVATGDFYWGQGLTVTVSSGSASAPTLPP 119
DB 90 SRDNSKNTLYLQNSLRADTAIVYICAKDWSGVETFDWGQGLTVTVSSGSASAPTLPP 149
QY 120 LVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQ 179
DB 150 LVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQ 209
QY 180 VLLPSKDVMOGTDHVKVC 197
DB 210 VLLPSKDVMOGTDHVVVC 227

RESULT 8
Q36BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]_
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
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RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015760; AAH15760.1; -.
DR PIR: S05271; S05271.
DR PIR: S24260; S24260.
DR HSP: F01861; LADQ.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003597; Ig cl.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF07654; Cl-set; 4.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS00835; IG_LIKE; 5.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 3.
DR PROSITE: PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8E263D9 CRC64;

Query Match 73.1%; Score 760; DB 2; Length 597;
Best Local Similarity 75.4%; Pred. No. 5.8e-59;
Matches 153; Conservative 14; Mismatches 30; Indels 6; Gaps 3;

QY 1 LVKPSSETLCTVSGGSISSYWNWIRQPGKGLWIGIYYS-GSTNPNLSKSRVTI 59
DB 30 LVQPGSLRLSCAASGFTSFSSYGMHWVRQAPGKGLWVAISYDGSNKYIADSVKGRFTI 89
QY 60 SVDTSKNPSLSSVTAADTAIVYICARD-RGVATG----FDYWGQGLTVTVSSGSASA 114
DB 90 SRDNSKNTLYLQNSLRADTAIVYICAKDPRGYSAGNYTRDYWGQGLTVTVSSGSASA 149
QY 115 PTLFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKY 174
DB 150 PTLFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKY 209
QY 175 AATSOVLLPSKDVMOGTDHVKVC 197
DB 210 AATSOVLLPSKDVMOGTDHVVVC 232

RESULT 9
Q6GMV2 PRELIMINARY; PRT; 606 AA.
AC Q6GMV2
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]_
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RC TISSUE=Primary B-Cells;
RC Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073758; AAH73758.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B51114E4C55 CRC64;

Query Match 73.1%; Score 759.5; DB 2; Length 606;
Best Local Similarity 71.7%; Pred. No. 6.6e-59;
Matches 152; Conservative 12; Mismatches 33; Indels 15; Gaps 3;

QY 1 LVKPSLTLCTVSGSGSYSSYNNWIRPPGKGLWIGIYSGS-TYNPPLSKSRVTI 59
DB 30 LVKPGSLRLSCAAGTFTSDYNNWIRQAPGKGLWISYSSSYNYADSVKGRFTI 89
DB 90 SRDANKSLYLQNSLRAEDTAVYICARGGNGIAAGRVVYAEVYVYGVMDVWGQTTV 149
QY 106 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGF 165
DB 150 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGF 209
QY 166 PSVLGGKYAATSQVLLPSKDVWQGTDEHKVC 197
DB 210 PSVLGGKYAATSQVLLPSKDVWQGTDEHKVC 241

RESULT 10
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini, Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RC TISSUE=Primary B-Cells;
RC Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS08335; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; B3A9B7D0FDB1386E CRC64;

Query Match 59.1%; Score 614; DB 2; Length 465;
Best Local Similarity 64.1%; Pred. No. 4.1e-46;
Matches 127; Conservative 20; Mismatches 41; Indels 10; Gaps 6;

QY 1 LVKPSLTLCTVSGSGSYSSYNNWIRPPGKGLWIGIYSGSYNNPPLSKSRVTIS 60
DB 30 LVKPSLTLCTVSGSGSYSSYNNWIRQAPGKGLWIGRIYTSSTYNNPPLSKSRVTMS 89
QY 61 VDTSKNQPSLKLSSVTAADTAVYICARDRGVGTGATGFDYWGQGLTVTVSSGSASAPTLFPL 120
DB 90 VDTSKNQPSLKLSSVTAADTAVYICARGR---FTYFDYWGQGLTVTVSSASTKGPSVPL 146
QY 121 VSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPSVLR-GGKYAATSQ 179
DB 147 APSSKSTSG-GTAAAGCLVKDIFPEPVTWSW-NSGALTSGVHTFPAVLQSSGLYSLSSV 203
QY 180 VLLPSKDVWQGTDEHKVC 197
DB 204 VTFSSSL--GTQTY-IC 218

RESULT 11
Q6GMX1 PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
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RC TISSUE-Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [12]
RP SEQUENCE FROM N.A.
RC TISSUE-Spleen;
RA Strausberg R.;
DR EMBL; BC073773; AAH73773.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABA5C62DDE9D CRC64;

Query Match 57.4%; Score 596.5; DB 2; Length 476;
Best Local Similarity 59.7%; Pred. No. 1.5e-44;
Matches 123; Conservative 26; Mismatches 42; Indels 15; Gaps 7;

QY 1 LVKPSSETLCTVSGSGSISS--YYNWIROPKGLWIGYIYSGSTNYPNLSKSRVT 58
DB 30 LVKPSQTLSTCTVSGSGSISSGGDYNSWIRQPPKGLWIGYIYSGSTNYPNLSKSRVT 89

QY 59 ISVDTSKNQFSLKLSVTAADTAVYICARD-----RGVATGFDYWGQGLTVTVSSGSA 112
DB 90 ISLDTSKNQFSLKMSVTAADTAVFCARAGWGSFRSWAIDGFIWGGTWTWVSSAST 149

QY 113 SAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDIDSTRGFPVLR-G 171
DB 150 KGPSVFPPLAPSSKSTSG-GTAAIGCLVKDYFPPEPVTWSN--NSGALTSGVHTFPVLDSS 206

QY 172 GKVAATSOVLPLSKDVMQGTDEHKV 197
DB 207 GLYSUSSVTVFPSSSL--GTQTY-IC 229

RESULT 12
Q6GMX7 PRELIMINARY; PRT; 477 AA.
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [12]
RP SEQUENCE FROM N.A.
RC TISSUE-Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00047; IG; 3.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CF85 CRC64;

Query Match 54.1%; Score 562; DB 2; Length 477;
Best Local Similarity 60.6%; Pred. No. 1.8e-41;
Matches 120; Conservative 22; Mismatches 38; Indels 18; Gaps 7;

QY 1 LVKPSSETLCTVSGSGSISSYYNWIROPKGLWIGYIYSGSTNYPNLSKSRVTIS 60
DB 30 LVKPSSETLCTVSGSGSISSYYNWIROPKGLWIGYIYSGSTNYPNLSKSRVTLS 89

QY 61 VDTSKNQFSLKLSVTAADTAVYICARDGVGAT---GFDYWGQGLTVTVSSGSAAPTL 117
DB 90 LDTSKNQFSLRLNSVTAADTAVYICAH---GSSWDFAFDYWGQGLTVTVSSASPTSPKV 145

QY 118 PPLVSCNSPDSSTSSVAVGCLAQDFLPD---SITFSWKYKNSDIDSTRGFP--SVLRGG 172
DB 146 PPL-SLSTPD--GNVVVAVCLVQGFPOEPLSVTWSESGQN-----VTARNFPSPQDASGD 199

QY 173 KYAATSOVLPLSKDVMQOG 190
DB 200 LYTSSQTLTPATQCPDG 217

RESULT 13
Q7TMT6 PRELIMINARY; PRT; 614 AA.
ID Q7TMT6
AC Q7TMT6;

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DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE MG60843 protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshitaki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAH53409.1; -.
DR HSSP; P01820; 1G77.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
DR SEQUENCE 614 AA; 67746 MW; 839BAF3B8D124F89 CRC64;

Query Match 53.4%; Score 554.5; DB 2; Length 614;
Best Local Similarity 52.8%; Pred. No. 1.1e-40;
Matches 105; Conservative 39; Mismatches 52; Indels 3; Gaps 3;

Qy 1 LVKPSLTLCTVSGSGSISSYYNNWIRQPPGKLEWIGYIY-YSGSTNYPNPSLKSRTYI 59
Db 30 LVKPCASVKISCKASGYAFSSSMWVQRPGKLEWIGRVYPGDNTYNGKFGKATL 89
Qy 60 SVDTSKNQFSLKLSVTAADTAIVYCARDRGVATGPDYWGQGLTVTVSSGSASAPTLP 119
Db 90 TADKSSSTAYMQLSLTSEDSAVYCARDYG--SSYRFAYWGQGLTVTVSAESQSFPNVP 148
Qy 120 LVSCNPSDTSVAVGCLAQDFLPDSITFSWKYKNNSD-LSSTRGPPSVLRGGKYAATS 178
Db 149 LVSCPSLSDKNLVAMGCLARDLFPSTISFTWYQNNAEVIGIRTFITLRTGGKYLATS 208
Qy 179 QVLLPSKDVMOQGTDEHKVC 197
Db 209 QVLLSPKILEGSDYLVC 227

RESULT 14
Q6P418 PRELIMINARY; PRT; 576 AA.
ID Q6P418
```

```
Q6P418;
AC 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE IGHD protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshitaki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063384; AAH63384.1; -.
DR HSSP; P01820; 1A7N.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00409; Igv; 1.
DR SMART; SM00407; Igc1; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
DR SEQUENCE 576 AA; 63363 MW; FBB97C949D720F1E CRC64;

Query Match 53.3%; Score 554; DB 2; Length 576;
Best Local Similarity 59.9%; Pred. No. 1.1e-40;
Matches 118; Conservative 16; Mismatches 57; Indels 6; Gaps 4;

Qy 1 LVKPSLTLCTVSGSGSISSYYNNWIRQPPGKLEWIGYIYSGSTNYPNPSLKSRTYI 59
Db 37 LVKPSGTLTLCAVSGSGSISSNNWVQRPGKLEWIGEIYHSGSTNYPNPSLKSRTYI 96
Qy 60 SVDTSKNQFSLKLSVTAADTAIVYCARDRGVATGPDYWGQGLTVTVSSGSASAPTLP 119
Db 97 SVDKSKNQFSLKLSVTAADTAIVYCASLGIYIYGMVWGQGLTVTVSSAPTAPDVP 156
Qy 120 LVSCNPSDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAAT-S 178
Db 157 IISGRHPKNSPVVLACLITGYHTSVTVTWYMGTS--QPQRTFPIQRDSYMTSS 214
Qy 179 QVLLPSKDVMOQGTDEHK 195
ID Q6P418
```

Db 215 QLSTPLQWRQG--EYK 229

RESULT 15

Q7Z379 PRELIMINARY; PRT; 478 AA.
AC Q7Z379;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686K04218 (Fragment).
GN Name=DKFZp686K04218;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538066; CAD97996.1; --
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 478 AA; 51620 MW; 4AFCE541F3217CA1 CRC64;

Query Match 53.2%; Score 553; DB 2; Length 478;
Best Local Similarity 58.4%; Pred. NO. 1.1e-40;
Matches 115; Conservative 29; Mismatches 39; Indels 14; Gaps 7;
QY 1 LVKPSRTLSLCTVSGGSISS--YYNWIROPKGLWIGYIYSGSTNYPNPSLKSRVT 58
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 58
29 LVKPSQTLTCTVSGGSISSGSDYFWSWIRQAPGRGLEWNGIYIYSGSTNYPNPSLESRLS 88
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 118
59 ISVDTSKNQFSLKSSVTAADTAVYYCARDRGVGTGPDYWGQGLTVTVSSGSASAPTILF 118
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 147
89 ISIDTSKNQFSLRLNSLTAAATAVYFCARGVGLG-TAFDIWGQGTVTTVSSASPTSPKVF 147
QY |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 173
119 PLVSCENSPSDTSSVAVGCLAQDFLPD---SITFSWKYKNNSDISSTRGFP--SVLRGK 173
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 201
148 PL-SLDSTPQD-GNVVVAQLVQGFPPQEPPLSVTWSESGQN----VTARNFPPSQDASGDL 201
QY 174 YAAATQVLPLPSKDVMOG 190
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 218
202 YTTSSQLTLPATQCPDG 218

Search completed: March 8, 2005, 06:35:46
Job time : 74.5696 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 91.3346 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039

Sequence: 1 LVKPSETLSLCTVSGGIS.....SOVLLPSKDVNQGTDEHKVC 197

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1039	100.0	197	2 AAY34300	Aay34300 IgM antib
2	889.5	85.6	205	2 AAY34299	Aay34299 IgM antib
3	880.5	84.7	190	2 AAY34304	Aay34304 IgM antib
4	854.5	82.2	202	2 AAY34303	Aay34303 IgM antib
5	753.5	72.5	223	2 AAY08598	Aay08598 Anti-huma
6	751	72.3	266	8 ADF69305	Adf69305 Human lun
7	750.5	72.2	596	4 AAM23924	Aam23924 Human EST
8	747.5	71.9	223	8 ADL70773	Adl70773 Anti-TNFA
9	746.5	71.8	588	2 AAW71880	Aaw71880 Anti-huma
10	746.5	71.8	588	3 AAB12917	Aab12917 Anti-huma
11	743	71.5	228	8 ADL70776	Adl70776 Anti-TNFA
12	732.5	70.5	588	2 AAW71881	Aaw71881 Anti-huma
13	732.5	70.5	588	3 AAB12918	Aab12918 Anti-huma
14	730.5	70.3	533	7 ADB65070	Adb65070 Human lmm
15	709	68.2	627	7 ADE597370	Ade597370 Human lmm
16	708.5	68.2	595	7 ADM05427	Adm05427 Human pro
17	702.5	67.6	571	8 ADP84570	Adp84570 Chimeric
18	698	67.2	199	2 AAY34302	Aay34302 IgM antib
19	698	67.2	203	2 AAY34301	Aay34301 IgM antib
20	692.5	66.7	569	8 ADP19330	Adp19330 Chimeric
21	689	66.3	570	8 ADP19329	Adp19329 Chimeric
22	634	61.0	466	7 ADE28419	Ade28419 Human ant
23	633.5	61.0	241	8 ADE584432	Ade584432 Human ant
24	633.5	61.0	241	8 ADE68574	Ade68574 Human ant
25	633	60.9	466	7 ADE28479	Ade28479 Human ant

ALIGNMENTS

RESULT 1

AAY34300

ID AAY34300 standard; protein; 197 AA.

XX AC AAY34300;

XX DT 19-NOV-1999 (first entry)

XX DE IgM antibody CEM 10.1 G10 heavy chain sequence.

XX KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

XX KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

XX KW organ transplant rejection disease; lymphoma; pancreatic disease;

XX KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX PN WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX DR WPI; 1999-540816/45.

XX N-PSDB; AAZ20401.

XX PT New monoclonal antibody, used for treating e.g. graft versus host

XX PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 60; Fig 25; 245pp; English.

XX CC This sequence represents the heavy chain of an antibody of the invention.
XX CC The antibody is a monoclonal antibody (mAb) with an isotype that fixes
XX CC complement and a variable region that binds to the epitope on CD147 bound
XX CC by the IgM mAb ABX-CBL, providing that the antibody is not CBL1. The mAb
XX CC can selectively kill activated T-cells, activated B-cells or resting or
XX CC activated monocytes. The products and methods can be used for treating
XX CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
XX CC versus host disease (GVHD), organ transplant rejection diseases (e.g. blood
XX CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

PS Claim 3; Page 12-13; 22pp; Japanese.

CC This invention describes novel recombinant anti-human TNF-alpha human

CC monoclonal antibody consisting of a heavy (H) chain and a light (L)

CC chain. The recombinant anti-human TNF-alpha human monoclonal antibody can

CC be produced stably in a high purity and in a large amount

XX

SQ Sequence 223 AA;

Query Match 72.5%; Score 753.5; DB 2; Length 223;

Best Local Similarity 74.2%; Pred. No. 8.2e-45;

Matches 147; Conservative 15; Mismatches 33; Indels 3; Gaps 2;

Qy 1 LVKSETLTLCTVSGGSISSYYWNWIRQPPKGLWIGYIYSGSTN-YNPCLKSRVTI 59

Db 11 VVQGRSLRSCASAGFTFSSYGHWHVRQAKGLWAVVSYDGSNKYYADSVKGRFTI 70

Qy 60 SVDTSKQFSLKLSVTAADTAIVYICARDRGVATGFDYWGQGTTLVTVSSGSASAPTLFP 119

Db 71 SRDNSKNTLYLQMSLRAEDTAIVYICAKDS--GDIAFDWQGTMTVTVSSGSASAPTLFP 128

Qy 120 LVSCNSPDSSTSSVAVGCLAQDFLSDITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQ 179

Db 129 LVSCNSPDSSTSSVAVGCLAQDFLSDITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQ 188

Qy 180 VLLPSKDVMOQGTDEHKVC 197

Db 189 VLLPSKDVMOQGTDEHVVC 206

RESULT 6

ADF69305

ID ADF69305 standard; protein; 266 AA.

XX

AC ADF69305;

XX

DT 26-FEB-2004 (first entry)

XX

DE Human lung specific protein sequence SEQ ID NO:62.

XX

XX human; lung specific nucleic acid; lung specific protein; lung cancer;

KW cytostatic; gene therapy.

KW

XX Homo sapiens.

OS

XX WO2003102137-A2.

PN

XX 11-DEC-2003.

PD

XX 30-MAY-2003; 2003WO-US016810.

PF

XX 31-MAY-2002; 2002US-0385301P.

PR

XX (DIAD-) DIADEXUS INC.

PA

XX Chen S, Macina RA, Sun Y, Liu C, Turner LR;

PI

XX WPI; 2004-053457/05.

DR

XX New human lung specific nucleic acid, useful for preparing a composition

XX for diagnosing or treating lung cancer.

PT

XX Claim 11; SEQ ID NO 62; 221pp; English.

PS

XX The present invention describes a human lung specific nucleic acid

CC molecule. Also described: (1) a method for determining the presence of a

CC lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising

CC the nucleic acid molecule; (3) a host cell comprising the vector; (4) a

CC method for producing a polypeptide encoded by the nucleic acid molecule;

CC (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody

CC or its fragment that specifically binds to the polypeptide; (7) a method

CC for determining the presence of a lung specific protein in a sample; (8)

CC a method for diagnosing and monitoring the presence and metastases of

CC lung cancer in a patient; (9) a kit for detecting a risk of cancer or

CC presence of cancer in a patient comprising a means for determining the

CC presence the nucleic acid molecule or polypeptide in a sample of a

CC patient; (10) a method of treating a patient with lung cancer; and (11) a

CC vaccine comprising the polypeptide or the nucleic acid encoding the

CC polypeptide. Human LSNA molecules and related proteins have cytostatic

CC activity, and can be used in gene therapy. They are useful for preparing

CC a composition for diagnosing or treating lung cancer. The present

CC sequence represents a human lung specific protein, which is used in the

CC exemplification of the present invention.

XX

SQ Sequence 266 AA;

Query Match 72.3%; Score 751; DB 8; Length 266;

Best Local Similarity 75.6%; Pred. No. 1.5e-44;

Matches 149; Conservative 15; Mismatches 31; Indels 2; Gaps 2;

Qy 3 KPSTLSLTCTVSGGSISSYYWNWIRQPPKGLWIGYIYSGS-TYNNPCLKSRVTISV 61

Db 24 KPGBSLKISCKSGSYSTSYWIGWVRQMPKGLWEMGIYPGDSITRYSPSQQTISA 83

Qy 62 DTSKNQFSLKLSVTAADTAIVYICARDGV-GATGFDYWGQGTTLVTVSSGSASAPTLPL 120

Db 84 DKSISTAYLOWSSLSKASDTAMYICARPIAVAGHYFYFDYWGQGTTLVTVSSGSASAPTLPL 143

Qy 121 VSCNSPDSSTSSVAVGCLAQDFLSDITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQ 180

Db 144 VSCNSPDSSTSSVAVGCLAQDFLSDITFSWKYKNNSDISSTRGFPSVLRGGKYAATSQ 203

Qy 181 LLPSKDVMOQGTDEHKVC 197

Db 204 LLPSKDVMOQGTDEHVVC 220

RESULT 7

AAM23924

ID AAM23924 standard; protein; 596 AA.

XX

AC AAM23924;

XX

DT 12-OCT-2001 (first entry)

XX

DE Human EST encoded protein SEQ ID NO: 1449.

XX

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;

KW gene therapy; nutrition.

XX

OS Homo sapiens.

XX

XX WO200154477-A2.

PN

XX 02-AUG-2001.

PD

XX 25-JAN-2001; 2001WO-US002687.

PF

XX 25-JAN-2000; 2000US-00491404.

PR

XX 17-JUL-2000; 2000US-00617746.

PR

XX 03-AUG-2000; 2000US-00631451.

PR

XX 15-SEP-2000; 2000US-00663870.

XX

XX (HYSE-) HYSEQ INC.

PA

XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;

PI Cao Y, Drmanac RA, Zhang J, Werhman T;

XX

XX WPI; 2001-476164/51.

DR

XX N-PSDB; AAH98583.

XX

XX Isolated polypeptide for treatment of diseases, diagnostics, raising

XX antibodies and research use.

XX

PS Claim 20; Page 1011-1012; 1275pp; English.

XX The present invention provides the protein and coding sequences of novel

CC proteins from a variety of organisms, including human, dog, cat, horse,

CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea

CC urchin and tomato. These were derived from expressed sequence tags (ESTs)

CC from the organism of interest. They can be used in diagnostics,

CC forensics, gene mapping, identification of mutations, to assess

CC biodiversity and for nutritional purposes. The present sequence is a

CC protein of the invention

XX Sequence 596 AA;

SQ

Query Match 72.2%; Score 750.5; DB 4; Length 596;

Best Local Similarity 73.3%; Pred. No. 3.7e-44;

Matches 148; Conservative 16; Mismatches 33; Indels 5; Gaps 2;

QY 1 LVKPESETLSLCTVSGGSISSVYWNWIRQPPKGLWIGYIYSG-STNYPNLSKSRVTI 59

DB 30 LVQPGSLRLSCASGFTFSSYGMHWVQAPKGLVWVSRINTDGSSTSYADSVKGRFTI 89

QY 60 SVDTSKNQFSLKLSVTAADTAVYYCARDRGVGATG----FDYWGQGLTVTVSSGSASAP 115

DB 90 SRDNAKNTLYLQMSLRAEDTAVYYCARADNCSTSCYKCFDYWGQGLTVTVSSGSASAP 149

QY 116 TLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYA 175

DB 150 TLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYA 209

QY 176 ATSQVLLPSKDVMOQTDEHKVC 197

DB 210 ATSQVLLPSKDVMOQTDEHVC 231

RESULT 8

ADL70773

ID ADL70773 standard; protein; 223 AA.

XX

AC ADL70773;

XX

XX 03-JUN-2004 (first entry)

DT

XX

DE Anti-TNFAlpa antibody VH region, SEQ ID 46.

XX

XX Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;

KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;

KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnery;

KW Antiparkinsonian; Nootropic; Cardiant; Antinaemic; Antiatherosclerotic;

KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;

KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFAlpa;

KW antibody; VH region.

XX

OS Unidentified.

XX

XX WO2004020588-A2.

PN

XX

PD 11-MAR-2004.

XX

PF 28-AUG-2003; 2003WO-US026779.

XX

PR 30-AUG-2002; 2002US-0406977P.

PR 10-MAR-2003; 2003US-00384060.

PR 09-JUL-2003; 2003US-0485404P.

XX

PA (BIOR-) BIOREXIS PHARM CORP.

XX

PI Prior CP, Turner AJ, Sadeghi H;

XX

DR WPI; 2004-239175/22.

XX

PT Novel library containing several fusion proteins each of which comprises

PT first transferrin polypeptide fused to at least one second peptide,

PT useful for screening for transferrin fusion protein having the particular

PT activity.

XX Example 8; SEQ ID NO 46; 243pp; English.

XX The present invention relates to a library (I) of modified fusion

CC proteins of transferrin (Tf) and therapeutic proteins with increased

CC serum half-life or serum stability. Preferred fusion proteins include

CC those modified so that the Tf moiety exhibits no or reduced

CC glycosylation, iron binding and/or Tf receptor binding. The transferrin

CC fusion proteins are useful for treating, preventing or ameliorating

CC disorders or diseases of endocrine system, nervous system, immune system,

CC respiratory system, cardiovascular system, diseases and/or disorders

CC relating to cell proliferation, and/or diseases or disorders relating to

CC blood. The modified fusion proteins are useful in diagnosis, prognosis,

CC prevention and/or treatment of autoimmune disorders; diseases and

CC disorders of haematopoietic cells (e.g., leukaemia, neutropenia, anaemia

CC and thrombocytopenia); allergic reactions such as allergic asthma,

CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and

CC eczema; inflammatory conditions e.g., inflammation associated with

CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,

CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders

CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel

CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders

CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative

CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The

CC fusion protein is also useful as an adjuvant to enhance antibacterial or

CC antifungal immune responses, antiparasitic immune responses, etc. The

CC fusion protein is also useful for treating monoclonal gammopathy of

CC undetermined significance (MGUS), Waldenström's disease, plasmacytomas,

CC adult respiratory distress syndrome, for stimulating wound repair, for

CC preventing or treating infections of joints, bones, skin, etc. The fusion

CC protein is also useful for treating or preventing thrombosis, myocardial

CC infarction, cancers, thrombocytopenia, sickle cell anaemia,

CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,

CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf

CC and a specific example of a SCA that can be fused to Tf is anti-tumour

CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence

XX from an anti-TNFAlpa antibody.

SQ Sequence 223 AA;

Query Match 71.9%; Score 747.5; DB 8; Length 223;

Best Local Similarity 73.7%; Pred. No. 2.1e-44;

Matches 146; Conservative 15; Mismatches 34; Indels 3; Gaps 2;

QY 1 LVKPESETLSLCTVSGGSISSVYWNWIRQPPKGLWIGYIYSGTN-YNPSLKSRTVI 59

DB 11 VVQPCSLRLSCASGFTFSSYGMHWVQAPKGLWVAVISYDGSNKYYADSVKGRFTI 70

QY 60 SVDTSKNQFSLKLSVTAADTAVYYCARDRGVGATGFDYWGQGLTVTVSSGSASAPTLPP 119

DB 71 SRDNSKNTLYLQMSLRAEDTAVYYCAKDS--GDIAFDIWGQGTWTVTVSSGSASAPTLPP 128

QY 120 LVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSO 179

DB 129 LVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSO 188

QY 180 VLLPSKDVMOQTDEHKVC 197

DB 189 VLLPSKDVMOQTDEHVC 206

RESULT 9

AAW71880

ID AAW71880 standard; protein; 588 AA.

XX

AC AAW71880;

XX

DT 18-JAN-1999 (first entry)

XX

DE Anti-human Fas humanised antibody CH11 heavy chain HmuH.

XX

KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;

autoimmune disease; rheumatoid arthritis; therapy; human; antibody engineering.

XX Homo sapiens.
OS
OS Synthetic.

Key	Location/Qualifiers
Peptide	1. .19
Protein	/label= sig_peptide
	20. .588
Region	/label= Mat_protein
	50. .54
Region	/label= CDR1
	/note= "complementa- heavy chain"
	69. .84
	/label= CDR2
Region	/note= "complementa- heavy chain"
	118. .124
	/label= CDR3
	/note= "complementa- heavy chain"

EP866131-A2.

23-SEP-1998.

20-MAR-1998: 98EP-00302113.

21-MAR-1997: 97JP-00067938.

(SANYO) SANKYO CO. LTD.

Serizawa N. Haruyama H. Takahashi T. Nakahara K. Yonehara S.

WPI; 1998-482965/42.

N-PSDB; AAV61363.

PT Production of anti-Fas protein humanised antibodies - for use in inducing
PT apoptosis on Fas expressing cells in the treatment of auto:immune
PT diseases, especially rheumatoid arthritis.

Claim 21: Page 105-107; 187pp; English.

This is the amino acid sequence of a humanised anti-Fas antibody CH11 heavy chain, designated HmuH. HmuH is based on the heavy chain (see AAW71888) of murine anti-human Fas monoclonal antibody CH11. The humanised sequence was designed following selection of donor residues from CH11 to be grafted onto acceptor molecule 21.28'. 2 Heavy chain sequences (see AAW71880-81) have been designed, and each can be used in combination with any of 4 light chain sequences (see AAW71876-79) to provide novel, claimed humanised CH11 IgM antibodies that lack a J chain. These humanised anti-human Fas antibodies are capable of inducing apoptosis in cells expressing Fas (e.g. synoviocytes) and are useful in the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA sequences encoding the humanised antibodies are claimed, as are vectors such as pHMuH5-1 including the HmuH nucleotide sequence (see AAW61363), and host cells such as *Escherichia coli* pHMuH5-1 (FERM BP-5863).

AA
SQ
Sequence 588 AA;

Query Match 71.8%; Score 746.5; DB 2; Length 588;
Best Local Similarity 72.4%; Pred. No. 7e-44;
Matches 142; Conservative 19; Mismatches 30; Indels 5

Qy	3	KPSETLSLCTVGGSGISYWNWIRPPGKGLWIGIY- YGSTWNPSSLKSRTVISV	61
		: : : : : :	
Db	32	KPGASVKVECKASGYTFDYNHWVRAPGGLEWMGIYPYNGTGTGNQKFASKATLV	91
		: : : : : :	
Qy	62	DPSKNQFSLKLASVAADTAIVYCARDRGVGATGFDMVGQTLTVSSSGSASAPTLPPLV	121
		: : : : : :	
Db	92	DNSASTAYWEISLSRSEPTAVYYCAR----SYAMDVMGQTLTVSSSGSASAPTLPPLV	147
		: : : : : :	

	Qy	Db	Qy	Db
122	SCENSPDTSVA	CGCQAQDF	PDPSITFSWKYKNSD	ISSTRGPPSVLRGGKYAATSOVL
148	SCENSPDTSVA	CGCQAQDF	PDPSITFSWKYKNSD	ISSTRGPPSVLRGGKYAATSOVL
182	LPISKDVNMQGT	DEHKVC	197	
208	LPISKDVNMQGT	DEHVVC	223	

RESULT 10
XAP12017

ID AAB12917 standard; protein; 588 AA.

AA AAB12917;
AC

16-NOV-2000 (first entry)

DE Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #86.

AA Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW immunosuppression; autoimmune disease; treatment; rheumatism;
KW anti-Fas antibody.

OS Synthetic.

XX PN JP2000154149-A.

XX PD 06-JUN-2000.

XX
PF 17-SEP-1999: 99JP-00263984

XX
PR 18-SEP-1998: 98JP-00264598-

XX
PA (SANY) SANKYO CO LTD.

XX
DR WPI: 2000-454476/40.

DR N-PSDB; AAA78271.

PT Anti-human Fas humanizing antibody-containing antirheumatic agents.

PS Claim 1; Page 75-77; 109pp; Japanese.

The present invention relates to antirheumatic agents which comprise as active ingredients an immunoglobulin M (IgM) protein. The IgM protein does not include a segment, has apoptosis inducing activity, and consists of a light and heavy chain polypeptide produced synthetically. The agents of the invention exhibit antirheumatic and immunosuppressive activity and can be used to treat autoimmune diseases, especially rheumatism. The IgM molecule used in the invention has human Fas-antigen binding properties. Included in the invention are nucleotide sequences of the IgM light and heavy chains (see AAA78267-A78272) and the corresponding protein sequences (see AAB12913-B12918 and AAB12919), and nucleotide sequences of the humanised anti-human Fas Ig CH11 (see AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also included are anti-human Fas antibody CDR peptides (AAB12902-B12907). Primers specific for the anti-human Fas antibody, light, heavy and kappa chains used in the invention are represented by sequences AAA78213-A78266. Primers used for sequencing the human Ig DNA used in the invention are represented by sequences AAA78277-A78318 and AAA78335-A78337, while humanised anti-Fas Ig DNA sequencing primers are represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in the production of the agent of the invention.

Sequence 588 AA:

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Query Match      71.8%; Score 746.5; DB 3; Length 588;
Best Local Similarity 72.4%; Pred. No. 7e-44;
Matches 142; Conservative 19; Mismatches 30; Indels 5
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FT Region 118..124
FT /label= CDR3
FT /note= "complementarity determining region 3 from CH11
FT heavy chain"
XX
XX
XX EP866131-A2.
XX
XX 23-SEP-1998.
XX
XX 20-MAR-1998; 98EP-00302113.
XX
XX 21-MAR-1997; 97JP-00067938.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;
XX
XX WPI; 1998-482965/42.
XX
XX N-PSDB; AAV61364.
XX
XX Production of anti-Fas protein humanised antibodies - for use in inducing
XX apoptosis on Fas expressing cells in the treatment of auto:immune
XX diseases, especially rheumatoid arthritis.
XX
XX Claim 22; Page 111-113; 187pp; English.
XX
XX This is the amino acid sequence of a humanised anti-Fas antibody CH11
XX heavy chain, designated HmuM. HmuM is based on the heavy chain (see
XX AA771888) of murine anti-human Fas monoclonal antibody CH11. The
XX humanised sequence was designed following selection of donor residues
XX from CH11 to be grafted onto acceptor molecule 21.28'CL. 2 Heavy chain
XX sequences (see AA771880-81) have been designed, and each can be used in
XX combination with any of 4 light chain sequences (see AA771876-79) to
XX provide novel, claimed humanised CH11 IgM antibodies that lack a J chain.
XX These humanised anti-human Fas antibodies are capable of inducing
XX apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in
XX the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA
XX sequences encoding the humanised antibodies are claimed, as are vectors
XX such as pHmuM1-1 including the HmuM nucleotide sequence (see AAV61364),
XX and host cells such as Escherichia coli pHmuM1-1 (FERM BP-5864)
XX
XX Sequence 588 AA;
XX
XX Query Match 70.5%; Score 732.5; DB 2; Length 588;
XX Best Local Similarity 71.4%; Pred. No. 6.6e-43;
XX Matches 140; Conservative 19; Mismatches 32; Indels 5; Gaps 2;
QY 3 KPSETLSLCTVSGGSISYYNNMIRPPGKLEWIGYIY-YSGSTNNPSLKRVTISV 61
Db 32 KPGASVKVCKASGVTFTDYNMHWKQAHGKSLKLEWGMVYIPYNGGTGYNQKFKSKATLTV 91
QY 62 DTSKNQFSLKLSVTAADTAVYICARDRGVATGFDYWGQGLTVTVSSGSASAPFLPLV 121
Db 92 DNSASTAYMELSLRSED TAVYICAR----SYAMDYWGQGLTVTVSSGSASAPFLPLV 147
QY 122 SCENSPDTSVAVGCLAQDFLPDSITFSWKYKXNSDISSTRGPPSVLRGGKYAATSQVL 181
Db 148 SCENSPDTSVAVGCLAQDFLPDSITFSWKYKXNSDISSTRGPPSVLRGGKYAATSQVL 207
QY 182 LPSKDVMOGTDDEHKVC 197
Db 208 LPSKDVMOGTDDEHVVC 223
RESULT 13
AAB12918
ID AAB12918 standard; protein; 588 AA.
XX
XX AAB12918;
XX
XX 16-NOV-2000 (first entry)
XX
XX Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #88.
DE

XX Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW immunosuppression; autoimmune disease; treatment; rheumatism;
KW anti-Fas antibody.
XX
XX Synthetic.
XX OS
XX JP2000154149-A.
XX PN
XX 06-JUN-2000.
XX PD
XX 17-SEP-1999; 99JP-00263984.
XX PF
XX 18-SEP-1998; 98JP-00264598.
XX PR
XX (SANY) SANKYO CO LTD.
XX PA
XX WPI; 2000-454476/40.
XX DR
XX N-PSDB; AAA78272.
XX DR
XX Anti-human Fas humanizing antibody-containing antirheumatic agents.
PT
XX Claim 1; Page 80-81; 109pp; Japanese.
XX PS
XX The present invention relates to antirheumatic agents which comprise as
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC does not include a J segment, has apoptosis inducing activity, and
CC consists of a light and heavy chain polypeptide produced synthetically.
CC The agents of the invention exhibit antirheumatic and immunosuppressive
CC activity and can be used to treat autoimmune diseases, especially
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC binding properties. Included in the invention are nucleotide sequences of
CC the IgM light and heavy chains (see AAA78267-A78272) and the
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC chains used in the invention are represented by sequences AAA78213-
CC A78266. Primers used for sequencing the human Ig DNA used in the
CC invention are represented by sequences AAA78277-A78318 and AAA78335-
CC A78337, while humanised anti-Fas Ig DNA sequencing primers are
CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer
CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in
CC the production of the agent of the invention
XX
XX Sequence 588 AA;
XX
XX Query Match 70.5%; Score 732.5; DB 3; Length 588;
XX Best Local Similarity 71.4%; Pred. No. 6.6e-43;
XX Matches 140; Conservative 19; Mismatches 32; Indels 5; Gaps 2;
QY 3 KPSETLSLCTVSGGSISYYNNMIRPPGKLEWIGYIY-YSGSTNNPSLKRVTISV 61
Db 32 KPGASVKVCKASGVTFTDYNMHWKQAHGKSLKLEWGMVYIPYNGGTGYNQKFKSKATLTV 91
QY 62 DTSKNQFSLKLSVTAADTAVYICARDRGVATGFDYWGQGLTVTVSSGSASAPFLPLV 121
Db 92 DNSASTAYMELSLRSED TAVYICAR----SYAMDYWGQGLTVTVSSGSASAPFLPLV 147
QY 122 SCENSPDTSVAVGCLAQDFLPDSITFSWKYKXNSDISSTRGPPSVLRGGKYAATSQVL 181
Db 148 SCENSPDTSVAVGCLAQDFLPDSITFSWKYKXNSDISSTRGPPSVLRGGKYAATSQVL 207
QY 182 LPSKDVMOGTDDEHKVC 197
Db 208 LPSKDVMOGTDDEHVVC 223
RESULT 14
ADB65070
ID ADB65070 standard; protein; 533 AA.
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Db 32 KPGSSVKVCKASGGTFSSYAISWVRQAPQGQLEWVGIIPIFGTANYAQKFQGRVTITA 91
Qy 62 DTSKNQFSLKLSSVTAADTAVYYCARDRGVGA-----TGFDYWGQGLVTVS 108
Db 92 DESTSTAYMELSSURSEDTAVYYCAKTGILGYPYSSGWYPNSDYIYGGMDVWGQGLTVTVS 151
Qy 109 SGSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSV 168
Db 152 SGSASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSV 211
Qy 169 LRGGKYAATSQVLLPSKDVMOGTDEHKVC 197
Db 212 LRGGKYAATSQVLLPSKDVMOGTDEHVVC 240

Search completed: March 8, 2005, 06:17:07
Job time : 93.3346 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 104.543 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039

Sequence: 1 LVKPSSETLSLTCTVSGSGSIS.....SQVLLPSKDVNQGTDEHKVC 197

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	730.5	70.3	533	15	US-10-104-047-3224
2	709	68.2	627	13	US-10-047-542-47
3	708.5	68.2	595	15	US-10-108-260A-4112
4	634	61.0	466	15	US-10-292-088-30
5	633.5	61.0	241	15	US-10-684-109-71
6	633	60.9	466	15	US-10-292-088-86
7	631	60.7	466	15	US-10-292-088-70
8	626.5	60.3	230	10	US-09-972-656-72
9	625	60.2	179	15	US-10-309-762-171
10	622.5	59.9	241	16	US-10-684-109-106
11	620.5	59.7	239	16	US-10-684-109-100
12	618	59.5	464	15	US-10-292-088-22
13	609	58.6	580	14	US-10-310-719-37

14	607.5	58.5	241	16	US-10-684-109-88	Sequence 88, Appl
15	604.5	58.2	580	14	US-10-310-719-35	Sequence 35, Appl
16	598	57.6	223	10	US-09-972-656-66	Sequence 36, Appl
17	596	57.4	221	10	US-09-972-656-80	Sequence 80, Appl
18	591	56.9	229	10	US-09-972-656-82	Sequence 82, Appl
19	581.5	56.0	173	15	US-10-309-762-173	Sequence 173, App
20	581.5	56.0	235	16	US-10-684-109-112	Sequence 112, App
21	581	55.9	172	14	US-10-153-382-21	Sequence 21, Appl
22	576	55.4	193	15	US-10-264-049-4331	Sequence 4331, Ap
23	576	55.4	229	9	US-09-974-449-37	Sequence 37, Appl
24	573	55.1	250	14	US-10-194-975-110	Sequence 110, App
25	562.5	54.1	243	16	US-10-684-109-94	Sequence 94, Appl
26	556	53.5	487	9	US-09-800-729-145	Sequence 145, App
27	556	53.5	487	11	US-09-833-245-2194	Sequence 2194, Ap
28	547	52.6	467	14	US-10-211-357-8	Sequence 8, Appli
29	547	52.6	467	14	US-10-211-357-10	Sequence 10, Appl
30	547	52.6	467	14	US-10-211-357-12	Sequence 12, Appl
31	544.5	52.4	152	9	US-09-187-693-68	Sequence 68, Appl
32	542.5	52.2	476	9	US-09-758-173-12	Sequence 12, Appl
33	542.5	52.2	476	9	US-09-948-429B-12	Sequence 12, Appl
34	542.5	52.2	476	13	US-10-124-905-12	Sequence 12, Appl
35	542.5	52.2	476	14	US-10-124-807-12	Sequence 12, Appl
36	542.5	52.2	476	14	US-10-291-532-12	Sequence 12, Appl
37	534.5	51.4	118	15	US-10-292-088-109	Sequence 109, App
38	530.5	51.1	220	16	US-10-379-392-114	Sequence 114, App
39	529.5	51.0	220	16	US-10-379-392-167	Sequence 167, App
40	528.5	50.9	220	16	US-10-379-392-113	Sequence 113, App
41	526	50.6	119	14	US-10-125-687-5	Sequence 5, Appli
42	521.5	50.2	122	15	US-10-309-762-24	Sequence 24, Appl
43	521.5	50.2	122	15	US-10-309-762-25	Sequence 25, Appl
44	521.5	50.2	122	15	US-10-309-762-27	Sequence 27, Appl
45	521.5	50.2	122	15	US-10-309-762-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-10-104-047-3224
; Sequence 3224, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3224
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3224

Query Match	70.3%	Score	730.5;	DB	15;	Length	533;
Best Local Similarity	72.0%	Pred	No. 1.9e-46;				
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Gaps	1;						
QY	1	LVKPSSETLSLTCTVSGSGSISYYNNWIRQPPGKGLWIGYIYSGSTNNPPLKGRVTIS	60				
Db	30	LVQPGGSLRLSCAASGFDVSSNNYMSWRQSPCKPEWATMYGGNTYYAESVKGRFTVS	89				
QY	61	VDTSKNQPSLKLSSVTAAATVAYICARDRGVATGFDY---WGQGLTVTVSSGSASAPTL	117				
Db	90	RDGQNTLYLEMSRLRPDDTAVYYCRDRHNYADTSYGRKRWGQGLTVTVSSGSASAPTL	149				
QY	118	PFLVSCENSPSDTSSVAVGCLAQDLPDSITPFSWKYKNNSDISSSTRGFPFSLVRGGKYAAT	177				
Db	150	PFLVSCENSPSDTSSVAVGCLAQDLPDSITPFSWKYKNNSDISSSTRGFPFSLVRGGKYAAT	209				

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Qy 178 SQVLLPSKDVMOGTDDEHKVC 197
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Db 210 SQVLLPSKDVMOGTDDEHVC 229

RESULT 2
US-10-047-542-47
; Sequence 47, Application US/10047542
; Publication No. US2002016937A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIPI
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 47
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-47

Query Match 68.2%; Score 709; DB 13; Length 627;
Best Local Similarity 67.0%; Pred. No. 8.9e-45;
Matches 140; Conservative 19; Mismatches 36; Indels 14; Gaps 2;

Qy 3 KPSETLSLTCTVSGGSISSYVWNIROPPGKLEWI-GYIYVSGSTVNNPSLKSRVTISV 61
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Db 32 KPGSSVKVSKRAGSGTFSYAISWVRQAPGGQLEWNGIIPFGTANYAQKFGQGVTTA 91
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Qy 62 DTSKNQFSLKLSVTAADTAVYVCARDRGVCA-----TGFDYWGQGTLTVTS 108
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Qy 109 SGSASAPTLPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSV 168
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Qy 169 LRGGKYAATSQVLLPSKDVMOGTDDEHKVC 197
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Db 212 LRGGKYAATSQVLLPSKDVMOGTDDEHVC 240

RESULT 3
US-10-108-260A-4112
; Sequence 4112, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: NO. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4112
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4112

Query Match 68.2%; Score 708.5; DB 15; Length 595;
Best Local Similarity 70.5%; Pred. No. 9.2e-45;
Matches 141; Conservative 17; Mismatches 39; Indels 3; Gaps 2;

Qy 1 LVKPSSETLSLTCTVSGGSISSYVWNIROPPGKLEWIGIYVSGSTVNNPSLKSRVTI 59
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FILE REFERENCE: 6989.US.02
CURRENT APPLICATION NUMBER: US/10/684,109
CURRENT FILING DATE: 2003-10-10
PRIOR APPLICATION NUMBER: 10/269,711
PRIOR FILING DATE: 2002-10-14
NUMBER OF SEQ ID NOS: 115
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 71
LENGTH: 241
TYPE: PRT
ORGANISM: Homo sapiens
US-10-684-109-71

Query Match 61.0%; Score 633.5; DB 16; Length 241;
Best Local Similarity 67.4%; Pred. No. 1.4e-39;
Matches 128; Conservative 20; Mismatches 31; Indels 11; Gaps 6;
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DB 32 LKPSSETLSLCTVSGGSISSYYNNWIRQPPCKGLEWIGYIYSGSTNNPNSLKSRVTIS 91
QY 61 V--DTSKNQFSLKSSVTAADTAATVYYCARDR-GVGATGFDYWGQGTTLTVSSGSASAPTL 117
DB 92 VASPTSKNQFSLKLSVTAADTAATVYYCAERLGIG----DYWGQGTTLTVSSASTKGPSV 147
QY 118 PLVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPVLR-GGKYAA 176
DB 148 PFLAPCSRSTSE--STAALGCLVKDYFPPEVTVSW--NSGALTSGVHTFPAVLQSSGLYSL 204
QY 177 TSQVLLPSKD 186
DB 205 SSVTVPSNN 214

RESULT 6
US-10-292-088-86
Sequence 86, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 86
LENGTH: 466
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-088-86

Query Match 60.9%; Score 633; DB 15; Length 466;
Best Local Similarity 64.7%; Pred. No. 3e-39; Indels 14; Gaps 7;
Matches 132; Conservative 20; Mismatches 38; Indels 14; Gaps 7;
QY 1 LKPSSETLSLCTVSGGSISSYYNNWIRQPPCKGLEWIGYIYSGSTNNPNSLKSRVTIS 60
DB 30 LKPSSETLSLCTVSGGSISSYYNNWIRQPPCKGLEWIGYIYSGSTNNPNSLKSRVTIS 89
QY 61 VDTSKNQFSLKSSVTAADTAATVYYCARDRV-GATG-FDYWGQGTTLTVSSGSASAPTLF 118
DB 90 VDTSKNQFSLKSSVTAADTAATVYYCARRGGLYDYGWFPAPWGQGTTLTVSSASTKGPSV 149
QY 119 PLVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPVLR-GGKYAAT 177
DB 150 PLAPCSRSTSE--STAALGCLVKDYFPPEVTVSW--NSGALTSGVHTFPAVLQSSGLYSL 206

QY 178 SQVLLPSKDVNQGTD-----EHK 195
DB 207 SSVTVPSNNF--GTQTYTCNVNDHK 228
RESULT 7
US-10-292-088-70
Sequence 70, Application US/10292088
Publication No. US20030211100A1
GENERAL INFORMATION:
APPLICANT: BEDIAN, VAHE
APPLICANT: GLADUE, RONALD P.
APPLICANT: CORVALAN, JOSE
APPLICANT: JIA, XIAO-CHI
APPLICANT: FENG, XIAO
TITLE OF INVENTION: ANTIBODIES TO CD40
FILE REFERENCE: ABX-PF/3 US
CURRENT APPLICATION NUMBER: US/10/292,088
CURRENT FILING DATE: 2003-03-14
PRIOR APPLICATION NUMBER: 60/348,980
PRIOR FILING DATE: 2001-11-09
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 70
LENGTH: 466
TYPE: PRT
ORGANISM: Homo sapiens
US-10-292-088-70

Query Match 60.7%; Score 631; DB 15; Length 466;
Best Local Similarity 64.2%; Pred. No. 4.3e-39;
Matches 131; Conservative 21; Mismatches 38; Indels 14; Gaps 7;
QY 1 LKPSSETLSLCTVSGGSISSYYNNWIRQPPCKGLEWIGYIYSGSTNNPNSLKSRVTIS 60
DB 30 LKPSSETLSLCTVSGGSISSYYNNWIRQPPCKGLEWIGYIYSGSTNNPNSLKSRVTIS 89
QY 61 VDTSKNQFSLKSSVTAADTAATVYYCARDRV-GATG-FDYWGQGTTLTVSSGSASAPTLF 118
DB 90 VDTSKNQFSLKSSVTAADTAATVYYCARRGGLYDYGWFPAPWGQGTTLTVSSASTKGPSV 149
QY 119 PLVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNSDISSTRGFPVLR-GGKYAAT 177
DB 150 PLAPCSRSTSE--STAALGCLVKDYFPPEVTVSW--NSGALTSGVHTFPAVLQSSGLYSL 206
QY 178 SQVLLPSKDVNQGTD-----EHK 195
DB 207 SSVTVPSNNF--GTQTYTCNVNDHK 228

RESULT 8
US-09-972-656-72
Sequence 72, Application US/09972656
Publication No. US20030099647A1
GENERAL INFORMATION:
APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei-Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
TITLE OF INVENTION: Neutralizing Activity
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 72
LENGTH: 230
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-656-72
Query Match 60.3%; Score 626.5; DB 10; Length 230;
Best Local Similarity 61.7%; Pred. No. 4.5e-39;

```
Matches 127; Conservative 23; Mismatches 41; Indels 15; Gaps 6;
Qy 1 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
11 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 70
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 VDTSKNQFSLKLSVTAADTAIVYCCARDR-----VGATGFDYWGQGLTVTVSSGSA 112
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
71 VDTSKNQFSLKLSVTAADTAIVYCCARDR-----VGATGFDYWGQGLTVTVSSSAST 130
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
113 SAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLR-G 171
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
131 KGPSVFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSS 187
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
172 GKAAATSOVLLPSKDVMOGTDEHKYC 197
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
188 GLYSLSVVTVPPSSSL--GTQTY-IC 210
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 9
US-10-309-762-171
; Sequence 171, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudae, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Maehisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-171
Query Match 60.2%; Score 625; DB 15; Length 179;
Best Local Similarity 69.1%; Pred. No. 4.5e-39;
Matches 121; Conservative 17; Mismatches 29; Indels 8; Gaps 3;
Qy 1 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 64
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 VDTSKNQFSLKLSVTAADTAIVYCCARDRGVAT-----GPDYWGQGLTVTVSSGSAP 115
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 VDTSKNQFSLKLSVTAADTAIVYCCARDQHSSSVYIYGYGMDVWGQGLTVTVSSASTKGP 124
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
116 TLFPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLR 170
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 SVFPLAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQ 176
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 10
US-10-684-109-106
; Sequence 106, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: Antibodies
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-106
Query Match 59.7%; Score 620.5; DB 16; Length 239;
Best Local Similarity 65.4%; Pred. No. 1.3e-38;
Matches 123; Conservative 23; Mismatches 33; Indels 9; Gaps 5;
Qy 1 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
32 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 91
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 VDTSKNQFSLKLSVTAADTAIVYCCARDR--GVGATGFDYWGQGLTVTVSSGSASAPTLFP 119
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
92 ADTSKNQFSLKLSVTAADTAIYCCAREKLGIG---DYWGQGLTVTVSSASTKGPSVFP 147
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 LVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLR--GGKYAATS 178
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
148 LAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLS 204
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-106
Query Match 59.9%; Score 622.5; DB 16; Length 241;
Best Local Similarity 66.3%; Pred. No. 9.4e-39;
Matches 126; Conservative 21; Mismatches 33; Indels 11; Gaps 6;
Qy 1 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
32 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 91
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 V--DTSKNQFSLKLSVTAADTAIVYCCARDR--GVGATGFDYWGQGLTVTVSSGSASAPTL 117
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
92 VASPTSKNQFSLKLSVTAADTAIVYCCARDKKGIG---DYWGQGLTVTVSSASTKGPSV 147
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
118 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLR--GGKYAA 176
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
148 FPLAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSL 204
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
177 TSQVLLPSKD 186
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
205 SSVTVTPSSN 214
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RESULT 11
US-10-684-109-100
; Sequence 100, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: Antibodies
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-100
Query Match 59.7%; Score 620.5; DB 16; Length 239;
Best Local Similarity 65.4%; Pred. No. 1.3e-38;
Matches 123; Conservative 23; Mismatches 33; Indels 9; Gaps 5;
Qy 1 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
32 LVKPSLTLCTVSGGSISSYYNNWIRQPPGKGLEWIGYIYSGSTNNPNSLKSRTVIS 91
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 VDTSKNQFSLKLSVTAADTAIVYCCARDR--GVGATGFDYWGQGLTVTVSSGSASAPTLFP 119
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
92 ADTSKNQFSLKLSVTAADTAIYCCAREKLGIG---DYWGQGLTVTVSSASTKGPSVFP 147
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 LVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLR--GGKYAATS 178
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
148 LAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLS 204
Qy :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
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QY 179 QVLLPSKD 186
Db 205 VVTVPSSN 212

RESULT 12
US-10-292-088-22
; Sequence 22, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-XI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PP/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-22

Query Match 59.5%; Score 618; DB 15; Length 464;
Best Local Similarity 62.9%; Pred. No. 4e-38;
Matches 127; Conservative 20; Mismatches 43; Indels 12; Gaps 5;

QY 1 LVKPSETLSLCTVSGGSISSYYNNWIRQPPGKLEWIGYIYVSGSTNNPDLKSRVTIS 60
Db 30 LVKPSETLSLCTVSGGSISSYYNNWIRQPPGKLEWIGRVTTSSTNNPDLKSRVTMS 89

QY 61 VDTSKNQFSLKLSVTAADTAIVYCARDRGVATGDFYWGQGTTLVTVSSGSASAPTL 120
Db 90 VDTSKNQFSLKLSVTAADTAIVYCARDGLYRGYMDVWGQGTTLVTVSSASTKGPVFL 149

QY 121 VSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGKYAATSQ 179
Db 150 APCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTFAVLQSSGLYSLSV 206

QY 180 VLLPSKDVMOGTD-----EHK 195
Db 207 VVTVPSSNF--GIQTYTCNVVDHK 226

RESULT 13
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: dI-NHS76(gamma4h) (FN>AQ) -ala-IL2 (D20T) heavy chain fused to
```

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; OTHER INFORMATION: IL-2 variant
US-10-310-719-37

Query Match 58.6%; Score 609; DB 14; Length 580;
Best Local Similarity 63.1%; Pred. No. 2.3e-37;
Matches 128; Conservative 21; Mismatches 38; Indels 16; Gaps 7;

QY 1 LVKPSETLSLCTVSGGSISS--YYNNWIRQPPGKLEWIGYIYVSGSTNNPDLKSRVTI 59
Db 11 LVKPSETLSLCTCAVSGYISGYYGWIRQPPGKLEWIGSYTHSGSTYVNPDLKSRVTI 70

QY 60 SVDTSKNQFSLKLSVTAADTAIVYCARDRGVATGDFYWGQGTTLVTVSSGSASAPTL 119
Db 71 SVDTSKNQFSLKLSVTAADTAIVYCARGW---SKFDYWGQGTTLVTVSSASTKGPVFP 127

QY 120 LVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGKYAATS 178
Db 128 LAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTFAVLQSSGLYSL 184

QY 179 QVLLPSKDVMOGTD-----BHK 195
Db 185 VVTVPSSSL--GTKTYTCNVVDHK 205

RESULT 14
US-10-684-109-88
; Sequence 88, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-88

Query Match 58.5%; Score 607.5; DB 16; Length 241;
Best Local Similarity 64.2%; Pred. No. 1.2e-37;
Matches 122; Conservative 24; Mismatches 33; Indels 11; Gaps 6;
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```
QY 1 LVKPSETLSLCTVSGGSISSYYNNWIRQPPGKLEWIGYIYVSGSTNNPDLKSRVTIS 60
Db 32 LVKPSETLSLCTVSGASISNNYNNWIRQPPGKLEWIGYISYSGSTYVNPDLKGRVTMS 91

QY 61 V--DTSKNQFSLKLSVTAADTAIVYCARDR--GVGATGDFYWGQGTTLVTVSSGSASAPTL 117
Db 92 VASPTSKNQFSLKLSVTAADTAIVYCARGLIGIG---DYWGQGTTLVTVSSASTKGPV 147

QY 118 PPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGKYAA 176
Db 148 PPLAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTFAVLQSSGLYSL 204

QY 177 TSQVLLPSKD 186
Db 205 SSVTVPPSSN 214

RESULT 15
US-10-310-719-35
; Sequence 35, Application US/10310719
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/ Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NHS76(gamma2h) (FN>AQ) -ala-IL2 (D20T) heavy chain fused to IL2
; OTHER INFORMATION: variant
; US-10-310-719-35
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Query Match 58.2%; Score 604.5; DB 14; Length 580;
Best Local Similarity 63.2%; Pred. No. 5e-37;
Matches 129; Conservative 21; Mismatches 37; Indels 17; Gaps 8;

QY 1 LVKPSETLSLCTVSGGSISS--YYWNWIRQPPGKLEWIGYIYSGSTNYPNPSLKSRYTI 59
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 11 LVKPSETLSLCTCAVSGYSISGYYGWIRQPPGKLEWIGSIYHSGSTYYPNPSLKSRYTI 70
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 60 SVDTSKNQFSLKLSVTAADTAVYYCARDRGVGTGFDYWGQGTILVTYSSG--SASAPTLF 118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 71 SVDTSKNQFSLKLSVTAADTAVYYCARGKW---SKFDYWGQGTILVTYSSGASTKGPSVF 127
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 119 PLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLR--GKYYAAT 177
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 128 PLAPCSRSTSE--STAALGCLVKDYPPEPVTWSW--NSGALTSGVHTFPAVLQSSGLYSLS 184
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 178 SQVLLPSKDVMOGTD-----EHK 195
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 185 SVTVFSSNF--GTQTYTCNVDPHK 206
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Search completed: March 8, 2005, 07:05:48
Job time : 104.543 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 21.6614 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-25

Perfect score: 1039

Sequence: 1 LVKSEETLSLCTVSGGIS.....SQLLPKDVQGTDEHKVC 197

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	615	59.2	473	3	US-09-049-672A-4
2	581	55.9	172	4	US-09-472-087-7
3	581	55.9	172	4	US-09-472-087-7
4	572.5	55.1	472	3	US-08-793-450-8
5	556.5	53.6	832	4	US-08-630-820-7
6	556.5	53.6	832	4	US-09-273-453-7
7	556	53.5	487	4	US-09-800-729-145
8	549.5	52.9	219	3	US-09-460-384-37
9	547	52.6	467	3	US-08-523-894-10
10	547	52.6	467	3	US-08-523-894-10
11	547	52.6	467	3	US-08-523-894-12
12	542.5	52.2	476	3	US-08-487-550-12
13	542.5	52.2	476	4	US-09-526-098-12
14	542.5	52.2	476	4	US-09-383-916-12
15	526	50.6	119	3	US-09-025-769B-39
16	526	50.6	119	3	US-09-025-769B-65
17	526	50.6	119	4	US-09-490-070A-39
18	526	50.6	119	4	US-09-490-070A-65
19	526	50.6	119	4	US-09-490-153-39
20	526	50.6	119	4	US-09-490-153-65
21	526	50.6	119	4	US-09-490-324-39
22	526	50.6	119	4	US-09-490-324-65
23	521.5	50.2	118	3	US-09-025-769B-25
24	521.5	50.2	118	4	US-09-490-070A-25
25	521.5	50.2	118	4	US-09-490-153-25
26	521.5	50.2	118	4	US-09-490-324-25
27	508.5	48.9	476	3	US-08-487-550-4

28 508.5 48.9 476 4 US-09-526-098-4
29 508.5 48.9 476 4 US-09-383-916-4
30 506 48.7 244 3 US-08-918-148-79
31 506 48.7 244 4 US-09-138-091A-77
32 505.5 48.7 120 4 US-09-424-840B-20
33 501.5 48.3 255 3 US-09-171-945-57
34 501 48.2 273 3 US-08-397-411-6
35 501 48.2 446 3 US-08-397-411-7
36 494.5 47.6 306 3 US-09-171-945-95
37 494.5 47.6 613 3 US-09-171-945-113
38 494.5 47.6 716 3 US-09-171-945-125
39 489 47.1 467 4 US-08-030-175-42
40 486 46.8 260 3 US-09-171-945-93
41 486 46.8 467 4 US-08-030-175-41
42 479.5 46.2 117 3 US-08-851-362D-48
43 474.5 45.7 122 1 US-08-360-125-11
44 474.5 45.7 122 2 US-08-450-578-11
45 474.5 45.7 122 2 US-09-017-628-11

ALIGNMENTS

RESULT 1

US-09-049-672A-4

; Sequence 4, Application US/09049672A

; Patent No. 6135941

; GENERAL INFORMATION:

; APPLICANT: Hillman, Jennifer L.

; APPLICANT: Lal, Preeti

; APPLICANT: Tang, Y. Tom

; APPLICANT: Yue, Henry

; APPLICANT: Au-Young, Janice

; APPLICANT: Corley, Neil C.

; APPLICANT: Guegler, Karl J.

; APPLICANT: Baughn, Mariah R.

; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS

; NUMBER OF SEQUENCES: 28

; CORRESPONDENCE ADDRESS:

; ADDRESS: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: USA

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/049,672A

; FILING DATE: HEREWITH

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Cerrone, Michael C

; REGISTRATION NUMBER: 39,132

; REFERENCE/DOCKET NUMBER: PF-0497 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650-855-0555

; TELEFAX: 650-845-4166

; TELEX:

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 473 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; IMMEDIATE SOURCE:

; LIBRARY: PANCYT01

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; CLONE: 1513264
US-09-049-672A-4

Query Match      59.2%; Score 615; DB 3; Length 473;
Best Local Similarity 63.7%; Pred. No. 3e-47;
Matches 130; Conservative 20; Mismatches 40; Indels 14; Gaps 8;

Qy 1 LVKPESETLSLTCTVSGGSISS--YYWNWIRPPGKLEWIGYIYSGSTNPNPSLKSRVT 58
Db 30 LVKPESETLSLTCAVSGSISGSGYWNWIRPPGKLEWIGYIYSGSTNPNPSLKSRVT 89
Qy 59 ISVDTSKNQFSLKLSVTAADTAIVYCARD---RGVGTATGFDYWGQGTTLTVSSGSASA 114
Db 90 ISVDTSKNQFSLKLSVTAADTAIVYCARDVDGLRG-GNYGMDVWGQGTTLTVSSASTKG 148
Qy 115 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGK 173
Db 149 PSVFPPLAPSSKSTSG-GTAALGCLVKDYFPPEPTVSW--NSGALTSGVHTTFFAVLQSSGL 205
Qy 174 YAATSOVLLPSKDVWQGTDEHKVC 197
Db 206 YLSVSVTVPPSSSL--GTQTY-IC 226

RESULT 2
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      55.9%; Score 581; DB 4; Length 172;
Best Local Similarity 67.4%; Pred. No. 9.5e-45;
Matches 116; Conservative 17; Mismatches 33; Indels 6; Gaps 4;

Qy 1 LVKPESETLSLTCTVSGGSISS--YYWNWIRPPGKLEWIGYIYSGSTNPNPSLKSRVT 58
Db 5 LVKPSQILSLTCTVSGGSISSGGHYWNIROHPGKLEWIGYIYIGNTYNPNPSLKSRVT 64
Qy 59 ISVDTSKNQFSLKLSVTAADTAIVYCARDRGVGTATGFDYWGQGTTLTVSSGSASAPTLF 118
Db 65 ISVDTSKNQFSLKLSVTAADTAIVYCARDSG-DYYGIDVWGQGTTLTVSSASTKGPSVF 123
Qy 119 PLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR 170
Db 124 PLAPCSRSTSE-STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTTFFAVLQ 172

RESULT 4
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABRIHI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
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; CLONE: 1513264
US-09-049-672A-4

Query Match      59.2%; Score 615; DB 3; Length 473;
Best Local Similarity 63.7%; Pred. No. 3e-47;
Matches 130; Conservative 20; Mismatches 40; Indels 14; Gaps 8;

Qy 1 LVKPESETLSLTCTVSGGSISS--YYWNWIRPPGKLEWIGYIYSGSTNPNPSLKSRVT 58
Db 30 LVKPESETLSLTCAVSGSISGSGYWNWIRPPGKLEWIGYIYSGSTNPNPSLKSRVT 89
Qy 59 ISVDTSKNQFSLKLSVTAADTAIVYCARD---RGVGTATGFDYWGQGTTLTVSSGSASA 114
Db 90 ISVDTSKNQFSLKLSVTAADTAIVYCARDVDGLRG-GNYGMDVWGQGTTLTVSSASTKG 148
Qy 115 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGK 173
Db 149 PSVFPPLAPSSKSTSG-GTAALGCLVKDYFPPEPTVSW--NSGALTSGVHTTFFAVLQSSGL 205
Qy 174 YAATSOVLLPSKDVWQGTDEHKVC 197
Db 206 YLSVSVTVPPSSSL--GTQTY-IC 226

RESULT 2
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-7

Query Match      55.9%; Score 581; DB 4; Length 172;
Best Local Similarity 67.4%; Pred. No. 9.5e-45;
Matches 116; Conservative 17; Mismatches 33; Indels 6; Gaps 4;

Qy 1 LVKPESETLSLTCTVSGGSISS--YYWNWIRPPGKLEWIGYIYSGSTNPNPSLKSRVT 58
Db 5 LVKPSQILSLTCTVSGGSISSGGHYWNIROHPGKLEWIGYIYIGNTYNPNPSLKSRVT 64
Qy 59 ISVDTSKNQFSLKLSVTAADTAIVYCARDRGVGTATGFDYWGQGTTLTVSSGSASAPTLF 118
Db 65 ISVDTSKNQFSLKLSVTAADTAIVYCARDSG-DYYGIDVWGQGTTLTVSSASTKGPSVF 123
Qy 119 PLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR 170
Db 124 PLAPCSRSTSE-STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTTFFAVLQ 172

RESULT 3
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 472 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-793-450-8

Query Match 55.1%; Score 572.5; DB 3; Length 472;
Best Local Similarity 59.4%; Pred. No. 26-43; Mismatches 22; Indels 11; Gaps 6;
Matches 120; Conservative 22; Mismatches 49; Indels 11; Gaps 6;
QY 1 LKPSSETLSLCTVSGSGSISSYYNNWIRQPPGKGLWIGIYIYSGSTNNPNSLKSRTVTS 60
DB 30 LKPSSETLSLCTVYGGSFSGYNNWIRQPPGKGLWIGIYIYSGSTNNPNSLKSRTVTS 89
QY 61 VDTSKNQPSLKLSSVTAADTAIVYCAR----DRGVGATGFDYWGQGTLLVTVSSGSGASAPT 116
DB 90 VDTSKNQPSLKLNSVTAADTAIVYCARAPEYKWKYHGDWFDWQGGTTLTVTVSSASTKGPS 149
QY 117 LPELVSCNSPDSSTSSAVGCLAQDPLPDSITFSWKYKNNSDISSTRGFPVLR-GGKYA 175
DB 150 VFPLAPSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLYS 206
QY 176 ATSOVLPSKDVMOGTDSHKVC 197
DB 207 LSSVTVFPSSSL--GTQTY-IC 225

RESULT 5
US-08-630-820-7
Sequence 7, Application US/08630820
Patent No. 6008023
GENERAL INFORMATION:
APPLICANT: OPPER, Martin
BOSSLET, Klaus
CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES.
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,820
FILING DATE: 10-APR-1996
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: DE 19513676.4
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-820-7
Query Match 53.6%; Score 556.5; DB 3; Length 832;
Best Local Similarity 58.6%; Pred. No. 1.1e-41; Mismatches 27; Indels 9; Gaps 6;
Matches 116; Conservative 27; Mismatches 46; Indels 9; Gaps 6;
QY 1 LKPSSETLSLCTVSGSGSISSYYNNWIRQPPGKGLWIGIYIYSGSTNNPNSLKSRTVTS 59
DB 12 LVRPSQTLSLCTVSGFTISSGYSWHWVRQPPGKGLWIGIYIYSGIITNNPNSLKSRTVM 71
QY 60 SVDTSKNQPSLKLSSVTAADTAIVYCARDRGVGATGFDYWGQGTLL--VTVSSGSGASAPT 117
DB 72 LVDTSKNQPSLKLSSVTAADTAIVYCARVDYHWFVDMVGQGLVTVTVSSASTKGPSV 131
QY 118 FPLVSCNSPDSSTSSAVGCLAQDPLPDSITFSWKYKNNSDISSTRGFPVLR-GGKYAA 176
DB 132 FPLAPCSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLYS 188
QY 177 TSQVLLPSKDVMOGTDEH 194
DB 189 SSVTVFPSSSL--GTQTY 204
RESULT 6
US-09-273-453-7
Sequence 7, Application US/09273453
Patent No. 6602688
GENERAL INFORMATION:
APPLICANT: OPPER, Martin
BOSSLET, Klaus
CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES.
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,453
FILING DATE: 22-Mar-1999
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/630,820
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-273-453-7

REFERENCE/DOCKET NUMBER: 012712-165
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 467 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-523-894-12

Query Match 52.6%; Score 547; DB 3; Length 467;
Best Local Similarity 57.8%; Pred. No. 3.9e-41;
Matches 118; Conservative 23; Mismatches 49; Indels 14; Gaps 7;

Qy 1 LVKPSLTLCTCTVSGGIS-SYYWNWIRQPPGKLEWIGYIYS-GSTNNPSLKSRVT 58
Db 30 LVKPSLTLCTCSVSGGISGDIYFWIRQSPGKLEWIGYIYGGGGTNNPSLNNRVS 89
Qy 59 ISVDTSKNQLSLSSVTAADTAIVYICARDRGVGTGFDYWGQGLVTVSSGSASAPTLF 118
Db 90 ISIDTSKNLFLSKLRSVTAADTAIVYICASNILKYLHLLYWGQGLVTVSSASTKGPSVF 149
Qy 119 PLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLR-GKYAAT 177
Db 150 PLAFCSRSTSE-STAAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFAVLQSSGLYSLS 206
Qy 178 SQVLLPSKDVMOGTD-----EHK 195
Db 207 SWVTVPSSSL--GTNTYTCNVDPHK 228

RESULT 12

US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
AND USE THEREOF AS
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
AND USE THEREOF AS
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,550
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-487-550-12

Query Match 52.2%; Score 542.5; DB 3; Length 476;
Best Local Similarity 56.8%; Pred. No. 1e-40;
Matches 117; Conservative 22; Mismatches 52; Indels 15; Gaps 8;

Qy 1 LVKPSLTLCTCTVSGGIS-SYYWNWIRQPPGKLEWIGYIY-YSGSTNNPSLKSRVT 58
Db 30 LVKPSLTLCTCAVSGGISGGYCWGIRQPPGKLEWIGSYSSGNTYNNPSLKSQVT 89
Qy 59 ISVDTSKNQLSLSSVTAADTAIVYICARDRGVGTG-----FDYWGQGLVTVSSGSA 112
Db 90 ISIDTSKNQPSLKLNSMTAADTAIVYICVRDLFSVVGVMVNNWFDVPGVGLVTVSSAST 149

Qy 113 SAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLR-G 171
Db 150 KGPSVFFPLAPSSKSTSG-GTAAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTFFAVLQSS 206
Qy 172 GKYAATSQVLLPSKDVMOGTDDEHKVC 197
Db 207 GLYSLSSVTVTPSSSL--GTQTY-IC 229

RESULT 13

US-09-526-098-12
; Sequence 12, Application US/09526098
; Patent No. 6492134

GENERAL INFORMATION:

APPLICANT: Anderson, Darrell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
AND USE THEREOF AS
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:

APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-526-098-12

Query Match 52.2%; Score 542.5; DB 4; Length 476;
Best Local Similarity 56.8%; Pred. No. 1e-40;
Matches 117; Conservative 22; Mismatches 52; Indels 15; Gaps 8;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.4472 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 783

Sequence: 1 SQSPSSLSASVGERVTTCR.....VVCLLNNFYPREAKEHOKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	556.5	72.9	215	2 JE0244	Ig kappa chain NIG
2	552.5	72.4	215	2 JE0242	Ig kappa chain NIG
3	541.5	71.0	215	2 JE0243	Ig kappa chain NIG
4	512.5	67.2	215	2 A23746	Ig kappa chain V-I
5	496	65.0	125	2 S40353	Ig kappa chain V-J
6	490	64.2	230	2 S33161	Ig kappa chain - s
7	487	63.8	123	2 S40313	Ig kappa chain V-J
8	485	63.6	234	2 S14237	Ig kappa chain pre
9	481	63.0	141	2 A49134	Ig kappa chain V-I
10	481	63.0	240	2 S06084	Ig kappa chain pre
11	478	62.6	108	1 K1HUGL	Ig kappa chain V-I
12	478	62.6	216	2 JE0241	Ig kappa chain Am3
13	478	62.6	234	2 S01320	Ig kappa chain pre
14	475	62.3	214	2 S68212	Ig kappa chain (Ma
15	468	61.3	108	1 K1HWE	Ig kappa chain V-I
16	462	60.6	132	2 S40334	Ig kappa chain - h
17	459	60.2	126	2 S40335	Ig kappa chain V-J
18	458	60.0	144	2 P0106	Ig kappa chain pre
19	458	60.0	220	2 A31790	Ig kappa chain V r
20	457	59.9	210	2 A56169	Ig kappa chain V r
21	454	59.5	131	2 S40352	Ig kappa chain V-J
22	453.5	59.4	235	2 S25058	Ig kappa chain - m
23	453	59.4	218	2 J05810	monoclonal antibody
24	452	59.2	107	2 S36262	Ig lambda chain V
25	452	59.2	125	2 S40349	Ig kappa chain V-J
26	451.5	59.2	225	2 S37484	Ig kappa chain - m
27	450	59.0	218	2 S68241	Ig kappa chain V r
28	449	58.8	117	2 S41809	Ig kappa chain V r
29	448	58.7	125	2 S40333	Ig kappa chain V-J

RESULT 1
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Te
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VKV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 72.9%; Score 556.5; DB 2; Length 215;
Best Local Similarity 74.0%; Pred. No. 5e-38;
Matches 108; Conservative 15; Mismatches 22; Indels 1; Gaps 1;

Qy 1 SQSPSSLSASVGERVTTCRASQIRDELGHVQKPGKPKRLIYVASSLSQSGVSPRSG 60
Db 5 TQSPATLSVSPGERATLSCRASQSVHNSLAWYQKPGQAPRLIYRSTRATGIPARFSG 64
Qy 61 SCSTGTEFTLTSSLOPEDFATYVCLQNGY-PRTFGQGTKEIKRTVAAPSVFIPPSDE 119
Db 65 SCSTGDFILTSSLOSEDFALYYCQYNTWPLTFGGGTKEIKRTVAAPSVFIPPSDE 124
Qy 120 QLKSGTASVVCLLNNFYPREAKEHOK 145
Db 125 QLKSGTASVVCLLNNFYPREAKVQWK 150

RESULT 2
JE0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mult
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 72.4%; Score 552.5; DB 2; Length 215;
Best Local Similarity 74.0%; Pred. No. 1e-37;
Matches 108; Conservative 13; Mismatches 24; Indels 1; Gaps 1;

ALIGNMENTS


```

Db      141 LRTGTVSVVCLVNDFPKD 159
:::| | ||||| : |:| ::
RESULT 7
S40313
IG kappa chain V-J region - human
C:Species: Homo sapiens (man)
C>Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40313
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A>Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40313
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-123 <LIE>
A:Cross-references: EMBU:X72423; NID:g441314; PIDN:CAA51091.1; PID:g441315
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:32-106/Domain: immunoglobulin homology <IMM>

Query Match          63.8%; Score 487; DB 2; Length 123;
Best Local Similarity 90.3%; Pred. No. 1.2e-32;
Matches   93; Conservative    7; Mismatches   3; Indels     0; Gaps    0;

QY       1 SOSPSLSASVGSRVTITCRASGIIRDELGWYOOKPGKAPKRLIYVASSIQSGVPSPFSFG 60
DB        21 TQPSSLSASVGDRVTITCRASGIIRDLAWFOOQGKGAKPRLIYDAALLSGVPSRFSG 80

QY       61 SGSGTEFTLTISSLQPEDPATYYCLOHNGYPRTFGGTKEIK 103
DB        81 SGSGTEFTLTISSLQPEDPATYYCLOYGYPTFGGTKEIK 123

RESULT 8
S14237
Ig kappa chain precursor (15C5) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S14237
R; Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A>Title: Construction and characterization of a recombinant murine monoclonal antibody
A:Reference number: S14236; MUID:91006173; PMID:2209622
A:Accession: S14237
A:Molecule type: mRNA
A:Residues: 1-234 <VAN>
A:Cross-references: EMBU:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623
C:Superfamily: immunoglobulin v region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>

Query Match          63.6%; Score 485; DB 2; Length 234;
Best Local Similarity 66.2%; Pred. No. 3.2e-32;
Matches   92; Conservative    20; Mismatches  27; Indels     0; Gaps    0;

QY       1 SOSPSLSASVGSRVTITCRASGIIRDELGWYOOKPGKAPKRLIYVASSIQSGVPSPFSFG 60
DB        25 TQSPSMYSALSGRVTVTCKASQINDSYLSWIQQKFQKSPTKIYRGRLVLAVGPSPFSFG 84

QY       61 SCGGTEFTLTISLLQPEDEATYYCLOHNGYPRTFGGTKEIKRTVAAPSVFIFPPSEDEQ 120
DB        85 SCGGQDYSTISSLVEDGVVVYLRYDEPFPTFGSGTKLEIKRADAAPTVSIFPPSSEQ 144

QY      121 LKSGTASVCILNNFYPRE 139
DB      145 LTSGGASVWCFLNNFYPKD 163


RESULT 9
A49134
```

Ig kappa chain V-I region (ISE) - human (fragment)

C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49134; S25115
R:Rocca, A.; Khamlichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.L.
Clin. Exp. Immunol. 91, 506-509, 1993
A:Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light
A:Reference number: A49134; MUID:93185310; PMID:7690298
A:Accession: A49134
A>Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-141 <ROC>
A:Cross-references: EMBL:X67322; NID:G33268; PIDN:CAA47736.1; PID:G33269
A:Note: sequence extracted from NCBI backbone (NCBIP:127088)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 481; DB 2; Length 141;
Best Local Similarity 81.7%; Pred. No. 4.1e-32;
Matches 94; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 1 SQSPSSLSASVGRVITTCRASGIRDELGWQOKPKAKRLIYVASSLSQGVPSRFSG 60
DB 27 TQSPSSLSASVGRVITTCRASGINTLAWYQOKPKAPNLLIYKATLQSGVPSRFSA 86
QY 61 SSGSGTEFTLTISLQPEDFATYYCLQHNQYPRTEGQGTKEIKRTVAAPSVFIFP 115
DB 87 SSGSGTEFTLTISGLQPDFFATYYCHQYDSFPWTFGQGTKEIKRTVAAPSVFIFP 141

RESULT 10
S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1-2.3. rat myeloma immunoglobulin kappa chain cDNA.
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-240/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 481; DB 2; Length 240;
Best Local Similarity 64.8%; Pred. No. 6.9e-32;
Matches 94; Conservative 19; Mismatches 26; Indels 6; Gaps 1;

QY 1 SQSPSSLSASVGRVITTCRASOGI-----RDELGWYQOKPKAPKRLIYVASSLSQGV 54
DB 25 TQSPSSLSASVAGTIVINCKSSLSFGNQKNYLAHYQOKPGQSPKLLIYWASTRQSGV 84
QY 55 PSRFGSGSGTEFTLTISLQPEDFATYYCLQHNQYPRTEGQGTKEIKRTVAAPSVFIF 114
DB 85 PDRFIGSGSGTDFTLTISVQAEALAIYCLQYYETPYTFGAGTKLELKRAADAPTVSIF 144
QY 115 PSDEQLKSGTASVVCLLNNFYPRE 139
DB 145 PPSTEQLATGGASVVCCLMNNFYPRD 169

RESULT 11
KHUGL
Ig kappa chain V-I region (Gal) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004

C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence revision 24-Apr-1984 #text change 09-Jul-2004
19 kappa chain V 1 region (Eur) #human connective sequences

Search completed: March 8, 2005, 06:39:22
Job time : 10.4972 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 54.8971 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 763

Sequence: 1 SQSSSLASVGERVTTCR.....VVCLLNFPYRAKEHQKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Length	DB	ID	Description
1	665	87.2	236	2	Q6GMW1	Q6gmw1 homo sapien
2	633	83.0	236	2	Q6GMX8	Q6gmx8 homo sapien
3	631	82.7	236	2	Q6PIH5	Q6pih5 homo sapien
4	628	82.3	236	2	Q6PIH7	Q6pih7 homo sapien
5	621	81.4	236	2	Q723V4	Q723v4 homo sapien
6	620	81.3	236	2	Q6GMX9	Q6gmx9 homo sapien
7	606	79.4	236	2	Q6GMX0	Q6gmx0 homo sapien
8	604	79.2	234	2	Q72473	Q72473 homo sapien
9	601	78.8	236	2	Q6PIH4	Q6pih4 homo sapien
10	552.5	72.4	235	2	Q6GMW0	Q6gmw0 homo sapien
11	536	70.2	236	2	Q6PIH8	Q6pih8 homo sapien
12	530.5	69.5	235	2	Q6GMV9	Q6gmv9 homo sapien
13	530.5	69.5	235	2	Q6PJF2	Q6pjf2 homo sapien
14	527	69.1	236	2	Q6P5S8	Q6p5s8 homo sapien
15	503	65.9	236	2	Q7TS98	Q7ts98 mus musculus
16	497.5	65.2	239	2	Q8NEK0	Q8nek0 homo sapien
17	496.5	65.1	239	2	Q8TCD0	Q8tcd0 homo sapien
18	484	63.4	240	2	Q6PIH6	Q6pih6 homo sapien
19	478	62.6	108	1	KV16G_HUMAN	P01599 homo sapien
20	476.5	62.5	239	2	Q6P491	Q6p491 homo sapien
21	468	61.3	108	1	KV1R_HUMAN	P01610 homo sapien
22	446	58.5	238	2	Q66JS7	Q66js7 mus musculus
23	442	57.9	108	2	Q9UL70	Q9ul70 homo sapien
24	433	56.7	108	1	KV1V_HUMAN	P04430 homo sapien
25	431.5	56.6	219	2	Q65ZC0	Q65zc0 mus musculus
26	429.5	56.3	243	2	Q6NTU5	Q6ntu5 xenopus lae
27	428	56.1	244	2	Q65ZC8	Q65zc8 homo sapien
28	426	55.8	108	2	Q9UL77	Q9ul77 homo sapien
29	424	55.6	108	1	KV1H_HUMAN	P01600 homo sapien
30	421	55.2	237	2	Q75Z36	Q75z36 xenopus lae
31	420.5	55.1	107	2	Q96SA9	Q96sa9 homo sapien

RESULT 1

ID	Q6GMW1	PRELIMINARY;	PRT;	236 AA.
AC	Q6GMW1;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Splicein;			
RX	MEDLINE=24388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schestz T.E.,			
RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Splicein;			
RL	Strausberg R.;			
DR	Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.			
DR	EMBL; BC073791; AAH3791.1; --			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG_MHC.			
DR	InterPro; IPR003596; IG_v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	Pfam; PF00047; IG; 2.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			

Q65zc9 homo sapien
P01598 homo sapien
Q9ul79 homo sapien
P01594 homo sapien
Q96pf6 homo sapien
P01605 homo sapien
P01604 homo sapien
P01611 homo sapien
P01603 homo sapien
P04431 homo sapien
P01596 homo sapien
Q63zx4 mus musculus
P01607 homo sapien
P01597 homo sapien

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KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 87.2%; Score 665; DB 2; Length 236;
Best Local Similarity 89.7%; Pred. No. 1.4e-58;
Matches 130; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
27 TQSPSSLSASVGDRTVITCRASQIGISNDLGNWYQKPGKAPKLLIYAASSLSQSGVPSRFSG 86
QY 61 SSGSGTEFTLTISLQPEDFATYYCLQHNHGYPRTEGQGTKEIKRTVAAPSFIPPPSDEQ 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
87 SSGSGTDFLTISLQPEDFATYYCLQDYNYPWTFTGQGTKEIKRTVAAPSFIPPPSDEQ 146
QY 121 LKSGTASVCLNNFYPREAKEHOK 145
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
147 LKSGTASVCLNNFYPREAKVQWK 171

RESULT 2
Q6GMX8 PRELIMINARY; PRT; 236 AA.
ID Q6GMX8 AC Q6GMX8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
```

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DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 83.0%; Score 633; DB 2; Length 236;
Best Local Similarity 85.5%; Pred. No. 2.2e-55;
Matches 124; Conservative 7; Mismatches 14; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
27 TQSPSSLSASVGDRTVITCRASQIGISNLGNWYQKPGKAPKLLIYAASSLSQSGVPSRFSG 86
QY 61 SSGSGTEFTLTISLQPEDFATYYCLQHNHGYPRTEGQGTKEIKRTVAAPSFIPPPSDEQ 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
87 SSGSGTDFLTISLQPEDFATYYCQAHSPFTFTGPGTKVDIKRTVAAPSFIPPPSDEQ 146
QY 121 LKSGTASVCLNNFYPREAKEHOK 145
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
147 LKSGTASVCLNNFYPREAKVQWK 171

RESULT 3
Q6PIT5 PRELIMINARY; PRT; 236 AA.
ID Q6PIT5 AC Q6PIT5
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029444; AAH29444.1; -.
DR HSP; P01607; IAR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEE351 CRC64;

Query Match      82.7%; Score 631; DB 2; Length 236;
Best Local Similarity 84.8%; Pred.No. 3.6e-55;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGGERVTITCRASQGIIRDELGWYQKPGKAPKELIYVASSLSQSGVPSRFSG 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 TQSPSSLSASGGERVTITCRASQGISSALAWYQKPGKAPKELIYDASTMESGVPSRFSG 86
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGTEFTLTSSLOPEDPATYICLQHGNYPRTFQGGTKVEIKRTVAAPSVFIPPPSDEQ 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 SSGSGTEFTLTSSLOPEDPATYICQFKSYPRTFQGGTKLEIKRTVAAPSVFIPPPSDEQ 146
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 LKSGTASVVCLNNFPYPREAKEHQK 145
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 LKSGTASVVCLNNFPYPREAKVQWK 171
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; 1AB2.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; I.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.

Query Match      82.3%; Score 628; DB 2; Length 236;
Best Local Similarity 86.2%; Pred.No. 7.2e-55;
Matches 125; Conservative 3; Mismatches 17; Indels 0; Gaps 0;

QY 1 SQSPSSLSASGGERVTITCRASQGIIRDELGWYQKPGKAPKELIYVASSLSQSGVPSRFSG 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 TQSPSSLSASGGERVTITCRASQGISSYLAWYQKPGKAPKELIYAASTLQSGVPSRFSG 86
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 SSGSGTEFTLTSSLOPEDPATYICLQHGNYPRTFQGGTKVEIKRTVAAPSVFIPPPSDEQ 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 87 SSGSGTEFTLTSSLOPEDPATYICQQLNSPPPTFGGTKVEIKRTVAAPSVFIPPPSDEQ 146
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 LKSGTASVVCLNNFPYPREAKEHQK 145
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 LKSGTASVVCLNNFPYPREAKVQWK 171
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; Cl-set; I.
DR SMART; SM00406; IG; 1.
DR SMART; PS00835; IG_LIKE; 2.
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DR PROSITE, PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7BFE4ED3084BC6 CRC64;

Query Match 81.4%; Score 621; DB 2; Length 236;
Best Local Similarity 84.1%; Pred. No. 3.6e-54;
Matches 122; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

QY 1 SOSPSLSASGVRTITCRASQGIIRDELGHVYQKPGKAPKRLIYVASSLSQGVPSRFSG 60
Db 27 TQSPSSLSASGVDTITITCRASQDISLNLAWPQKPGKAPKSLIYGASSLSQGVQSKFSG 86
QY 61 SSGSTFTLTSSLOPEDFATYYCLQHNGYPRTFQGGTKVEIKRTVAAPSFIFFPSDEQ 120
Db 87 SSGSTDFLTLTSSLOPEDFATYYCQYKSYPTVTFQGGTKLEIKRTVAAPSFIFFPSDEQ 146
QY 121 LKSGTASVCLNNFYPREAKEHQK 145
Db 147 LKSGTASVCLNNFYPREAKVQWK 171

RESULT 6
Q6GMX9 PRELIMINARY; PRT; 236 AA.
ID Q6GMX9
AC Q6GMX9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalious D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE, PS0835; IG Like; 2.
DR PROSITE, PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;

Query Match 81.3%; Score 620; DB 2; Length 236;
Best Local Similarity 84.1%; Pred. No. 4.6e-54;
Matches 122; Conservative 5; Mismatches 18; Indels 0; Gaps 0;

QY 1 SOSPSLSASGVRTITCRASQGIIRDELGHVYQKPGKAPKRLIYVASSLSQGVPSRFSG 60
Db 27 TQSPSSLSASGVRTITCRASQNVSRWLAWYQORPEKAPKSLIYATSSLSQGVPSRFSG 86
QY 61 SSGSTFTLTSSLOPEDFATYYCLQHNGYPRTFQGGTKVEIKRTVAAPSFIFFPSDEQ 120
Db 87 SSGSTDFLTLTSSLOPEDFATYYCQYNTYPLTFGGGKVEIKRTVAAPSFIFFPSDEQ 146
QY 121 LKSGTASVCLNNFYPREAKEHQK 145
Db 147 LKSGTASVCLNNFYPREAKVQWK 171

RESULT 7
Q6GMX0 PRELIMINARY; PRT; 236 AA.
ID Q6GMX0
AC Q6GMX0;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Maruina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalious D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 79.4%; Score 606; DB 2; Length 236;
Best Local Similarity 82.8%; Pred. No. 1.2e-52;
Matches 120; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

QY 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 27 TQSPSSLSASVGERVTITCRASQGINNNYVQLKPGKAPNLLIYVASSLSQSGVPSRFSG 86
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SSGSGTEFTLTSSLOPEDFATYICLOHNGYPRFTGCGTKVEIKRTVAAPSVFIPPSDEQ 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 87 SSGSGTDFLTSSLRPDDFATYICQSYNIPLTFCGGTNVEIKRTVAAPSVFIPPSDEQ 146
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LKSGTASVVCLLNNFYPREAKEHQK 145
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 147 LKSGTASVVCLLNNFYPREAKEVQWK 171
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 79.2%; Score 604; DB 2; Length 234;
Best Local Similarity 82.1%; Pred. No. 1.8e-52;
Matches 119; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 25 TQSPSSSFGASGDRVTITCRASQSIGSLAWYQKPGKAPQLLIYVASSLSQSGVPSRFSG 84
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 61 SSGSGTEFTLTSSLOPEDFATYICLOHNGYPRFTGCGTKVEIKRTVAAPSVFIPPSDEQ 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 85 SASGTDFTLTSSLRPDDFATYICQSYNIPLTFCGGTNVEIKRTVAAPSVFIPPSDEQ 144
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 121 LKSGTASVVCLLNNFYPREAKEHQK 145
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DQ 145 LKSGTASVVCLLNNFYPREAKEVQWK 169
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
Q6PIH4 PRELIMINARY; PRT; 236 AA.
AC Q6PIH4
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034146; AAH34146.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25871 MW; BE01A28CD06BEE26 CRC64;

Query Match 78.8%; Score 601; DB 2; Length 236;
Best Local Similarity 82.1%; Pred. No. 3.7e-52;
Matches 119; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASGVGVTTTCRASQIGIRDELGWYQKPKAPKRLIYVASSLSGVPSPRSFG 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 66
27 TQSPSTLSASGVDRVTIACRASQISDWLAWYQKPKAPKRLIYDASRLSGVPSPRSFG 86
Qy 61 SSGSTETLTSSSQPEDFATYVCLQHNQYVPTFGQTKVKEIKRTVAAPSVFIPPPSDEQ 120
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 126
87 SSGSTERSLTISGLQDDFATYVCPYNSPSFQGGTKVKEIKRTVAAPSVFIPPPSDEQ 146
Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 147
147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 10
Q6GMW0 PRELIMINARY; PRT; 235 AA.
ID Q6GMW0
AC Q6GMW0;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
EX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IG; 2.
DR SMART; SM00407; IGC1; 1.

DR PROSITE; PS0835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 72.4%; Score 552.5; DB 2; Length 235;
Best Local Similarity 74.0%; Pred. No. 2.8e-47;
Matches 108; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

Qy 1 SQSPSSLSASGVGVTTTCRASQIGIRDELGWYQKPKAPKRLIYVASSLSGVPSPRSFG 60
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 66
25 TQSPATLSVSGERATLSCRASQISNNLAWYQKPKAPKRLIYGASSRVITGIPRSFG 84
Qy 61 SSGSTETLTSSSQPEDFATYVCLQHNQYVPTFGQTKVKEIKRTVAAPSVFIPPPSDE 119
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 125
85 SSGSTETLTSSSQSDEFAVYFCQYNDMLLYTFQGGTKVKEIKRTVAAPSVFIPPPSDE 144
Qy 120 QKSGTASVVCLLNNFYPREAKEHQK 145
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: 146
145 QKSGTASVVCLLNNFYPREAKVQWK 170

RESULT 11
Q6PIL8 PRELIMINARY; PRT; 236 AA.
ID Q6PIL8
AC Q6PIL8;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
EX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032451; AAH32451.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
```

DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match 70.2%; Score 536; DB 2; Length 236;
Best Local Similarity 71.4%; Pred.No. 1.3e-45;
Matches 105; Conservative 15; Mismatches 25; Indels 2; Gaps 2;

QY 1 SOSPSLSASVGERVTITCRASQGRDE-LGWYQQKPGKAPRLIYVASLQSGVSPRFS 59
DB 25 TOSPGTSLSPERATLSRASQSUSLYAWYQQKPGAPRLIYGVRATGIPDRFS 84
QY 60 GSGSGTEFTLTSSLPEDFAFYICLQH-NGYPRTFGGTKVEIKRTVAAPSVFPPSD 118
DB 85 GSGSGTDPTLTISRLEPEDFAVYCYQYGTSRPTFGGTGLDRIKRTVAAPSVFPPSD 144
QY 119 EQLKSGTSASVCLLNFPYPREAKEHOK 145
DB 145 EQLKSGTSASVCLLNFPYPREAKVQWK 171

RESULT 12

ID	Q6GMV9	PRELIMINARY;	PRT;	235 AA.
AC	Q6GMV9;			
DT	05-JUL-2004 (TREMBLrel. 27, Created)			
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)			
DE	Hypothetical protein.			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RC	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haieh F., Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshikiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RT				
RL				
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RC	Strausberg R.;			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; BC073793; ANH73793.1; -.			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG MHC.			
DR	Pham; PF07654; Cl-set; 1.			
DR	Pham; PF00047; IG; 2.			

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DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 69.5%; Score 530.5; DB 2; Length 235;
Best Local Similarity 70.5%; Pred. No. 4.5e-45;
Matches 103; Conservative 17; Mismatches 25; Indels 1; Gaps 1;

Qy 1 SQSPSSLSASVGERVTITCRASQGRDE-LGWYQKPGKAPKRLIYVASSLQSGVPSRFS 59
Db 25 TQSPATLSLSPGERATLSRASQIVSSAYLAWYQKPGQAPRLLMFGSSSRATGIPDRFS 84

Qy 60 GSGSGTEFTLTISLQPEDFATYICLQHGNGYPRFTFGQGTKEIKRTVAAPSVFIPPSPDE 119
Db 85 GSGSGTDFLTITSLRLEPDEFAVYFCQYSGQGTGFGPQTKVDIKRTVAAPSVFIPPSPDE 144

Qy 120 QLKSGTASVCLNNFYPREAKEHOK 145
Db 145 QLKSGTASVCLNNFYPREAKVQWK 170

RESULT 14
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=glandular pool- thyroid;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,
RA Kryzyski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IGV.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 236 AA; 26454 MW; 2C506BFB5EA10F4C CRC64;

Query Match 65.9%; Score 503; DB 2; Length 236;
Best Local Similarity 69.1%; Pred. No. 2.7e-42;
Matches 96; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQGRDELGLWYQKPGKAPKRLIYVASSLQSGVPSRFS 60
Db 27 TQSPSSMYASLGERVTITCRASQDINSYLSWFOQPGKSPKLIYRANRLVDGVPDRFS 86

Qy 61 GSGSGTEFTLTISLQPEDFATYICLQHGNGYPRFTFGQGTKEIKRTVAAPSVFIPPSPDEQ 120
Db 87 GSGGQDYSLTITSLSEYEDMGIIYCLQVDEPRTTGGGTGKLEIKRADAAPTYSVFIPPSPSEQ 146

Qy 121 LKSGTASVCLNNFYPRE 139
Db 147 LTSGGASVVCFLNNFYPRKD 165
```

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DR InterPro; IPR003596; IGV.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BBE4FF5F27 CRC64;

Query Match 69.1%; Score 527; DB 2; Length 236;
Best Local Similarity 70.7%; Pred. No. 1e-44;
Matches 104; Conservative 16; Mismatches 25; Indels 2; Gaps 2;

Qy 1 SQSPSSLSASVGERVTITCRASQGI-RDELGWYQKPGKAPKRLIYVASSLQSGVPSRFS 59
Db 25 TQSPGTUSFSPGERATLSRASQIVSSHLAWYQORPGQAPRLIYLGASSRATGIPDRFS 84

Qy 60 GSGSGTEFTLTISLQPEDFATYICLQHGNGYPR-TFGQGTKEIKRTVAAPSVFIPPSPD 118
Db 85 GSGSGTDFLTITRLEPDEFAVYFCQYGTSPSLTFGGGTRVEIKRTVAAPSVFIPPSPD 144

Qy 119 EQLKSGTASVCLNNFYPREAKEHOK 145
Db 145 EQLKSGTASVCLNNFYPREAKVQWK 171

RESULT 15
Q7TS98 PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93383497; PubMed=8372513;
RA Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 1116NS19.9 heavy and light chain
RT cDNAs and expression of antibody fragments in Escherichia coli.";
RL Year Immunol. 7:56-62 (1993).
DR EMBL; S65921; AAB28160.1; -.
DR HSSP; P01837; 1KB5.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IGV.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 236 AA; 26454 MW; 2C506BFB5EA10F4C CRC64;

Query Match 65.9%; Score 503; DB 2; Length 236;
Best Local Similarity 69.1%; Pred. No. 2.7e-42;
Matches 96; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQGRDELGLWYQKPGKAPKRLIYVASSLQSGVPSRFS 60
Db 27 TQSPSSMYASLGERVTITCRASQDINSYLSWFOQPGKSPKLIYRANRLVDGVPDRFS 86

Qy 61 GSGSGTEFTLTISLQPEDFATYICLQHGNGYPRFTFGQGTKEIKRTVAAPSVFIPPSPDEQ 120
Db 87 GSGGQDYSLTITSLSEYEDMGIIYCLQVDEPRTTGGGTGKLEIKRADAAPTYSVFIPPSPSEQ 146

Qy 121 LKSGTASVCLNNFYPRE 139
Db 147 LTSGGASVVCFLNNFYPRKD 165
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Search completed: March 8, 2005, 06:35:47
Job time : 55.8971 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 68.1532 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 763

Sequence: 1 SQSPSSLASVGERVTTCR.....VVCLLNFPYREAHQKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	763	100.0	147	2	AAY34310 IgM antib
2	698	91.5	236	5	ABG77164 Germline
3	698	91.5	236	8	ADR28586 Human ant
4	697	91.3	184	8	ADS84439 Human ant
5	697	91.3	184	8	ADR68581 Human ant
6	696	91.2	236	5	ABG77160 Germline
7	696	91.2	236	8	ADR28582 Human ant
8	695	91.1	147	2	AAY34312 IgM antib
9	691	90.6	234	8	ADR584470 Human ant
10	691	90.6	234	8	ADR68612 Human ant
11	690	90.4	215	8	ADH10328 Anti-HIV-
12	690	90.4	234	8	ADS844464 Human ant
13	690	90.4	234	8	ADR68606 Human ant
14	689	90.3	152	8	ADK52390 Human ant
15	688	90.2	234	8	ADS84476 Human ant
16	688	90.2	234	8	ADS84452 Human ant
17	688	90.2	234	8	ADR68618 Human ant
18	688	90.2	234	8	ADR68594 Human ant
19	686	89.9	236	8	ADP07905 Human imm
20	683	89.5	152	8	ADK52354 Human ant
21	682	89.4	234	8	ADR684458 Human ant
22	682	89.4	234	8	ADR68600 Human ant
23	675	88.5	236	5	ABG77163 Amino aci
24	675	88.5	236	8	ADR28585 Human ant
25	670	87.8	236	5	ABG77159 Amino aci

26	670	87.8	236	8	ADR28581	Adr28581 Human ant
27	665	87.2	164	7	ADD28242	Ad28242 Human ant
28	662	86.8	212	6	AAO31100	Aao31100 Human A2-
29	653	85.6	233	8	ADR46823	Adr46823 Human ant
30	651	85.3	214	7	ADFL1431	Adfl1431 18B2 anti
31	649	85.1	236	5	AAU74297	Aau74297 Anti-huma
32	648.5	85.0	234	2	AAK38162	Aak38162 Human imm
33	646	84.7	224	4	AAW75043	Aaw75043 TRO005 Hu
34	644	84.4	214	2	AAV08600	Aav08600 JP1112785
35	642	84.1	214	8	ADFL11669	Adfl11669 anti-CD11
36	642	84.1	224	4	AAW75040	Aaw75040 TRO005 Hu
37	642	84.1	236	2	AAK42065	Aak42065 Human ant
38	641	84.0	136	5	ABG77135	Abg77135 Anti-IGF-
39	641	84.0	136	8	ADR28536	Adr28536 Human ant
40	640	83.9	224	4	AAW75044	Aaw75044 TRO005 Hu
41	640	83.9	224	4	AAW75041	Aaw75041 TRO005 Hu
42	639	83.7	234	7	ADM47073	Adm47073 Mouse ant
43	638	83.6	164	2	AAV34317	Aav34317 IgG antib
44	638	83.6	214	7	ADFL1423	Adfl1423 2B11 anti
45	636.5	83.4	241	4	AAW82912	Aaw82912 Human imm

ALIGNMENTS

RESULT 1
AAY34310
ID AAY34310 standard; protein; 147 AA.
XX
AC AAY34310;
XX
DT 19-NOV-1999 (first entry)
XX
DE Igm antibody CEM 10.1 G10 kappa chain sequence.
XX

KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

XX WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX WPI; 1999-540816/45.

XX DR N-PSDB; AA220411.

XX PT New monoclonal antibody, used for treating e.g. graft versus host

XX FT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 61; Fig 25; 245pp; English.

XX CC This sequence represents the kappa chain of an antibody of the invention.

XX CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes

XX CC complement and a variable region that binds to the epitope on CD147 bound

XX CC by the Igm Mab ABX-CBL, providing that the antibody is not CBL1. The Mab

XX CC can selectively kill activated T-cells, activated B-cells or resting or

XX CC activated monocytes. The products and methods can be used for treating or

XX CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft

XX CC versus host disease (GVHD), organ transplant rejection diseases (e.g.

XX CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

PF 10-OCT-2003; 2003US-00684109.
PR 14-OCT-2002; 2002US-0418031P.
XX
XX (DEV)/ DEVRIES P J.
PA (OSTR)/ OSTROW D H.
PA (REIL)/ REILLY E B.
PA (GREE)/ GREEN L L.
PA (WIEL)/ WIELER J.
XX
PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
XX
XX WPI; 2004-661369/64.
DR N-PSDB; ADR68579, ADR68586.
XX
XX New antibody or its antibody fragment that activates an endogenous
PT activity or is capable of binding to a human erythropoietin receptor in a
PT mammal, useful for treating a mammal suffering aplasia or anemia.
XX
XX Claim 41; SEQ ID NO 78; 156pp; English.
XX
XX The invention describes an antibody or its fragment that activates an
CC endogenous activity or capable of binding to a human erythropoietin
CC receptor in a mammal, or that comprises at least one heavy or light chain
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC ID NO: 3 or 5) given in the specification or its fragment, but does not
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC given in the specification. Also described are: a method of activating or
CC modulating an endogenous activity of a human erythropoietin receptor in a
CC mammal; a pharmaceutical composition comprising a therapeutic amount of
CC an antibody or antibody fragment above and a pharmaceutical excipient; an
CC isolated and purified polynucleotide sequence selected from 28 sequences
CC comprising 322-370 bp (even SEQ ID NOs between SEQ ID NO: 2-56) given in
CC the specification, and their fragments, complements, and degenerate codon
CC equivalents; and an isolated and purified amino acid sequence selected
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOs between
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC their fragments. The antibody or its antibody fragment that activates or
CC modulates the activity of the receptor is useful in a method of treating
CC a mammal suffering aplasia or anemia. The antibodies are also useful for
CC treating disorders characterised by decreased or subnormal levels of
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
CC hypoxia and/or diseases characterised by inadequate blood circulation or
CC reduced blood flow. They are also useful for promoting wound healing or
CC for protecting against neural cell and/or tissue damage, resulting from
CC brain/spinal cord injury, stroke and the like. The antibodies are also
CC useful for identifying or diagnosing mammals having dysfunctional
CC erythropoietin receptor. This is the amino acid sequence of a human Ab12
XX antibody light chain polypeptide.
XX
XX Sequence 184 AA;
Query Match 91.3%; Score 697; DB 8; Length 184;
Best Local Similarity 93.1%; Pred. No. 1e-43;
Matches 135; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 1 SQSPSSLSASGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 60
Db 27 TQSPSSLSASVGDRTVITCRASQGIIRNDLWYQKPGKAPKRLIYVASSLSQGVPSRFSG 86
QY 61 SSGSGTEFTLTISLQPEDFATYYCLQHNQYPRFTGQGTKEIKRTVAAPSFIFFPSDEQ 120
Db 87 SSGSGTEFTLTISLQPEDFATYYCLQHNQYPTFTGQGTKEIKRTVAAPSFIFFPSDEQ 146
QY 121 LKSGTASVCLLNFPYPREAKEHOK 145
Db 147 LKSGTASVCLLNFPYPREAKVQWK 171
RESULT 6
ABG77160
ID ABG77160 standard; protein; 236 AA.
XX

AC ABG77160;
XX
XX 24-OCT-2002 (first entry)
XX
XX Germline protein sequence of anti-IGF-IR antibody AJ30/Jk2.
XX
XX Insulin-like growth factor I receptor; antibody; human; cytostatic;
KW osteopathic; antiatherosclerotic; antiapoptotic; IGF-IR; tumour;
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
KW acromegaly; gigantism; psoriasis; atherosclerosis.
XX
XX Homo sapiens.
XX
XX WO200253596-A2.
XX
XX 11-JUN-2002.
XX
XX 20-DEC-2001; 2001WO-US0511113.
XX
XX 05-JAN-2001; 2001US-0259927P.
XX
XX (PFIZ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX
XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
XX WPI; 2002-575410/61.
XX
XX Novel humanized, chimeric monoclonal antibody that specifically binds to
PT insulin-like growth factor I (IGF-I) receptor useful for inhibiting
PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
XX
XX Disclosure; Fig 19C; 172pp; English.
XX
XX This invention relates to a novel humanised, chimeric or human monoclonal
CC antibody or its antigen binding portion that specifically binds to
CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the
CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
CC phosphorylation. The antibodies of the invention are useful for
CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
CC subject. The antibody or its antigen-binding portion is also useful for
CC treating cancer in a human. The method for this further involves an anti
CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
CC antibodies may also be useful for increasing IGF-IR activity and thus
CC restoring IGF-IR activity in a condition characterised by low IGF-IR
CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
CC also useful for inducing apoptosis of specific cells in a patient, and to
CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,
CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
CC minimise the immunogenic and allergic responses intrinsic to mouse or
CC mouse-derived monoclonal antibodies and thus increase the efficacy
CC and safety of the administered antibodies. The present sequence
CC represents an anti-insulin-like growth factor I receptor antibody of the
XX invention
XX
XX Sequence 236 AA;
Query Match 91.2%; Score 696; DB 5; Length 236;
Best Local Similarity 92.4%; Pred. No. 1.5e-43;
Matches 134; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 SQSPSSLSASGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 60
Db 27 TQSPSSLSASVGDRTVITCRASQGIIRNDLWYQKPGKAPKRLIYVASSLSQGVPSRFSG 86
QY 61 SSGSGTEFTLTISLQPEDFATYYCLQHNQYPRFTGQGTKEIKRTVAAPSFIFFPSDEQ 120
Db 87 SSGSGTEFTLTISLQPEDFATYYCLQHNQYPTFTGQGTKEIKRTVAAPSFIFFPSDEQ 146
QY 121 LKSGTASVCLLNFPYPREAKEHOK 145
Db 147 LKSGTASVCLLNFPYPREAKVQWK 171

Db 2 QSPSSLSASVGDRTTITCRASQIRDLNLGWYQKPGKAPKRLIYAASLQSGVPSRFGS 61
 Qy 62 GSGTEFTLTISLQPEDFATYCYLQHNQYPRFTGGTKEIKRTVAAPSFIIPPSDEQL 121
 Db 62 GSGTEFTLTISLQPEDFATYCYLQHNQYPRFTGGTKEIKRTVAAPSFIIPPSDEQL 121
 Qy 122 KSGTASVCLNNFYPREAKEHOKSP 147
 Db 122 KSGTASVCLNNFYPREAKEHOKSP 147
 RESULT 9
 ID ADS84470 standard; protein; 234 AA.
 XX ADS84470;
 XX 18-NOV-2004 (first entry)
 XX Human anti-EPO-R antibody Ab467 light chain SEQ ID NO:109.
 XX human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
 XX Homo sapiens.
 OS WO2004035603-A2.
 PN 29-APR-2004.
 XX 14-OCT-2003; 2003WO-US032243.
 PF 14-OCT-2002; 2002US-00269711.
 PR 10-OCT-2003; 2003US-00684109.
 XX (ABBO) ABBOTT LAB.
 PA Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 PI WPI; 2004-348433/32.
 DR N-PSDB; ADS84468, ADS84469.
 XX New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.
 XX Disclosure; SEQ ID NO 109; 192pp; English.
 XX The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,
 CC complements and degenerate codon equivalents; and (5) an isolated and
 CC purified amino acid sequence, and their fragments. The EPO receptor
 CC binding antibody has antianemic, neuroprotective and vulnerary
 CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from

CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence represents a human anti-EPO-R antibody light
 CC chain, which is given in the exemplification of the present invention.
 XX Sequence 234 AA;
 SQ
 Query Match 90.6%; Score 691; DB 8; Length 234;
 Best Local Similarity 91.7%; Pred. No. 3.5e-43;
 Matches 133; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 SQSPSSLSASVGERVTITCRASQIRDLNLGWYQKPGKAPKRLIYAASLQSGVPSRFGS 60
 Db 25 TQSPSSLSASVGDRTTITCRASQIRDLNLGWYQKPGKAPKRLIYAASLQSGVPSRFGS 84
 Qy 61 GSGTEFTLTISLQPEDFATYCYLQHNQYPRFTGGTKEIKRTVAAPSFIIPPSDEQ 120
 Db 85 GSGTEFTLTISLQPEDFATYCYLQHNQYPRFTGGTKEIKRTVAAPSFIIPPSDEQ 144
 Qy 121 LKSGTASVCLNNFYPREAKEHOK 145
 Db 145 LKSGTASVCLNNFYPREAKEHOK 169
 RESULT 10
 ADS84470
 ID ADS84470 standard; protein; 234 AA.
 XX ADS84470;
 XX 02-DEC-2004 (first entry)
 XX Human antibody Ab467 light chain polypeptide seqid 109.
 XX antianemic; respiratory; vulnerary; gene therapy; vaccine;
 KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
 KW wound healing; neural cell damage; tissue damage; brain injury;
 KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;
 KW AB467.
 XX Homo sapiens.
 OS US2004175379-A1.
 PN 09-SEP-2004.
 PD 10-OCT-2003; 2003US-00684109.
 PF 14-OCT-2002; 2002US-0418031P.
 PR (DEVRI) DEVRIES P J.
 PA (OSTR) OSTROW D H.
 PA (REIL) REILLY E B.
 PA (GREE) GREEN L L.
 PA (WIEL) WIELER J.
 XX Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
 PI WPI; 2004-661369/64.
 DR N-PSDB; ADS84610.
 XX New antibody or its antibody fragment that activates an endogenous
 PT activity or is capable of binding to a human erythropoietin receptor in a
 PT mammal, useful for treating a mammal suffering aplasia or anemia.
 XX Disclosure; SEQ ID NO 109; 156pp; English.
 PS The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin
 CC receptor in a mammal, or that comprises at least one heavy or light chain

CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
 CC the specification, and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This sequence represents a human Ab467 antibody
 CC light chain polypeptide.
 XX
 SQ Sequence 234 AA;

Query Match 90.6%; Score 691; DB 8; Length 234;
 Best Local Similarity 91.7%; Pred. No. 3.5e-43;
 Matches 133; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 60
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 25 TQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 84
 QY 61 SSGSGTEFTLTISLQPEDFATYCYCLOHNGYPRFGQTKVEIKRTVAAPSVFIFFPSDEQ 120
 Db 85 SSGSGTEFTLTISLQPEDFATYCYCLOHNSYPLTFGGGTKVEIKRTVAAPSVFIFFPSDEQ 144
 QY 121 LKSGTASVVCLNNFPYPREAKEHQK 145
 Db 145 LKSGTASVVCLNNFPYPREAKEQWK 169

RESULT 11
 ADH10328
 ID ADH10328 standard; protein; 215 AA.
 XX
 AC ADH10328;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Anti-HIV-gp120-antibody light chain sequence.
 XX
 KW Glycoprotein; gp120; anti-HIV; vaccine; antibody S8; human; antibody S19;
 KW antibody S20.
 XX
 OS Homo sapiens.
 XX
 PN EP1371660-A1.
 XX
 PD 17-DEC-2003.
 XX
 PF 14-JUN-2002; 2002EP-00380126.
 XX
 PR 14-JUN-2002; 2002EP-00380126.
 XX
 PA (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
 PA (PHAA) PHARMACIA SPAIN.
 XX
 PI Toran JL, Martinez Alonso C;
 XX

DR WPI; 2004-055251/06.
 DR N-PSDB; ADH10327.
 XX
 PT Novel antibody or its fragment comprising a light chain and/or heavy
 PT chain which is capable of binding to glycoprotein gp120 of human
 PT immunodeficiency virus (HIV) useful for treating HIV infection.
 XX
 PS Claim 1; SEQ ID NO 2; 56pp; English.
 XX
 CC The invention relates to an antibody (I) or its fragment comprising heavy
 CC chain and/or light chain, capable of binding to glycoprotein gp120
 CC protein of HIV, anti-HIV vaccine (I) or a chemical compound identified by
 CC (I) is useful for preventing and treating HIV infections. They are also
 CC useful for inhibiting binding of HIV to a viral co-receptor. The present
 CC sequence represents the light chain sequence of anti-HIV-gp120 antibody
 CC S8, S19 and S20.
 XX
 SQ Sequence 215 AA;

Query Match 90.4%; Score 690; DB 8; Length 215;
 Best Local Similarity 91.7%; Pred. No. 3.8e-43;
 Matches 133; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 60
 Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 3 TQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQGVPSRFSG 62
 QY 61 SSGSGTEFTLTISLQPEDFATYCYCLOHNGYPRFGQTKVEIKRTVAAPSVFIFFPSDEQ 120
 Db 63 SSGSGTEFTLTISLQPEDFATYCYCLOHNSYPLTFGGGTKVEIKRTVAAPSVFIFFPSDEQ 122
 QY 121 LKSGTASVVCLNNFPYPREAKEHQK 145
 Db 123 LKSGTASVVCLNNFPYPREAKEQWK 147

RESULT 12
 ADS84464
 ID ADS84464 standard; protein; 234 AA.
 XX
 AC ADS84464;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human anti-EPO-R antibody Ab430 light chain SEQ ID NO:103.
 XX
 KW human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianemic; neuroprotective; vulnerrary; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO2004035603-A2.
 XX
 PD 29-APR-2004.
 XX
 PF 14-OCT-2003; 2003WO-US032243.
 XX
 PR 14-OCT-2002; 2002US-00269711.
 PR 10-OCT-2003; 2003US-00684109.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 XX
 DR WPI; 2004-348433/32.
 DR N-PSDB; ADS84462, ADS84463.
 XX
 PT New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating

Db	25	TQSPSSLGASVGDRTTTCRTSQGIRNDLGWYQQKPGHAPKRLIYAASSLQSGVPSRFSG	84
Qy	61	SGSGTEFTLTISLQPEDFATYYCLQHNQYPRTFGGGTKEIKRTVAAPSVFIPEPSDEQ	120
Db	85	SGSGTEFTLTISLQPEDFATYYCLQHNQYPRTFGGGTKEIKRTVAAPSVFIPEPSDEQ	144
Qy	121	LKSGTASVVCLLNNFYPREAKEHQK	145
Db	145	LKSGTASVVCLLNNFYPREAKVQWK	169

Search completed: March 8, 2005, 06:17:08
Job time : 69.1532 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 78.009 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 763

Sequence: 1 SQSPSSLSASVGERVTTCR.....VVCLLNYPREAKEHQKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	698	91.5	236	15	US-10-038-591-52
2	697	91.3	184	16	US-10-684-109-78
3	696	91.2	236	15	US-10-038-591-48
4	692	90.7	153	15	US-10-309-762-245
5	691	90.6	234	16	US-10-684-109-109
6	690	90.4	215	16	US-10-462-040A-2
7	690	90.4	234	16	US-10-684-109-103
8	688	90.2	234	16	US-10-684-109-91
9	688	90.2	234	16	US-10-684-109-115
10	682	89.4	234	16	US-10-684-109-97
11	675	88.5	236	15	US-10-038-591-51
12	670	87.8	236	15	US-10-038-591-47
13	662	86.8	212	14	US-10-320-231A-77

14	651	85.3	214	15	US-10-408-501-44	Sequence 44, Appl
15	649.5	85.1	163	15	US-10-364-743-20	Sequence 20, Appl
16	649	85.1	236	9	US-09-859-053-30	Sequence 30, Appl
17	649	85.1	236	16	US-10-625-105-30	Sequence 3, Appl
18	642	84.1	214	15	US-10-423-299-3	Sequence 2, Appl
19	641	84.0	136	15	US-10-038-591-2	Sequence 36, Appl
20	638	83.6	214	15	US-10-408-501-36	Sequence 1, Appl
21	636.5	83.4	241	14	US-10-221-945-1	Sequence 66, Appl
22	636	83.4	223	16	US-10-693-629-66	Sequence 19, Appl
23	631	82.7	233	16	US-10-663-244-150	Sequence 166, Appl
24	630	82.6	214	14	US-10-153-382-19	Sequence 11, Appl
25	628	82.3	211	15	US-10-379-392-166	Sequence 170, App
26	628	82.3	214	15	US-10-364-553-11	Sequence 48, Appl
27	628	82.3	214	16	US-10-379-392-170	Sequence 8, Appl
28	628	82.3	234	15	US-10-292-088-48	Sequence 4, Appl
29	628	82.3	237	14	US-10-020-786-8	Sequence 5, Appl
30	628	82.3	237	14	US-10-227-694-4	Sequence 2, Appl
31	628	82.3	237	17	US-10-754-212-5	Sequence 11, Appl
32	625	81.9	214	9	US-09-940-166A-2	Sequence 11, Appl
33	625	81.9	214	9	US-09-811-384-11	Sequence 6, Appl
34	625	81.9	214	15	US-10-404-286-11	Sequence 1, Appl
35	625	81.9	214	16	US-10-762-967-2	Sequence 11, Appl
36	625	81.9	237	9	US-09-940-166A-6	Sequence 2, Appl
37	625	81.9	237	14	US-10-227-694-1	Sequence 1, Appl
38	625	81.9	237	16	US-10-762-967-6	Sequence 6, Appl
39	625	81.9	237	17	US-10-754-212-2	Sequence 2, Appl
40	624	81.8	208	15	US-10-634-581-1	Sequence 1, Appl
41	624	81.8	211	16	US-10-379-392-144	Sequence 144, App
42	624	81.8	214	9	US-09-949-559-128	Sequence 128, App
43	624	81.8	214	10	US-09-875-221A-128	Sequence 128, App
44	624	81.8	214	14	US-10-310-454-4	Sequence 4, Appl
45	624	81.8	214	17	US-10-728-420B-113	Sequence 113, App

ALIGNMENTS

RESULT 1

US-10-038-591-52
; Sequence 52, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-52

Query Match	91.5%	Score 698;	DB 15;	Length 236;
Best Local Similarity	93.1%	Pred. No. 5.5e-43;		
Matches 135;	Conservative 4;	Mismatches 6;	Indels 0;	Gaps 0;
QY	1	SQSPSSLSASVGERVTTCRASQGRDELGWVQQKPGKAPKRLIYVASSLSQGVSRFSG	60	
Db	27	TQSPSSLSASVGDRTTTCRASQGRINDLGMVQQKPGKAPKRLIYVASSLSQGVSRFSG	86	
QY	61	SGSGTEFTLTSSLOPEDFATYVCLQHNQYPTFCQGTKEIKRTVAAPSVFIFPPSDEQ	120	
Db	87	SGSGTEFTLTSSLOPEDFATYVCLQHNQYPTFCQGTKEIKRTVAAPSVFIFPPSDEQ	146	

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Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
      |||||
Db 147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 2
US-10-684-109-78
; Sequence 78, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: Antibodies
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-78

Query Match 91.3%; Score 697; DB 16; Length 184;
Best Local Similarity 93.1%; Pred. No. 5,1e-43;
Matches 135; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
      :|||||
Db 27 TQSPSSLSASVGDRTTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 86

Qy 61 SSGSGTEFTLTSSLOPEDFATYCYCLOHNGYPRTFQGGTKVEIKRTVAAPSFIIPPSPDEQ 120
      :|||||
Db 87 SSGSGTEFTLTSSLOPEDFATYCYCLOHNTYPTTFQGGTKVEIKRTVAAPSFIIPPSPDEQ 146

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
      |||||
Db 147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 3
US-10-038-591-48
; Sequence 48, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-48
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Query Match 91.2%; Score 696; DB 15; Length 236;
Best Local Similarity 92.4%; Pred. No. 7,6e-43;
Matches 134; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
      :|||||
Db 27 TQSPSSLSASVGDRTTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 86

Qy 61 SSGSGTEFTLTSSLOPEDFATYCYCLOHNGYPRTFQGGTKVEIKRTVAAPSFIIPPSPDEQ 120
      :|||||
Db 87 SSGSGTEFTLTSSLOPEDFATYCYCLOHNSYPTTFQGGTKLEIKRTVAAPSFIIPPSPDEQ 146

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
      |||||
Db 147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 4
US-10-309-762-245
; Sequence 245, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudae, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: AGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-245

Query Match 90.7%; Score 692; DB 15; Length 153;
Best Local Similarity 92.4%; Pred. No. 1e-42;
Matches 134; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
      :|||||
Db 5 TQSPSSLSASVGDRTTITCRASQGIIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 64

Qy 61 SSGSGTEFTLTSSLOPEDFATYCYCLOHNGYPRTFQGGTKVEIKRTVAAPSFIIPPSPDEQ 120
      :|||||
Db 65 SSGSGTEFTLTSSLOPEDFATYCYCLOHNSYPLTFGGGTKVEIKRTVAAPSFIIPPSPDEQ 124

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
      |||||
Db 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 5
US-10-684-109-109
; Sequence 109, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: Antibodies
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
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; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-109

Query Match
Best Local Similarity 90.6%; Score 691; DB 16; Length 234;
Matches 133; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 25 TQSPSSLSASVGDRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 84

Qy 61 SSGTEFTLTSSLOPEDFATYVCLQHNQYPRTFQGGTKVEIKRTVAAPSVFIFFPSDEQ 120
Db 85 SSGTEFTLTSSLOPEDFATYVCLQHNQSYPCFQGGTKLEIKRTVAAPSVFIFFPSDEQ 144

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 145 LKSGTASVVCLLNNFYPREAKVQWK 169

RESULT 6
US-10-462-040A-2
; Sequence 2, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP-B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Light chain
US-10-462-040A-2

Query Match
Best Local Similarity 90.4%; Score 690; DB 16; Length 215;
Matches 133; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 3 TQSPSSLSASVGDRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 62

Qy 61 SSGTEFTLTSSLOPEDFATYVCLQHNQYPRTFQGGTKVEIKRTVAAPSVFIFFPSDEQ 120
Db 63 SSGTEFTLTSSLOPEDFATYVCLQHNQSYPLTFQGGTKVEIKRTVAAPSVFIFFPSDEQ 122

Qy 121 LKSGTASVVCLLNNFYPREAKEHOK 145
Db 123 LKSGTASVVCLLNNFYPREAKVQWK 147

RESULT 7
US-10-684-109-103
; Sequence 103, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-103

Query Match
Best Local Similarity 90.4%; Score 690; DB 16; Length 234;
Matches 133; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 25 TQSPSSLSASVGDRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 84

Qy 61 SSGTEFTLTSSLOPEDFATYVCLQHNQYPRTFQGGTKVEIKRTVAAPSVFIFFPSDEQ 120
Db 85 SSGTEFTLTSSLOPEDFATYVCLQHNQSYPTFGPGTKVDIKRTVAAPSVFIFFPSDEQ 144

RESULT 8
US-10-684-109-91
; Sequence 91, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-91

Query Match
Best Local Similarity 90.2%; Score 688; DB 16; Length 234;
Matches 132; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 25 TQSPSSLSASVGDRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 84

Qy 61 SSGTEFTLTSSLOPEDFATYVCLQHNQYPRTFQGGTKVEIKRTVAAPSVFIFFPSDEQ 120
Db 85 SSGTEFTLTSSLOPEDFATYVCLQHNQSYPCFQGGTKLEIKRTVAAPSVFIFFPSDEQ 144
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```
Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
| | | | | | | | | | | | | | | | | |
Db 145 LKSGTASVVCLLNNFYPREAKVQWK 169

RESULT 9
US-10-684-109-115
; Sequence 115, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-115

Query Match 90.2%; Score 688; DB 16; Length 234;
Best Local Similarity 91.7%; Pred. No. 2.9e-42;
Matches 133; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 60
Db 25 TQSPSSLSASVGDRTTTCRTSQIRNDLWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 84

Qy 61 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGQGTKEIKRTVAAPSFIIPPDSDEQ 120
Db 85 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGGKVEIKRTVAAPSFIIPPDSDEQ 144

Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
| | | | | | | | | | | | | | | | | |
Db 145 LKSGTASVVCLLNNFYPREAKVQWK 169

RESULT 10
US-10-684-109-97
; Sequence 97, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-97

Query Match 89.4%; Score 682; DB 16; Length 234;
Best Local Similarity 91.7%; Pred. No. 2.9e-42;
Matches 133; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 60
Db 25 TQSPSSLSASVGDRTTTCRTSQIRNDLWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 84

Qy 61 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGQGTKEIKRTVAAPSFIIPPDSDEQ 120
Db 85 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGGKVEIKRTVAAPSFIIPPDSDEQ 144

Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
| | | | | | | | | | | | | | | | | |
Db 145 LKSGTASVVCLLNNFYPREAKVQWK 169

RESULT 11
US-10-038-591-51
; Sequence 51, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 51
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-51

Query Match 88.5%; Score 675; DB 15; Length 236;
Best Local Similarity 90.3%; Pred. No. 2.5e-41;
Matches 131; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 60
Db 27 TQSPSSLSASVGDRTTTCRASQDIRDLGWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 86

Qy 61 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGQGTKEIKRTVAAPSFIIPPDSDEQ 120
Db 87 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGQGTVEIIRTVAAPSFIIPPDSDEQ 146

Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
| | | | | | | | | | | | | | | | | |
Db 147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 12
US-10-038-591-47
; Sequence 47, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
```

```
Best Local Similarity 91.0%; Pred. No. 7.8e-42;
Matches 132; Conservative 5; Mismatches 8; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 60
| | | | | | | | | | | | | | | | | |
Db 25 TQSPSSLSASVGDRTTTCRASQDIRDLGWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 84

Qy 61 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGQGTKEIKRTVAAPSFIIPPDSDEQ 120
| | | | | | | | | | | | | | | | | |
Db 85 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGGKVEIKRTVAAPSFIIPPDSDEQ 144

Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
| | | | | | | | | | | | | | | | | |
Db 145 LKSGTASVVCLLNNFYPREAKVQWK 169

RESULT 11
US-10-038-591-51
; Sequence 51, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 51
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-51

Query Match 88.5%; Score 675; DB 15; Length 236;
Best Local Similarity 90.3%; Pred. No. 2.5e-41;
Matches 131; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 60
Db 27 TQSPSSLSASVGDRTTTCRASQDIRDLGWYQKPGKAPKRLIYVASSLSQSGVPSRPSG 86

Qy 61 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGQGTKEIKRTVAAPSFIIPPDSDEQ 120
Db 87 SSGSTEFTLTSSLOPEDFATYVCLQHNQYPRRTFGQGTVEIIRTVAAPSFIIPPDSDEQ 146

Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
| | | | | | | | | | | | | | | | | |
Db 147 LKSGTASVVCLLNNFYPREAKVQWK 171

RESULT 12
US-10-038-591-47
; Sequence 47, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
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; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-47

Query Match      87.8%; Score 670; DB 15; Length 236;
Best Local Similarity 89.0%; Pred. No. 5.7e-41;
Matches 129; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 27 TQFPSSLSASVGDVRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 86

Qy 61 SSGTTEFTLTSSSQPEDFATYYCLQHNQYPRTFQGTQKVEIKRTVAAPSFIPPPSDEQ 120
Db 87 SSGTTEFTLTSSSQPEDFATYYCLQHNQYPRTFQGTQKVEIKRTVAAPSFIPPPSDEQ 146

Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
Db 147 LKSGTASVVCLLNNFYPREAKEVQWK 171

RESULT 13
US-10-320-231A-77
; Sequence 77, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 77
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-77

Query Match      86.8%; Score 662; DB 14; Length 212;
Best Local Similarity 89.7%; Pred. No. 2e-40;
Matches 130; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 3 TQSPSSLSASVGDVRTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 62

Qy 61 SSGTTEFTLTSSSQPEDFATYYCLQHNQYPRTFQGTQKVEIKRTVAAPSFIPPPSDEQ 120
Db 63 SSGTDFLTSSSQPEDFATYYCQYSGMPYTFQGTQKVEIKRTVAAPSFIPPPSDEQ 122

Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
Db 123 LKSGTASVVCLLNNFYPREAKEVQWK 147

RESULT 14
US-10-408-901-44
; Sequence 44, Application US/10408901
; Publication No. US2004002313A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 44
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-44

Query Match      85.3%; Score 651; DB 15; Length 214;
Best Local Similarity 88.3%; Pred. No. 1.2e-39;
Matches 128; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQIGISTWLAWYQKPEKAPKSLIYAASSLSQSGVPSRFSG 64

Qy 61 SSGTTEFTLTSSSQPEDFATYYCLQHNQYPRTFQGTQKVEIKRTVAAPSFIPPPSDEQ 120
Db 65 SSGTDFLTSSSQPEDFATYYCQYNSYPTTQGTQKVEIKRTVAAPSFIPPPSDEQ 124

Qy 121 LKSGTASVVCLLNNFYPREAKEHQK 145
Db 125 LKSGTASVVCLLNNFYPREAKEVQWK 149

RESULT 15
US-10-364-743-20
; Sequence 20, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178Alan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 163
; TYPE: PRT
; ORGANISM: human
US-10-364-743-20

Query Match      85.1%; Score 649.5; DB 15; Length 163;
Best Local Similarity 87.6%; Pred. No. 1.2e-39;
Matches 127; Conservative 6; Mismatches 11; Indels 1; Gaps 1;

Qy 1 SQSPSSLSASVGERVTITCRASQIGIRDELGWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 7 TQSPSSLSASVGDVRTITCRASQIGVRNALVWY-QKPGKAPERLIYAASILQSGVPSRFSG 65

Qy 61 SSGTTEFTLTSSSQPEDFATYYCLQHNQYPRTFQGTQKVEIKRTVAAPSFIPPPSDEQ 120
Db 66 SSGTTEFTLTGGSQPEDFATYYCLQHNQYPRTFQGTQKVEIKRTVAAPSFIPPPSDEQ 125
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QY 121 LKSGTASVCLNNFYPREAKEHQK 145
126 LKSGTASVCLNNFYPREAKVQWK 150
Db

Search completed: March 8, 2005, 07:05:49
Job time : 79.009 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.1636 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-26

Perfect score: 763

Sequence: 1 SQSPSSLASGVRVTTCR.....VVCLLNFPYPREAKEHQKSP 147

Scoring table: BLASUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A-COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B-COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A-COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B-COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PTUS-COMB.pep:*
6: /cgn2_6/prodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	85.1	236	4	US-09-859-053-30
2	642	84.1	236	1	US-08-157-101A-5
3	630	82.6	214	4	US-09-472-087-96
4	627	82.2	214	2	US-07-934-373C-39
5	627	82.2	214	3	US-08-437-642B-39
6	627	82.2	214	5	PCT-US93-07832-39
7	625	81.9	214	2	US-07-934-373C-40
8	625	81.9	214	2	US-08-788-800-11
9	625	81.9	214	3	US-08-437-642B-40
10	625	81.9	214	3	US-09-097-309-2
11	625	81.9	214	3	US-09-097-171A-2
12	625	81.9	214	3	US-09-460-587-2
13	625	81.9	214	4	US-09-940-166A-2
14	625	81.9	214	5	PCT-US93-07832-40
15	625	81.9	233	2	US-07-934-373C-25
16	625	81.9	233	3	US-08-437-642B-25
17	625	81.9	233	4	US-08-146-206C-25
18	625	81.9	233	4	US-09-705-686-25
19	625	81.9	233	4	US-09-705-392A-25
20	625	81.9	233	4	US-09-705-398-25
21	625	81.9	233	5	PCT-US93-07832-25
22	625	81.9	237	3	US-09-097-309-6
23	625	81.9	237	3	US-09-097-171A-10
24	625	81.9	237	3	US-09-422-712B-2
25	625	81.9	237	3	US-09-607-756-2
26	625	81.9	237	3	US-09-460-587-6
27	625	81.9	237	4	US-09-940-166A-6

28	619	81.1	139	4	US-09-472-087-22	Sequence 22, Appl
29	619	81.1	139	4	US-09-472-087-96	Sequence 96, Appl
30	619	81.1	491	4	US-10-011-125A-2	Sequence 2, Appl
31	618	81.0	233	4	US-08-030-175-43	Sequence 43, Appl
32	616.5	80.8	233	3	US-08-812-586-45	Sequence 45, Appl
33	616.5	80.8	233	4	US-09-535-832A-42	Sequence 42, Appl
34	615	80.6	214	3	US-09-679-397-1	Sequence 1, Appl
35	615	80.6	214	4	US-09-680-148-1	Sequence 1, Appl
36	615	80.6	214	4	US-09-304-465A-1	Sequence 1, Appl
37	615	80.6	237	2	US-08-463-587A-25	Sequence 25, Appl
38	615	80.6	237	2	US-08-463-667A-3	Sequence 3, Appl
39	615	80.6	237	3	US-08-923-854-25	Sequence 25, Appl
40	615	80.6	237	5	PCT-US91-09133-26	Sequence 26, Appl
41	613	80.3	218	5	PCT-US96-13152-2	Sequence 2, Appl
42	611	80.1	218	2	US-08-887-352B-15	Sequence 15, Appl
43	611	80.1	218	2	US-08-887-352B-17	Sequence 17, Appl
44	611	80.1	218	2	US-08-887-352B-19	Sequence 19, Appl
45	611	80.1	218	2	US-08-887-352B-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1

US-09-859-053-30

; Sequence 30, Application US/09859053

; Patent No. 6803039

; GENERAL INFORMATION:

; APPLICANT: Teuji, Takashi

; APPLICANT: Tezuka, Katsunari

; APPLICANT: Horii, No. 6803039uaki

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

; FILE REFERENCE: 06501-079001

; CURRENT APPLICATION NUMBER: US/09/859,053

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: JP 2001-99508

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: JP 2000-147116

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 30

; LENGTH: 236

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-859-053-30

Query Match 85.1%; Score 649; DB 4; Length 236;

Best Local Similarity 88.3%; Pred. No. 3.5e-55;

Matches 128; Conservative 5; Mismatches 12; Indels 0; Gaps 0;

QY 1 SQSPSSLASGVRVTTCRASQGIIRDELGWVQKPGKAPKLLIYVASSLQSGVPSRFSG 60

Db 27 TQSPSSVSASGDRVTTCRASQGISRLLAWYQKPGKAPKLLIYVASSLQSGVPSRFSG 86

QY 61 SGSGTEFTLTSSLOPEDFATYVCLOHNGYPRTFQGTKEIKRTVAAPSVFIFFPSDEQ 120

Db 87 SGSGTDFLTSSLOPEDFATYVCQANSFPWTFQGTKEIKRTVAAPSVFIFFPSDEQ 146

QY 121 LKSGTASVCLLNFPYPREAKEHQK 145

Db 147 LKSGTASVCLLNFPYPREAKEVQWK 171

RESULT 2

US-08-157-101A-5

; Sequence 5, Application US/08157101A

; Patent No. 5808032

; GENERAL INFORMATION:

; APPLICANT: KURIHARA, TATSUYA

; APPLICANT: MATSUKURA, SHIGEKAZU

Query Match 82.6%; Score 630; DB 4; Length 214;
Best Local Similarity 86.2%; Pred. No. 2.1e-53;
Matches 125; Conservative 4; Mismatches 16; Indels

1	SQSPSLASVCERTVITTCRASGGIRDELGWYQQKPGKAPKRLIIVASSLQSGVSRFSG	60
y		
b		
5	TQSPSLASVGDRTVITTCRASQSNYSYLDWYQQKPGKAPKLLIYAASSLQSGVSRFSG	64
y		
b		
61	SGSGTEFTLTISLQPEPATYVCIQHNYPPTFGQGTKEIKRTVAAPSVIFPPSDEQ	120
y		
b		
65	SGSGTDFLTITSSLOPEPATYVCQOYSTPTTFPGTKEIKRTVAAPSVIFPPSDEQ	124
y		
b		
121	LKSGTASVVCLNNFYPREAKEHQK	145
y		
b		
125	LKSGTASVVCLNNFYPREAKVQWK	149
y		
b		

```

RESULT 4
US-07-934-373C-39
; Sequence 39, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESS: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

```

[illegible]

```

; Sequence 71, Application US/09472087
; Patent No. 682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647

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Query Match 82.2%; Score 627; DB 2; Length 214;
Best Local Similarity 84.8%; Pred. No. 4.2e-53;


```

RESULT 7
US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-40

Query Match      81.9%; Score 625; DB 2; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQGIKRWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 5 TQSPSSLSASVGERVTITCRASQDINNLYNQKPGKAPKRLIYVASSLSQSGVPSRFSG 64
Qy 61 SSGSGTEFTLTISLQPEDFATYICLQHNQYPRFTQGGTKVEIKRTVAAPSVFIPPPSDEQ 120
Db 65 SSGSGTDYTLTISLQPEDFATYICQGGNTLPTFTQGGTKVEIKRTVAAPSVFIPPPSDEQ 124
Qy 121 LKSGTASVCLNNFYPREAKEHQK 145
Db 125 LKSGTASVCLNNFYPREAKVQWK 149

RESULT 8
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Gross, Gerald E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-788-800-11

Query Match      81.9%; Score 625; DB 2; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 1 SQSPSSLSASVGERVTITCRASQGIKRWYQKPGKAPKRLIYVASSLSQSGVPSRFSG 60
Db 5 TQSPSSLSASVGERVTITCRASQDINNLYNQKPGKAPKRLIYVASSLSQSGVPSRFSG 64
Qy 61 SSGSGTEFTLTISLQPEDFATYICLQHNQYPRFTQGGTKVEIKRTVAAPSVFIPPPSDEQ 120
Db 65 SSGSGTDYTLTISLQPEDFATYICQGGNTLPTFTQGGTKVEIKRTVAAPSVFIPPPSDEQ 124
Qy 121 LKSGTASVCLNNFYPREAKEHQK 145
Db 125 LKSGTASVCLNNFYPREAKVQWK 149

RESULT 9
US-08-437-642B-40
; Sequence 40, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA: PCT/US92/05126
; APPLICATION NUMBER: 07/715272
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-40

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQQKPGKAPKELIYVASSLSQGVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQDINNVLNMYQQKPGKAPKLLIYTTSLHSGVPSRFSG 64
QY 61 SSGTEFTLTISLQPEDFATYYCLQHNQYPRTFQGGTKVEIKRTVAAPSVFIFFPSDEQ 120
Db 65 SSGGTDYTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSVFIFFPSDEQ 124
QY 121 LKSGTASVCLNNFYPREAKEHQK 145
Db 125 LKSGTASVCLNNFYPREAKVQWK 149

RESULT 10
US-09-097-309-2
; Sequence 2, Application US/09097309
; Patent No. 6121428
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,309
; FILING DATE: 12-Jun-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050951
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P110SR1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-309-2

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQQKPGKAPKELIYVASSLSQGVPSRFSG 60
Db 5 TQSPSSLSASVGDVRTITCRASQDINNVLNMYQQKPGKAPKLLIYTTSLHSGVPSRFSG 64
QY 61 SSGTEFTLTISLQPEDFATYYCLQHNQYPRTFQGGTKVEIKRTVAAPSVFIFFPSDEQ 120
Db 65 SSGGTDYTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSVFIFFPSDEQ 124
QY 121 LKSGTASVCLNNFYPREAKEHQK 145
Db 125 LKSGTASVCLNNFYPREAKVQWK 149

RESULT 11
US-09-097-171A-2
; Sequence 2, Application US/09097171A
; Patent No. 6171586
; GENERAL INFORMATION:
; APPLICANT: Lam, Xanthe M.
; APPLICANT: Oeswein, James Q.
; APPLICANT: Ongpipattanakul, Boonsri
; APPLICANT: Shahrokh, Zahra
; APPLICANT: Wang, Sharon X.
; APPLICANT: Weissburg, Robert P.
; APPLICANT: Wong, Rita L.
; TITLE OF INVENTION: Antibody Formulation
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,171A
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/874897
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P1089R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-171A-2

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
DB 5 TQSPSSLSASVGDVRTITCRASQDINNLYNQKPGKAPKLLIYTTSLHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 120
DB 65 SGSGETDYTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
DB 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 12
US-09-460-587-2
; Sequence 2, Application US/09460587
; Patent No. 6322997
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/460,587
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-460-587-2

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
DB 5 TQSPSSLSASVGDVRTITCRASQDINNLYNQKPGKAPKLLIYTTSLHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 120
DB 65 SGSGETDYTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
DB 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 13
US-09-940-166A-2
; Sequence 2, Application US/09940166A
; Patent No. 6716598
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/940,166A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-940-166A-2

Query Match      81.9%; Score 625; DB 4; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
DB 5 TQSPSSLSASVGDVRTITCRASQDINNLYNQKPGKAPKLLIYTTSLHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 120
DB 65 SGSGETDYTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
DB 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 14
PCT-US93-07832-40
; Sequence 40, Application PC/TUS9307832
; GENERAL INFORMATION:
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; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-171A-2

Query Match      81.9%; Score 625; DB 3; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
DB 5 TQSPSSLSASVGDVRTITCRASQDINNLYNQKPGKAPKLLIYTTSLHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 120
DB 65 SGSGETDYTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
DB 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 13
US-09-940-166A-2
; Sequence 2, Application US/09940166A
; Patent No. 6716598
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/940,166A
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/097,309
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-940-166A-2

Query Match      81.9%; Score 625; DB 4; Length 214;
Best Local Similarity 84.8%; Pred. No. 6.5e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 SOSPSLSASVGERVTITCRASQGRDELGWYQKPGKAPKELIYVASSLOSQVPSRFSG 60
DB 5 TQSPSSLSASVGDVRTITCRASQDINNLYNQKPGKAPKLLIYTTSLHSGVPSRFSG 64
QY 61 SGSGETFTLTISLQPEDFATYYCLOHNGYPRTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 120
DB 65 SGSGETDYTLTISLQPEDFATYYCQGGNTLPTTFQGGTKVEIKRTVAAPSVEIFPPSDEQ 124
QY 121 LKSGTASVVCLLNNFYPREAKEHOK 145
DB 125 LKSGTASVVCLLNNFYPREAKVQWK 149

RESULT 14
PCT-US93-07832-40
; Sequence 40, Application PC/TUS9307832
; GENERAL INFORMATION:
```

APPLICANT: Genentech, Inc.
 TITLE OF INVENTION: Immunoglobulin Variants
 NUMBER OF SEQUENCES: 40
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 460 Point San Bruno Blvd
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genetech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07832
FILING DATE: 19930820

Query Match	81.9%	Score 625;	DB 5;	Length 214;
Best Local Similarity	84.8%;	Pred. No. 6.5e-53;		
Matches 123; Conservative	6;	Mismatches 16;	Indels 0;	Gaps 0;

Qy	1	SQSPSSLSASVGERVTITCRASQIGRDELGHYQQKPGKAPKLLIYVAASSLQSGLGVPSPFSG	60
Dd	5	TQSPSSLSASVGDRVTITCRASODINLYNMQKPGKAPKLLIYYTTLHSGVPSRFSG	64
		:	:
Qy	61	SGSGTEFTLISSLOPEDFATYYCLOHNGVPRTEFGQTKEVEIKETVAAPSFIPIPPSDEQ	120
Dd	65	SGSGTDYTLTISSLOPEDFATYYCOQGNLPPTFGQTKEVEIKETVAAPSFIPIPPSDEQ	124
		:	:
Qy	121	LKSGTASVWCLLNPFYPREAKEHK	145
Dd	125	LKSGTASVWCLLNPFYPREAKVOMK	149

RESULT 15
US-07-934-373C-25
; Sequence 25, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco

STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:

```

Query Match      81.9%; Score 625; DB 2; Length 233;
Best Local Similarity 84.8%; Pred. No. 7.2e-53;
Matches 123; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy      1  SQSPSSLSASVGRVTTTCRASQIDELGWQOKGKAPKRLIYVASSLSQGVPSFSG 60
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      24  TQSPSSLSASVGRVTTTCRASQDINLYNWYQOKGKAPKRLIYVTSLHSGVPSFSG 83
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      61  SSGSGTEFTLTISSLPQEDFATYYCLOHNGYPRPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      84  SSGSGTDYTLTISSLPQEDFATYYCQGGNTLPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 143
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy      121  LKSGTASVCLLNNFYPREAKEHQK 145
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      144  LKSGTASVCLLNNFYPREAKVQWK 168
      : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: March 8, 2005, 05:54:04
Job time : 27.1636 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.4271 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-27

Perfect score: 1085

Sequence: 1 KPGASVKVSKASGYTFTS.....QVLLPSKDVMOGTDHEHVCK 203

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	894	82.4	627	2 S14683	Ig mu chain precu
2	695.5	64.1	231	2 B23746	Ig Fab region IV-J
3	598	55.1	288	2 S29690	Ig heavy chain VJ1
4	525.5	48.4	110	2 PH1670	Ig heavy chain V r
5	510	47.0	127	2 S34014	Ig heavy chain V r
6	507.5	46.8	136	2 S31600	Ig heavy chain V r
7	501.5	46.2	246	2 S38950	Ig gamma chain - m
8	501.5	46.2	446	2 S40295	Ig gamma-2a chain
9	491	45.3	160	2 PL0105	anti-PR2 erythrocy
10	486	44.8	592	2 S25705	Ig mu chain - shee
11	485.5	44.7	118	2 PH1666	Ig heavy chain V r
12	483	44.5	469	2 S37483	Ig gamma-2a chain
13	482.5	44.5	132	2 S31596	Ig heavy chain V r
14	479	44.1	171	2 S23623	Ig heavy chain V r
15	473.5	43.6	241	2 S69131	Ig heavy chain (DO
16	468.5	43.2	568	2 A34891	Ig heavy chain pre
17	465	42.9	129	2 S46393	Ig heavy chain V r
18	463	42.7	452	1 MHU	Ig mu chain C regi
19	463	42.7	453	2 S37768	Ig mu chain C regi
20	463	42.7	473	1 MHUM	Ig mu chain C regi
21	463	42.7	474	2 S15590	Ig heavy chain - h
22	462	42.6	98	2 S26918	Ig heavy chain V r
23	454	41.8	129	2 S36260	Ig heavy chain V r
24	453.5	41.8	118	2 S36265	Ig heavy chain V r
25	451.5	41.6	135	2 S49530	anti-Sm antibody V
26	451	41.6	475	2 S01321	Ig gamma-2b chain
27	449.5	41.4	114	2 PH1667	Ig heavy chain V r
28	449	41.4	123	2 D33548	Ig heavy chain V-1
29	449	41.4	142	2 A32483	Ig heavy chain V r

30	447	41.2	131	2 S26792	Ig heavy chain V r
31	444.5	41.0	474	1 G2MS11	Ig gamma-2b chain
32	443	40.8	109	2 PH1668	Ig heavy chain V r
33	439	40.5	549	2 S04845	Ig heavy chain pre
34	438.5	40.4	214	2 PC4202	monoclonal antibod
35	437.5	40.3	110	2 PH1669	Ig heavy chain V r
36	437	40.3	119	2 PH0961	Ig heavy chain V r
37	436	40.2	160	2 S05271	Ig heavy chain pre
38	431	39.7	133	2 C33548	Ig heavy chain V-1
39	429.5	39.6	136	2 PH0960	Ig heavy chain V r
40	424.5	39.1	120	2 S31999	Ig heavy chain V r
41	424.5	39.1	132	2 PH0954	Ig heavy chain V r
42	423	39.0	125	2 S68170	Ig heavy chain V r
43	422	38.9	122	2 S36271	Ig heavy chain V r
44	419	38.6	127	2 PH0955	Ig heavy chain V r
45	418.5	38.6	124	2 S19665	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human Igm heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <PRI>
A:Cross-references: EMBL:X17115; NID:g33450; PIDN:CRA34971.1; PID:g33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match	82.4%;	Score 894;	DB 2;	Length 627;
Best Local Similarity	83.4%;	Pred. No. 3.1e-62;		
Matches 176;	Conservative 7;	Mismatches 20;	Indels 8;	Gaps 1;
QY	1	KPGASVKVSKASGYTFTSYDINNVROATGQGLEWMMGMPNSGNTGYAQKFGQGRVTWN	60	
Db	31	KPGSSVKVSKASGTFSSYAISWRQAPQGQLEWMGIIPIFGTANYAQKFGQGRVIT	90	
QY	61	RNTSISTAYMELSSLSRSDTAVYYCARGHGGSYF-----YSYIGMDVMVGQGTVTTV	112	
Db	91	ADESTSTAYMELSSLSRSDTAVYYCAKTIILGPYSSGWPNSDYVYGGMDVMVGQGTVTTV	150	
QY	113	SSGSASAPTLPLVSCENSPDTSVAVQCLAQDPLPSITFSWKYKNSDISSTRGPPS	172	
Db	151	SSGSASAPTLPLVSCENSPDTSVAVQCLAQDPLPSITFSWKYKNSDISSTRGPPS	210	
QY	173	VLRGKYAATSOVLPLSKDVMOGTDHEHVCK 203		
Db	211	VLRGKYAATSOVLPLSKDVMOGTDHEHVCK 241		

RESULT 2

B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: B23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin.
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: B23746

A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-231 <LEO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;140-209/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 695.5; DB 2; Length 231;
Best Local Similarity 68.8%; Pred. No. 3.2e-47;
Matches 139; Conservative 22; Mismatches 36; Indels 5; Gaps 2;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTWNR 61
Db 12 KPSETLSLTAVGYGSPDYFWSWIRQPPGKGLEWIGBIN-HSGSTNYPNPSLKSRVTISV 70
QY 62 NTSISTAYMELSSLRSEDATAVYVCARGHGGSFYFYCYMDVWGQGTITVTSSGSASAPT 121
Db 71 DTSKNQFSLKLSVTAADTA VYVCARPHDTSGHYWNV----WGQGLTVTVSSGSASAPT 126
QY 122 LPPLVSCNSPDSSTSSAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGGKYAA 181
Db 127 LPPLVSCNSPDSSTSSAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGGKYAA 186
QY 182 TSQVLLPSKDVNQGTDEHVCK 203
Db 187 TSQVLLPSKDVNQGTDEHVCK 208

RESULT 3
S29690
Ig heavy chain VDJ region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C;Accession: S29690
R;Dammer, P.M.; Bos, N.A.; Kroese, F.G.M.
submitted to the EMBL Data Library, October 1992
A;Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.
A;Reference number: S29690
A;Accession: S29690
A;Molecule type: mRNA
A;Residues: 1-288 <DM>
A;Cross-references: EMBL:X68782; NID:G56442; PID:G1334294
A;Experimental source: strain D2B
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 55.1%; Score 598; DB 2; Length 288;
Best Local Similarity 55.7%; Pred. No. 1.6e-39;
Matches 113; Conservative 37; Mismatches 45; Indels 8; Gaps 2;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTWNR 61
Db 10 RGGSSVKISCKASGYTFTDYMHVWVKQRPQEGVLWIGRINPANGNTEYAEKPKSRATLTA 69
QY 62 NTSISTAYMELSSLRSEDATAVYVCARGHGGSFYFYCYMDVWGQGTITVTSSGSASAPT 121
Db 70 DKSSNTAYQLSSLRSEDATATFCTING-----TVVPFDYWGQGVAVTVSSGSQSPT 122
QY 122 LPPLVSCNSPDSSTSSAVGCLAQDFLPDSITFSWKYKNNSDI-SSTRGFPSPVLRGGKYA 180
Db 123 VLPLVSCSPISDENLVAMGCLARDFLPSSISFSWNYQNTEVMQGVRTFTLRTGDKYT 182
QY 181 ATSQVLLPSKDVNQGTDEHVCK 203
Db 183 ATSQVLLSAKNLVGSDYLVCK 205

RESULT 4
PH1670
Ig heavy chain V region (clone 2A12) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996
C;Accession: PH1670

R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1670
A;Molecule type: mRNA
A;Residues: 1-110 <HIL>
A;Experimental source: B cell
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match 48.4%; Score 525.5; DB 2; Length 110;
Best Local Similarity 86.8%; Pred. No. 2.6e-34;
Matches 99; Conservative 3; Mismatches 5; Indels 7; Gaps 1;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTWNR 60
Db 4 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMT 63
QY 61 RNTSISTAYMELSSLRSEDATAVYVCARGHGGSFYFYCYMDVWGQGTITVTSS 114
Db 64 RNTSISTAYMELSSLRSEDATAVYVCARGKGGEF-----DIWGQGLTVTVSS 110

RESULT 5
S34014
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996
C;Accession: S34014; S30535
R;Mariette, X.; Teapla, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal antibodies to the human IgG1 C1q binding site
A;Reference number: S34001; MUID:93209281; PMID:7681398
A;Accession: S34014
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-127 <MAR>
A;Cross-references: EMBL:Z18321
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 47.0%; Score 510; DB 2; Length 127;
Best Local Similarity 83.2%; Pred. No. 5e-33;
Matches 99; Conservative 5; Mismatches 7; Indels 8; Gaps 2;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTWNR 60
Db 12 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMT 71
QY 61 RNTSISTAYMELSSLRSEDATAVYVCARGHGGSFYFYCYMDVWGQGTITVTSS 114
Db 72 RNTSISTAYMELSSLRSEDATAVYFCARALSIGAVIRGY---YYALDVGQGTITVS 127

RESULT 6
S31600
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31600
R;Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate from the germ-line and somatic hypermutation
A;Reference number: S31585
A;Accession: S31600
A;Molecule type: mRNA
A;Status: preliminary
A;Residues: 1-136 <CU1>
A;Cross-references: EMBL:Z14165; NID:G30994; PID:CAA78534.1; PID:G30995
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 46.8%; Score 507.5; DB 2; Length 136;
Best Local Similarity 84.3%; Pred. No. 8.3e-33;
Matches 97; Conservative 2; Mismatches 7; Indels 9; Gaps 1;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNSGNTGYAOKFGQGRVTMNR 60
DB 31 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNSGNTGYAOKFGQGRVTMNT 90
QY 61 RNTSISTAYMELSLRSEDATVYVCARGHGGSYFYSGMDVWGQGTFTVTSSG 115
DB 91 RNTSISTAYMELSLRSEDATVYVCARWRD-----AFDIWGQGTMTVTSSG 136

RESULT 7

IG gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bielefeldt, S.; Hoppe-Seyler, J.; 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha 1 chain of IgG2a
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 46.2%; Score 501.5; DB 2; Length 246;
Best Local Similarity 51.6%; Pred. No. 4.6e-32;
Matches 99; Conservative 33; Mismatches 41; Indels 19; Gaps 6;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNSGNTGYAOKFGQGRVTMNR 61
DB 13 RPGASVKISCKASGYTFTDYIHWVKRPGEGLEWIGWYIPGSGNTKYNEKFKGKATLV 72
QY 62 NTSISTAYMELSLRSEDATVYVCARGHGGSYFYSGMDVWGQGTFTVTSSGSASAPT 121
DB 73 DTSSSTAYMQLSLTSEDSAVYFCARGGK-----FAMDYWGQGTSTVTSSAKTTAPS 124
QY 122 LPPLVS-CENSPSDT--SSVAVGCLAQDFLPDSITFSWKYKNSDISS--TRGPPSVLRGG 177
DB 125 VYPLAPVC-----GDTTGSSTVLGCLVKGYFPEPVLTLW---NSGSLSSGVTHTFPVQLQSD 177
QY 178 KYAATSOVLPLPS 189
DB 178 LYTLLSSVTVTSS 189

RESULT 8

IG gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bielefeldt, S.; Hoppe-Seyler, J.; 993-1000, 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha 1 chain of IgG2a
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
A:Cross-references: UNIPROT:Q99L25
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid

F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-117/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyroglutamic acid (Gln) #status experimental
F:122-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 46.2%; Score 501.5; DB 2; Length 446;
Best Local Similarity 51.6%; Pred. No. 8.7e-32;
Matches 99; Conservative 33; Mismatches 41; Indels 19; Gaps 6;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNSGNTGYAOKFGQGRVTMNR 61
DB 13 RPGASVKISCKASGYTFTDYIHWVKRPGEGLEWIGWYIPGSGNTKYNEKFKGKATLV 72
QY 62 NTSISTAYMELSLRSEDATVYVCARGHGGSYFYSGMDVWGQGTFTVTSSGSASAPT 121
DB 73 DTSSSTAYMQLSLTSEDSAVYFCARGGK-----FAMDYWGQGTSTVTSSAKTTAPS 124
QY 122 LPPLVS-CENSPSDT--SSVAVGCLAQDFLPDSITFSWKYKNSDISS--TRGPPSVLRGG 177
DB 125 VYPLAPVC-----GDTTGSSTVLGCLVKGYFPEPVLTLW---NSGSLSSGVTHTFPVQLQSD 177
QY 178 KYAATSOVLPLPS 189
DB 178 LYTLLSSVTVTSS 189

RESULT 9

anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C:Accession: P10105
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma secretory cell line to the human B cell lymphoma secretory cell line
A:Reference number: P10105; MUID:89235583; PMID:2541221
A:Accession: P10105
A:Molecule type: mRNA
A:Residues: 1-160 <SIL>
A:Note: The authors translated the codon GAC for residues 108 and 109 as Glu
C:Comment: The antibody is one of the cold agglutinins that preferentially bind red blood cells
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; hemagglutinin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:34-117/Domain: immunoglobulin homology <IMM>
F:49-54/Region: complementarity-determining 1
F:69-84/Region: complementarity-determining 2
F:118-131/Domain: D region <DRG>
F:132-144/Domain: J4 segment <JSG>
F:145-160/Domain: C region <CRG>

Query Match 45.3%; Score 491; DB 2; Length 160;
Best Local Similarity 74.2%; Pred. No. 1.9e-31;
Matches 98; Conservative 9; Mismatches 19; Indels 6; Gaps 3;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNSGNTGYAOKFGQGRVTMNR 61
DB 32 KPGASVKVSKASGYTFTSYGISWRQAPGQGLEWIGWYIPGSGNTKYNEKFKGKATLV 91
QY 62 NTSISTAYMELSLRSEDATVYVCARG--GH--GGSFYFYSGMDVWGQGTFTVTSSGSAS 118
DB 92 DTSTSTAYMELNLRSDDTAVYVCARAPGYCSGGG---CYRGGDYWGQGTTLVTSSGSRS 148
QY 119 APTLPFLVSCEN 130

RESULT 14

S23623
Ig heavy chain V region precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S23623
R;Olee, T.; Lu, E.W.; Huang, D.P.; Soto-Gil, R.W.; Defetos, M.; Kozin, F.; Carson, D.A.; J. Exp. Med. 175, 831-842, 1992
A;Title: Genetic analysis of self-associated immunoglobulin G rheumatoid factors from t
A;Reference number: S23623; MUID:92156804; PMID:1740665
A;Accession: S23623
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-171 <OLE>
A;Cross-references: EMBL:X59702; NID:g32010; PIDN:CAA42223.1; PID:g32011
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 44.1%; Score 479; DB 2; Length 171;
Best Local Similarity 63.9%; Pred.No.1.8e-30;
Matches 94; Conservative 13; Mismatches 28; Indels 12; Gaps 3;

Qy 1 KPFGASVKVCKSGASYGTTFTSYDINWVRQAQGGLGWGNPNPSNGTGYAQKFGQRTVMN 60
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
31 KPFGASVKVCKSGSGYFTTAQHWRVAQPQLGLEWMGNPNPSGGTGYGQKPGQRTVLT 90
Qy ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
61 RNTSISTAYNELSLRSDDTAVYCARGHGGSFYFSYGM-----DVWGOGTTVTVS 114
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
91 RDTSISTAYNELSLRLTDATVYYCAI-----EIFYDGSDLKPSDFDIWGQGTMTVSS 145
Qy 115 GSASAPTLFLPLVCENSPDSTSVAG 141
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
146 ASTKGPSVFPLAPSKESTSG-GTAALG 171

RESULT 15

S69131
IG heavy chain (DOT) - human (fragment)
N;Alternate names: anti-riboflavin IgG Pd fragment
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C;Accession: S69131
R;Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A;Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A;Reference number: S69130; MUID:9525298; PMID:7737190
A;Accession: S69131
A:Molecule type: protein
A;Residues: 1-241 <STO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid
F;1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>
F;140-205/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 43.6%; Score 473.5; DB 2; Length 241;
Best Local Similarity 50.08; Pred.No.6.9e-30;
Matches 96; Conservative 34; Mismatches 53; Indels 9; Gaps 5;

Qy 1 KPFGASVKVCKSGASYGTTFTSYDINWVRQAQGGLGWGNPNPSNGTGYAQKFGQRTVMN 60
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
12 KVPGAIRISCKASGYAFNYIHWRVAQPLGLEWMGIENPVAGAVS-SKKPDLRVMS 70
Qy 61 RNTSISTAYNELSLRSDDTAVYCARGHGGSFYFSYGMVDVGOGTTTVTVSSGSASP 120
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
71 SDTSANTVSNQLRNLRSLDTGRYFCAR---VSYDFSQYGMVDVGOGTTTVIVSSASTKGP 126
Qy 121 TLPLPLVCENSPDSTSVAVGKAQDFLPDSITFSWKYNKSNDISSSTRGPSVL-RCGKY 179
Db ||||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
127 SVFPAPLPCSRSTS-STAAAGCLVKDPFBPTVSW--NSGALTGVHTTPFVLQSGLY 183
Qy 180 AATSQVLLPSKD 191

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 75.8103 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-27

Perfect score: 1085

Sequence: 1 KKGNSVKVSKASGYTFTS.....QVLLPSKDVMOQTDEHVCK 203

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	828.5	76.4	606	2	Q6GMV2	Q6gm22 homo sapien
2	784	72.3	597	2	Q96BB9	Q96bb9 homo sapien
3	765.5	70.6	613	2	Q8WUK1	Q8wuk1 homo sapien
4	724	66.7	595	2	Q8WUX4	Q8wux4 homo sapien
5	724	66.7	597	2	Q6GMX5	Q6gmx5 homo sapien
6	724	66.7	597	2	Q9BU10	Q9bu10 homo sapien
7	724	66.7	625	2	Q96AA6	Q96aa6 homo sapien
8	720	66.4	597	2	Q9BQB8	Q9bqb8 homo sapien
9	687.5	63.4	620	2	Q96EY0	Q96ey0 homo sapien
10	624	57.5	613	2	Q8VXC7	Q8vcx7 mus musculus
11	609.5	56.2	614	2	Q7TMT6	Q7tmt6 mus musculus
12	537.5	49.5	497	2	Q8WY24	Q8wy24 homo sapien
13	535.5	48.4	518	2	Q6N030	Q6n030 homo sapien
14	521	48.0	498	2	Q6N041	Q6n041 homo sapien
15	508.5	46.9	469	2	Q7Z7P5	Q7z7p5 homo sapien
16	507	46.7	470	2	Q7TMK1	Q7tmk1 mus musculus
17	506	46.6	500	2	Q9BRV0	Q9brv0 homo sapien
18	498.5	45.9	475	2	Q6N095	Q6n095 homo sapien
19	490	45.2	481	2	Q91WT1	Q91wt1 mus musculus
20	480.5	44.3	500	2	Q6N091	Q6n091 homo sapien
21	478	44.1	484	2	Q99LA6	Q99la6 mus musculus
22	477.5	44.0	473	2	Q9D8L4	Q9d8l4 mus musculus
23	477.5	44.0	480	2	Q6P089	Q6p089 homo sapien
24	476.5	43.9	482	2	Q8K172	Q8k172 mus musculus
25	474.5	43.7	463	2	Q99LC4	Q99lc4 mus musculus
26	474	43.7	480	2	Q6PJF1	Q6pjf1 homo sapien
27	472	43.5	465	2	Q6FJB2	Q6fjb2 mus musculus
28	471.5	43.5	472	2	Q6FJA7	Q6fja7 mus musculus
29	467.5	43.1	488	2	Q91WR1	Q91wr1 mus musculus
30	467	43.0	573	2	Q8WU38	Q8wu38 homo sapien
31	466.5	43.0	488	2	Q8K0F2	Q8k0f2 mus musculus

32	465	42.9	480	2	Q8K0Z4	Q8k0z4 mus musculus
33	463	42.7	454	1	MUC_HUMAN	P01871 homo sapien
34	462.5	42.6	593	2	Q6INMS	Q6inms xenopus lae
35	462	42.6	472	2	Q6N089	Q6n089 homo sapien
36	461	42.5	489	2	Q8VCX4	Q8vcx4 mus musculus
37	456	42.0	119	2	Q9UL94	Q9ul94 homo sapien
38	455	42.0	119	2	Q9UL95	Q9ul95 homo sapien
39	451	41.6	244	2	Q65ZC8	Q65zc8 homo sapien
40	451	41.6	481	2	Q91WT3	Q91wt3 mus musculus
41	448.5	41.3	159	2	Q96Q80	Q96q80 homo sapien
42	442	40.7	208	2	Q6ZP87	Q6zpb7 homo sapien
43	438.5	40.4	474	2	Q8R3H6	Q8r3h6 mus musculus
44	438	40.4	496	2	Q96DK0	Q96dk0 homo sapien
45	437.5	40.3	464	2	Q6FP95	Q6fp95 mus musculus

ALIGNMENTS

RESULT 1
Q6GMV2 PRELIMINARY; PRT; 606 AA.
ID AC Q6GMV2; DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny K.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalish D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
SEQUENCE FROM N.A.
TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC073758; AAH73758.1; -;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00407; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.

[illegible]

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]

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RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Lymph;
RA  Strauberg R.;
RL  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC073767; AAH73767.1; -.
DR  InterPro; IPR003599; IG.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG cl.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF07654; Cl-set; 4.
DR  Pfam; PF00047; Ig; 4.
DR  SMART; SM00409; IG; 2.
DR  SMART; SM00407; IGcl; 4.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS0835; IG-LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW  Hypothetical protein.
SQ  SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match      66.7%; Score 724; DB 2; Length 597;
Best Local Similarity 68.9%; Pred. No. 2.9e-54;
Matches 144; Conservative 21; Mismatches 30; Indels 14; Gaps 3;

QY  2 KPGASVKVCKASGYTFTSYDINWVROATGQGLEWMGWNPNSGNTGYAOKFQGRVTMNR 61
DB  32 KPSETLSITCGVYGSGFSGYWIRQPPGKLEWIGEIN-HSGSTNYPNLSKSRVITSV 90
QY  62 NTSISTAYMELSSRLSEDTAVYYCAR-----GGHGGSYFYSGYMDVMVGQGTITVTVSS 114
DB  91 DTSKKQLSLKSSVNAADTAVYYCARVITRASPGTDG-----RYGMDVMVGQGTITVTVSS 144
QY  115 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVL 174
DB  145 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVL 204
QY  175 RGGKYAATSOVLLPSKDVMOQGTDEHVUCK 203
DB  205 RGGKYAATSOVLLPSKDVMOQGTDEHVUCK 233

RESULT 6
ID  Q9BU10 PRELIMINARY; PRT; 597 AA.
AC  Q9BU10;
DT  01-JUN-2001 (TrEMBLrel. 17, Created)
DT  01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  IGHM protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Lymph;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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RA  Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
RT  and mouse cDNA sequences.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN  [2]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Lymph;
RA  Strauberg R.;
RL  Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC002963; AAH02963.1; -.
DR  HSSP; P01861; IADQ.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG cl.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF07654; Cl-set; 4.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS0835; IG-LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW  Hypothetical protein.
SQ  SEQUENCE 597 AA; 65274 MW; 2DAPAFB7E055851 CRC64;

Query Match      66.7%; Score 724; DB 2; Length 597;
Best Local Similarity 68.9%; Pred. No. 2.9e-54;
Matches 144; Conservative 21; Mismatches 30; Indels 14; Gaps 3;

QY  2 KPGASVKVCKASGYTFTSYDINWVROATGQGLEWMGWNPNSGNTGYAOKFQGRVTMNR 61
DB  32 KPSETLSITCGVYGSGFSGYWIRQPPGKLEWIGEIN-HSGSTNYPNLSKSRVITSV 90
QY  62 NTSISTAYMELSSRLSEDTAVYYCAR-----GGHGGSYFYSGYMDVMVGQGTITVTVSS 114
DB  91 DTSKKQLSLKSSVNAADTAVYYCARVITRASPGTDG-----RYGMDVMVGQGTITVTVSS 144
QY  115 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVL 174
DB  145 GSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVL 204
QY  175 RGGKYAATSOVLLPSKDVMOQGTDEHVUCK 203
DB  205 RGGKYAATSOVLLPSKDVMOQGTDEHVUCK 233

RESULT 7
ID  Q96AA6 PRELIMINARY; PRT; 625 AA.
AC  Q96AA6;
DT  01-DEC-2001 (TrEMBLrel. 19, Created)
DT  01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT  01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE  IGHM protein.
OS  Homo sapiens (Human).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX  NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  TISSUE=Lymph;
RX  MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA  Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA  Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA  Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA  Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
```



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RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.;
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W.,
RA Paney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC011857; AAH11857.2; -.
PIR; S15590; S15590.
HSSP; P01820; IGT9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 58125 MW; 950A1A4A6E8FF27B CRC64;

Query Match 63.4%; Score 687.5; DB 2; Length 620;
Best Local Similarity 67.8%; Pred. No. 4.4e-51;
Matches 137; Conservative 22; Mismatches 38; Indels 5; Gaps 2;

QY 2 KPGASVSKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTNMR 61
DB 39 KPSETLSTCTVSGSISSTYWSIRQAPAGLEWIGRIY-TSGSTNPNLSKGRVTMSV 97
QY 62 NTSISTAYMELSLRSEDYAVYCYARGHGGSYFYSGYGMVDMVGQGTVTTVSSGSASAPT 121
DB 98 DTSKNQPSLKLSSVTAADTAVYCA---SQPWELPTVGLFVWGQGLTVTVSSGSASAPT 153
QY 122 LFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLGGKYAA 181
DB 154 LFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLGGKYAA 213
QY 182 TSQVLLPSKDVMOGTDHEHVCK 203
DB 214 TSQVLLPSKDVMOGTDHEHVCK 235

RESULT 10
Q8VCX7 PRELIMINARY; PRT; 613 AA.
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

```

```

RA Alteschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
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RA Paney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
EMBL; BC018315; AAH18315.1; -.
PIR; C30562; C30562.
HSSP; P01751; IAGW.
DR MGP; MGI196448; Igh-6.
DR GO; GO:0019815; C:B-cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016084; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.
DR GO; GO:0030890; P:positive regulation of B-cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 57.5%; Score 624; DB 2; Length 613;
Best Local Similarity 58.6%; Pred. No. 1.4e-45;
Matches 119; Conservative 36; Mismatches 40; Indels 8; Gaps 3;

QY 2 KPGASVSKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTNMR 61
DB 32 KPGASVSKASGYTFTSYDINVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTNMR 91
QY 62 NTSISTAYMELSLRSEDYAVYCYARGHGGSYFYSGYGMVDMVGQGTVTTVSSGSASAPT 121
DB 92 DTSNTAYMQLSLTSDSAVYCAR--RLGRWTF-----DVWGAGTTVTVSSSESQSPFN 144
QY 122 LFPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSD-ISSTRGFPSPVLGGKYA 180
DB 145 VFPLVSCNSPDLSDKNLVAMGCLARDFLPSTISFTWYQNTVEIQGITFTFTLRTGGKYL 204
QY 181 ATSQVLLPSKDVMOGTDHEHVCK 203
DB 205 ATSQVLLSPKSLGSDGYLVCK 227

RESULT 11
Q7TWT6 PRELIMINARY; PRT; 614 AA.
AC Q7TWT6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC60843 protein.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RX MEDLINE=23288257; PubMed=1477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002)
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6Ncr; TISSUE=Hematopoietic Stem Cell;
RA Strausberg R.L.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053409; AAH53409.1; --
DR HSSP; P01820; 1G7J.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 614 AA; 67746 MW; 839BAF3BBD124F89 CRC64;

Query Match 56.2%; Score 609.5; DB 2; Length 614;
Best Local Similarity 57.1%; Pred. No. 2,5e-44;
Matches 116; Conservative 38; Mismatches 42; Indels 7; Gaps 3;

QY 2 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVTWNR 61
Db |||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
32 KPGASVKVCKASGYAFSSSSWNNVVKQRPFGKGLWIGRVYFGDGTNYNGKFGKATLTA 91
QY 62 NTSISTAYMELSSLRSDETVAVYCARGGHGGSYFYSGMDVMVGOGTTVTYSSGSASAPT 121
Db :|||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
92 DTSINTAYMVLSSLSTEDSAIFYCARGNLRGGRGFGYNWFDPMWGHGTLTVTVSSASPTNPK 151
QY 122 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSD--ISSTRGFP--SVLRGCK 178
Db :|||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
152 VFPLSCLSTQPD--GNVVIACLVGQFPPEPLSVTVSSESGQ--VTARNPPSQDASGDL 207
QY 179 YAATSVQLLPSKDVMOQTDEHVVC 202
Db :|||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
208 YTTSSQLTLPATQCLAG--KSVTC 229

RESULT 13
QGN030 PRELIMINARY; PRT; 518 AA.
ID Q6N030
AC Q6N030;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686I15212.
GN Name=DKFZp686I15212;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Foustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; --
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR000005; HTHaraC.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
```

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zheng S., Shao X., Cao J., Geng L., Pang Y., Dong Q.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF283666; AAL36987.1; --
DR HSSP; P01876; 1OW0.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;

Query Match 49.5%; Score 537.5; DB 2; Length 497;
Best Local Similarity 52.5%; Pred. No. 3.4e-38;
Matches 107; Conservative 26; Mismatches 62; Indels 9; Gaps 5;

QY 2 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVTWNR 61
Db |||||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
32 KPGASVKVCKASGYTFIAYDINWVRQAPGQGLEWMGMWNPQTGTEFAQKFGQRLTFSR 91
QY 62 NTSISTAYMELSSLRSDETVAVYCARGGHGGSYFYSGMDVMVGOGTTVTYSSGSASAPT 121
Db :|||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
92 DTSINTAYMVLSSLSTEDSAIFYCARGNLRGGRGFGYNWFDPMWGHGTLTVTVSSASPTNPK 151
QY 122 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTGFP--SVLRGCK 178
Db :|||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
152 VFPLSCLSTQPD--GNVVIACLVGQFPPEPLSVTVSSESGQ--VTARNPPSQDASGDL 207
QY 179 YAATSVQLLPSKDVMOQTDEHVVC 202
Db :|||:|||||:|:|||||:|||||:|:|||||:|:|||||:|:|||||:|:|||||:|:
208 YTTSSQLTLPATQCLAG--KSVTC 229

RESULT 13
QGN030 PRELIMINARY; PRT; 518 AA.
ID Q6N030
AC Q6N030;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686I15212.
GN Name=DKFZp686I15212;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Foustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640724; CAE45841.1; --
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR000005; HTHaraC.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 3.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00041; HTH ARAC FAMILY_1; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
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SQ SEQUENCE 518 AA; 57019 MW; 9385F98613BF6382 CRC64;
Query Match 49.4%; Score 535.5; DB 2; Length 518;
Best Local Similarity 54.2%; Pred. No. 5.3e-38; Indels 15; Gaps 6;
Matches 110; Conservative 28; Mismatches 50;
Qy 1 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAOKFQGRVTMN 60
Dd 31 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAOKFQGRVTMT 90
Qy 61 RNTSISTAYMELSLRSRSDTAVYICARGHGG----SYFYSYGMDVWGQGTVTTVSSGSA 117
Dd 91 RDTWTTTAYMDLSLSRSDTAVYICARDAPOGVTTTF-----DYMGGGLTVTVSSAST 144
Qy 118 SAPTLFPLVSCNSPDSSTSSVAVCLAQDFLPDSITFSWKYKNNSDLSSTGFPSVLAR-G 176
Dd 145 KGPSVFPLAPCSRSTSG-GTAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSS 201
Qy 177 GKYAATSOVLPLPSKDVMOGTDH 199
Dd 202 GLYSLSVVTVPSSSL-GTQTY 222

RESULT 14
Q6N041 PRELIMINARY; PRT; 498 AA.
AC Q6N041
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686G016217 (Fragment).
GN Name=DKFZp686G016217;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Anid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640710; CAE45829.1; --
DR HSSP; P01751; 1AGW.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; CI-set; 2.
DR SMART; SM00409; IG; 4.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON-TER 1
SQ SEQUENCE 498 AA; 54125 MW; 40B3208A84E03B46 CRC64;
Query Match 48.0%; Score 521; DB 2; Length 498;
Best Local Similarity 54.6%; Pred. No. 9.2e-37;
Matches 113; Conservative 25; Mismatches 55; Indels 14; Gaps 7;
Qy 1 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAOKFQGRVTMN 60
Dd 46 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAOKFQGRVSMT 105
Qy 61 RNTSISTAYMELSLRSRSDTAVYICARGHGGSYFYSYGMDVWGQGTVTTVSSGSA 120
Dd 106 RDTSTTIYMLSLRSRSDTAMFFCARAGPGYGTSAFY-FDYWGQGLTVTVSSASPTSP 164
Qy 121 TLFLVSCNSPDSSTSSVAVGCLAQDFLPD---SITFSWKYKNNSDISSTRGFP--SVLR 175
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Db 165 KVFPFL-SLDSTPQD-GNVVAVACLVGQFPQBPQLSVTWSESGQN-----VTARNFFPSQDAS 218
Qy 176 GKGYAATSOVLPLPSKDVMOGTDHVV 202
Dd 219 GDLYTSSQLTLPATQCPDG--KSVTC 243

RESULT 15
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; --
DR HSSP; P01857; 1HZZ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
Query Match 46.9%; Score 508.5; DB 2; Length 469;
Best Local Similarity 50.2%; Pred. No. 1e-35;
Matches 102; Conservative 34; Mismatches 52; Indels 15; Gaps 6;
Qy 1 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAOKFQGRVTMN 60
Dd 31 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMNPNPNSGNTGYAOKFQGRVTMT 90
Qy 61 RNTSISTAYMELSLRSRSDTAVYICARGHGG--GSFYFYGMDVWGQGTVTTVSSGSA 118
Dd 91 TDTATTSYMEFRSLRSDDTALFYCATKSRGQGVDF-----DSWGQGLTVTVSSASTK 143
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 94.1163 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-27

Perfect score: 1085

Sequence: 1 KPQASVKVSKASGYFTS.....QVLLPSKDVMOGTDHVVCK 203

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseq1980s.*

2: Geneseq1990s.*

3: Geneseq2000s.*

4: Geneseq2001s.*

5: Geneseq2002s.*

6: Geneseq2003as.*

7: Geneseq2003bs.*

8: Geneseq2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1085	100.0	203	2 AAY34301	Aay34301 Igm antib
2	985	90.8	199	2 AAY34302	Aay34302 Igm antib
3	894	82.4	627	7 ADE97370	Ad97370 Human imm
4	881.5	81.2	588	2 AAW71880	Aaw71880 Anti-huma
5	881.5	81.2	588	3 AAB12917	Aab12917 Anti-huma
6	867.5	80.0	588	2 AAW71881	Aaw71881 Anti-huma
7	867.5	80.0	588	3 AAB12918	Aab12918 Anti-huma
8	809	74.6	266	8 ADF69305	Adf69305 Human lun
9	783.5	72.2	571	8 ADP84970	Adp84970 ChimERIC
10	781	72.0	228	8 ADL70776	Adl70776 Anti-TNFA
11	775.5	71.5	595	7 ADM05427	Adm05427 Human pro
12	766.5	70.6	596	4 AAM23924	Aam23924 Human EST
13	763.5	70.4	223	2 AAY08598	Aay08598 Anti-huma
14	757.5	69.8	223	8 ADL70773	Adl70773 Anti-TNFA
15	736	67.8	570	8 ADL70773	Adl70773 ChimERIC
16	731.5	67.4	533	7 ADB65070	Adb65070 Human pro
17	728.5	67.1	205	2 AAY34299	Aay34299 Igm antib
18	719.5	66.3	569	8 ADL9330	Adl9330 ChimERIC
19	707.5	65.2	202	2 AAY34303	Aay34303 Igm antib
20	698	64.3	197	2 AAY34300	Aay34300 Igm antib
21	673.5	62.1	190	2 AAY34304	Aay34304 Igm antib
22	645	59.4	590	2 AAW31751	Aaw31751 H chain s
23	645	59.4	590	2 AAW71888	Aaw71888 Anti-huma
24	645	59.0	590	3 AAB12908	Aab12908 Anti-huma
25	638	58.8	476	2 AAW88464	Aaw88464 Monoclonal

26	601	55.4	576	8	ADF69325	Adf69325 Human lun
27	597	55.0	571	8	ADP84967	Adp84967 Murine an
28	596	54.9	470	5	AAU74296	Aau74296 Anti-huma
29	596	54.9	573	8	ADP84968	Adp84968 Murine an
30	592.5	54.6	228	6	ABR01526	Abt01526 Human ant
31	584.5	53.9	230	6	ABR01514	Abt01514 Human ant
32	583	53.7	221	6	ABR01537	Abt01537 Human ant
33	580.5	53.5	471	7	ADE28427	Ad28427 Human ant
34	559.5	51.6	125	7	ADK18814	Adk18814 Anti-huma
35	559.5	51.6	126	7	ADK18864	Adk18864 Anti-huma
36	559.5	51.6	126	7	ADK18595	Adk18595 Anti-huma
37	559.5	51.6	126	7	ADK18777	Adk18777 Anti-huma
38	559.5	51.6	126	8	ADL25408	Adl25408 Human mAb
39	559	51.5	125	7	ADK18614	Adk18614 Anti-huma
40	559	51.5	125	7	ADK18779	Adk18779 Anti-huma
41	559	51.5	125	7	ADK18919	Adk18919 Anti-huma
42	559	51.5	125	7	ADK18816	Adk18816 Anti-huma
43	559	51.5	125	8	ADL25444	Adl25444 Human mAb
44	557	51.3	451	8	ADR23350	Adr23350 Human CD7
45	554	51.1	451	8	ADR23348	Adr23348 Human CD7

ALIGNMENTS

RESULT 1

AAY34301

ID AAY34301 standard; protein; 203 AA.

XX AC AAY34301;

XX DT 19-NOV-1999 (first entry)

XX DE Igm antibody CEM 10.12 F3 heavy chain sequence.

KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX PN WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

DR N-PSDB; AAZ20402.

XX PT New monoclonal antibody, used for treating e.g. graft versus host

PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 60; Fig 26; 245pp; English.

XX CC This sequence represents the heavy chain of an antibody of the invention.

CC The antibody is a monoclonal antibody (mAb) with an isotype that fixes

CC complement and a variable region that binds to the epitope on CD147 mAb

CC by the Igm mAb ABX-CBL, providing that the antibody is not CBL1. The mAb

CC can selectively kill activated T-cells, activated B-cells or treating or

CC activated monocytes. The products and methods can be used for treating

CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft

CC versus host disease (GVHD), organ transplant rejection diseases (e.g.

CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 203 AA;
Query Match 100.0%; Score 1085; DB 2; Length 203;
Best Local Similarity 100.0%; Pred. No. 1.8e-72;
Matches 203; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KPGASVKVSKASGYFTSYDINWVRQATCGLEWGMWNPNSGNTGYAQKFGQRTVMN 60
Db 1 KPGASVKVSKASGYFTSYDINWVRQATCGLEWGMWNPNSGNTGYAQKFGQRTVMN 60
Qy 61 RNTSISTAYMELSLRSEDATVYICARGHGGSFYSYGMDVWGQTTVTVSSGSASAP 120
Db 61 RNTSISTAYMELSLRSEDATVYICARGHGGSFYSYGMDVWGQTTVTVSSGSASAP 120
Qy 121 TLFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFVLRGGKYA 180
Db 121 TLFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFVLRGGKYA 180
Qy 181 ATSQVLLPSKDVMOGTDEHVCK 203
Db 181 ATSQVLLPSKDVMOGTDEHVCK 203

RESULT 2
RAY34302
ID AAY34302 standard; protein; 199 AA.
XX
AC AAY34302;
XX
DT 19-NOV-1999 (first entry)
XX
DE IgM antibody CEM 10.12 G5 heavy chain sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
FN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
XX
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
DR N-PSDB; AAZ20403.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 60; Fig 27; 245pp; English.
XX
CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.

CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 199 AA;
Query Match 90.8%; Score 985; DB 2; Length 199;
Best Local Similarity 94.0%; Pred. No. 4.3e-65;
Matches 189; Conservative 1; Mismatches 7; Indels 4; Gaps 1;
Qy 1 KPGASVKVSKASGYFTSYDINWVRQATCGLEWGMWNPNSGNTGYAQKFGQRTVMN 60
Db 3 KPGASVKVSKASGYFTSYDINWVRQATCGLEWGMWNPNSGNTGYAQKFGQRTVMN 62
Qy 61 RNTSISTAYMELSLRSEDATVYICARGHGGSFYSYGMDVWGQTTVTVSSGSASAP 120
Db 63 RNTSISTAYMELSLRSEDATVYICAR----EEWLVRYYGMDVWGQTTVTVSSGSASAP 118
Qy 121 TLFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFVLRGGKYA 180
Db 119 TLFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFVLRGGKYA 178
Qy 181 ATSQVLLPSKDVMOGTDEHV 201
Db 179 ATSQVLLPSKDVMOGTDEHKV 199

RESULT 3
ADE97370
ID ADE97370 standard; protein; 627 AA.
XX
AC ADE97370;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human immunoadhesin-related protein - SEQ ID 47.
XX
KW immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;
KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;
KW intercellular adhesion molecule; ICAM-1, human.
XX
OS Homo sapiens.
XX
FN WO2003064992-A2.
XX
PD 07-AUG-2003.
XX
PF 25-OCT-2002; 2002WO-US034197.
XX
PR 26-OCT-2001; 2001US-00047542.
XX
PA (PLAN-) PLANET BIOTECHNOLOGY INC.
PA (LARR/) LARRICK J W.
PA (WYCO/) WYCOFF K L.
XX
PI Larrick JW, Wycoff KL;
XX
DR WPI; 2003-636816/60.
XX
PT New immunoadhesin, useful for treating anthrax and rhinovirus, comprises
PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and
PT J chain and secretory component associated with the chimeric toxin
PT receptor protein.
XX
PS Disclosure; SEQ ID NO 47; 289pp; English.
XX
CC The invention relates to a novel immunoadhesin comprising a chimeric
CC toxin receptor protein consisting of a toxin receptor protein linked to
CC at least a portion of an immunoglobulin heavy chain with a J (joining)
CC chain and secretory component (SC) associated with the chimeric toxin
CC receptor protein. The immunoadhesin comprises a chimeric bacterial or
CC viral toxin receptor protein and the immunoadhesin has plant-specific
CC glycosylation. The immunoadhesin of the invention demonstrates virucide

CC and antibacterial activities and may be useful for reducing the binding
 CC of a viral or bacterial antigen to a host cell and thus for treating or
 CC preventing anthrax, as well as human rhinovirus infection which results
 CC in the common cold. The current sequence is that of the human
 CC immunoadhesion-related protein of the invention.

XX Sequence 627 AA;

Query Match 82.4%; Score 894; DB 7; Length 627;
 Best Local Similarity 83.4%; Pred. No. 7.8e-58;
 Matches 176; Conservative 7; Mismatches 20; Indels 8; Gaps 1;

QY 1 KPGASVSVCKASGYTFTSYDINVRQATGCGLEWGMWNPNSGNTGYAQKFGQRTVMN 60
 DB 31 KPGSSVSVCKASGTTFTSYAISVWRQAPGQGLEWGMGIIPFTANYAQKFGQRTVT 90
 QY 61 RNTSISTAYMELSLRSRSDTAVYYCARGHGGSYF-----YSYVGMDVWGQTTT 112
 DB 91 ADESTSTAYMELSLRSRSDTAVYYCAKTIILGYSYGWPNSDYYVYGMVWGQTTT 150
 QY 113 SSGSASAPTLPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPS 172
 DB 151 SSGSASAPTLPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPS 210
 QY 173 VLRGKYAATSQVLLPSKDVMOGTDHVVCK 203
 DB 211 VLRGKYAATSQVLLPSKDVMOGTDHVVCK 241

RESULT 4
 AAW71880
 ID AAW71880 standard; protein; 588 AA.

XX AC AAW71880;

DT 18-JAN-1999 (first entry)

DE Anti-human Fas humanised antibody CH11 heavy chain HmuH.

XX Humanised antibody; Fas; CH11; monoclonal antibody; Mab; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human;
 KW antibody engineering.

XX Homo sapiens.
 OS Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= Sig_peptide

FT Protein 20..588

FT /label= Mat_protein

FT Region 50..54

FT /label= CDR1

FT /note= "complementarity determining region 1 from CH11

FT heavy chain"

FT Region 69..84

FT /label= CDR2

FT /note= "complementarity determining region 2 from CH11

FT heavy chain"

FT Region 118..124

FT /label= CDR3

FT /note= "complementarity determining region 3 from CH11

FT heavy chain"

XX EP866131-A2.

XX 23-SEP-1998.

XX 20-MAR-1998; 98EP-00302113.

XX 21-MAR-1997; 97JP-00067938.

XX (SANY) SANKYO CO LTD.

XX Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;
 XX WPI; 1998-482965/42.
 DR N-PSDB; AAV61363.
 XX Production of anti-Fas protein humanised antibodies - for use in inducing
 PT apoptosis on Fas expressing cells in the treatment of auto:immune
 PT diseases, especially rheumatoid arthritis.
 XX Claim 21; Page 105-107; 187pp; English.

XX This is the amino acid sequence of a humanised anti-Fas antibody CH11
 CC heavy chain, designated HmuH. HmuH is based on the heavy chain (see
 CC AAW71880) of murine anti-human Fas monoclonal antibody CH11. The
 CC humanised sequence was designed following selection of donor residues
 CC from CH11 to be grafted onto acceptor molecule 21.28'Cl. 2 Heavy chain
 CC sequences (see AAW71880-81) have been designed, and each can be used in
 CC combination with any of 4 light chain sequences (see AAW71876-79) to
 CC provide novel, claimed humanised CH11 IgM antibodies that lack a J chain.
 CC These humanised anti-human Fas antibodies are capable of inducing
 CC apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in
 CC the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA
 CC sequences encoding the humanised antibodies are claimed, as are vectors
 CC such as pMmuH5-1 including the HmuH nucleotide sequence (see AAV61363),
 CC and host cells such as Escherichia coli pMmuH5-1 (PERM BP-5863)
 XX Sequence 588 AA;

Query Match 81.2%; Score 881.5; DB 2; Length 588;

Best Local Similarity 83.3%; Pred. No. 6.1e-57;
 Matches 169; Conservative 10; Mismatches 15; Indels 9; Gaps 1;

QY 1 KPGASVSVCKASGYTFTSYDINVRQATGCGLEWGMWNPNSGNTGYAQKFGQRTVMN 60

DB 31 KPGASVSVCKASGYTFTSYDINVRQAPGQGLEWGMGIIPFTANYAQKFGQRTVT 90

QY 61 RNTSISTAYMELSLRSRSDTAVYYCARGHGGSYFYSYGMDVWGQTTT VSSGSASAP 120

DB 91 VDNSASTAYMELSLRSRSDTAVYYCAR-----SYYAMDYWGQTTLT VSSGSASAP 141

QY 121 TLFPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPVLRGGKYA 180

DB 142 TLFPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPVLRGGKYA 201

QY 181 ATSQVLLPSKDVMOGTDHVVCK 203

DB 202 ATSQVLLPSKDVMOGTDHVVCK 224

RESULT 5

AAAB12917

XX ID AAB12917 standard; protein; 588 AA.

XX AC AAB12917;

XX 16-NOV-2000 (first entry)

XX Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #86.

DE Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
 KW immunosuppression; autoimmune disease; treatment; rheumatism;
 KW anti-Fas antibody.

XX Synthetic.

XX JP2000154149-A.

XX 06-JUN-2000.

XX 17-SEP-1999; 99JP-00263984.

XX 18-SEP-1998; 98JP-00264598.

Db 202 ATSQVLLPSKDVMOGTDEHVCK 224
RESULT 7
ID AAB12918
XX AAB12918 standard; protein; 588 AA.
XX AAB12918;
AC AAB12918;
XX 16-NOV-2000 (first entry)
XX Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #88.
DE Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
XX immunosuppression; autoimmune disease; treatment; rheumatism;
KW anti-Fas antibody.
XX Synthetic.
OS JP2000154149-A.
XX 06-JUN-2000.
XX 17-SEP-1999; 99JP-00263984.
XX 18-SEP-1998; 98JP-00264599.
XX (SANY) SANKYO CO LTD.
XX WPI; 2000-454476/40.
XX N-PSDB; AAB78272.
XX Anti-human Fas humanizing antibody-containing antirheumatic agents.
PS Claim 1; Page 80-81; 109pp; Japanese.
XX The present invention relates to antirheumatic agents which comprise as
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC does not include a J segment, has apoptosis inducing activity, and
CC consists of a light and heavy chain polypeptide produced synthetically.
CC The agents of the invention exhibit antirheumatic and immunosuppressive
CC activity and can be used to treat autoimmune diseases, especially
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC binding properties. Included in the invention are nucleotide sequences of
CC the IgM light and heavy chains (see AAB78267-A78272) and the
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC AAB78202-A78206) and protein sequences (see AAB12908-B12910). Also
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC chains used in the invention are represented by sequences AAB78213-
CC A78266. Primers used for sequencing the human Ig DNA used in the
CC invention are represented by sequences AAB78277-A78318 and AAB78335-
CC A78337, while humanised anti-Fas Ig DNA sequencing primers are
CC represented by sequences AAB78321-A78334 and AAB78338-A78367. Primer
CC sequences AAB78207-A78212 are specific for murine Ig DNA, and are used in
CC the production of the agent of the invention
XX Sequence 588 AA;
Query Match 80.0%; Score 867.5; DB 3; Length 588;
Best Local Similarity 81.8%; Pred. No. 6.6e-56;
Matches 166; Conservative 12; Mismatches 16; Indels 9; Gaps 1;
QY 1 KPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMNPNNSGNTGYAOKFQGRVTMN 60
Db 31 KPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMNPNNSGNTGYAOKFQGRVTMN 90
QY 61 RNTSISTAYMELSLRSEDYAVYYCAR-----SYVMDYWGQGLTIVTVSSGSASAP 120
Db 91 VDNASTAYMELSLRSEDYAVYYCAR-----SYVMDYWGQGLTIVTVSSGSASAP 141
QY 121 TLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYA 180

Db 142 TLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYA 201
QY 181 ATSQVLLPSKDVMOGTDEHVCK 203
Db 202 ATSQVLLPSKDVMOGTDEHVCK 224
RESULT 8
ID ADF69305
XX ADF69305 standard; protein; 266 AA.
AC ADF69305;
XX 26-FEB-2004 (first entry)
XX Human lung specific protein sequence SEQ ID NO:62.
DE human; lung specific nucleic acid; lung specific protein; lung cancer;
KW cytostatic; gene therapy.
XX Homo sapiens.
XX WO2003102137-A2.
XX 11-DEC-2003.
XX 30-MAY-2003; 2003WO-US016810.
XX 31-MAY-2002; 2002US-0385301P.
XX (DIAD-) DIADEXUS INC.
XX Chen S, Macina RA, Sun Y, Liu C, Turner LR;
XX WPI; 2004-053457/05.
XX New human lung specific nucleic acid, useful for preparing a composition
PT for diagnosing or treating lung cancer.
XX Claim 11; SEQ ID NO 62; 221pp; English.
XX The present invention describes a human lung specific nucleic acid
CC molecule. Also described: (1) a method for determining the presence of a
CC lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising
CC the nucleic acid molecule; (3) a host cell comprising the vector; (4) a
CC method for producing a polypeptide encoded by the nucleic acid molecule;
CC (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody
CC or its fragment that specifically binds to the polypeptide; (7) a method
CC for determining the presence of a lung specific protein in a sample; (8)
CC a method for diagnosing and monitoring the presence and metastases of
CC lung cancer in a patient; (9) a kit for detecting a risk of cancer or
CC presence of cancer in a patient comprising a means for determining the
CC presence the nucleic acid molecule or polypeptide in a sample of a
CC patient; (10) a method of treating a patient with lung cancer; and (11) a
CC vaccine comprising the polypeptide or the nucleic acid encoding the
CC polypeptide. Human LSNA molecules and related proteins have cytostatic
CC activity, and can be used in gene therapy. They are useful for preparing
CC a composition for diagnosing or treating lung cancer. The present
CC sequence represents a human lung specific protein, which is used in the
CC exemplification of the present invention.
XX Sequence 266 AA;
Query Match 74.6%; Score 809; DB 8; Length 266;
Best Local Similarity 75.4%; Pred. No. 6e-52;
Matches 156; Conservative 18; Mismatches 21; Indels 12; Gaps 3;
QY 1 KPGASVKVSKASGYTFTSYDINVRQATGQGLEWMGMNPNNSGNTGYAOKFQGRVTMN 60
Db 23 KPGESLKISKSGSYFTSYWGNVRQMPGKLEWGMIIYPGDSIDTYSFQFQVITIS 82
QY 61 RNTSISTAYMELSLRSEDYAVYYCAR----GGHGGSYFYSGYGMVMDVWGQGTIVTVSSGS 116

XX Example 8; SEQ ID NO 49; 243pp; English.

XX The present invention relates to a library (I) of modified fusion

CC proteins of transferrin (Tf) and therapeutic proteins with increased

CC serum half-life or serum stability. Preferred fusion proteins include

CC those modified so that the Tf moiety exhibits no or reduced

CC glycosylation, iron binding and/or Tf receptor binding. The transferrin

CC fusion proteins are useful for treating, preventing or ameliorating

CC disorders or diseases of endocrine system, nervous system, immune system,

CC respiratory system, cardiovascular system, diseases and/or disorders

CC relating to cell proliferation, and/or diseases or disorders relating to

CC blood. The modified fusion proteins are useful in diagnosis, prognosis,

CC prevention and/or treatment of autoimmune disorders; diseases and

CC disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia

CC and thrombocytopenia); allergic reactions such as allergic asthma,

CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and

CC eczema; inflammatory conditions e.g., inflammation associated with

CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,

CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders

CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel

CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders

CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative

CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The

CC fusion protein is also useful as an adjuvant to enhance antibacterial or

CC antifungal immune responses, antiparasitic immune responses, etc. The

CC fusion protein is also useful for treating monoclonal gammopathy of

CC undetermined significance (MGUS), Waldenström's disease, plasmacytomas,

CC adult respiratory distress syndrome, for stimulating wound repair, for

CC preventing or treating infections of joints, bones, skin, etc. The fusion

CC protein is also useful for treating or preventing thrombosis, myocardial

CC infarction, cancers, thrombocytopenia, sickle cell anaemia,

CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,

CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf

CC and a specific example of a SCA that can be fused to Tf is anti-tumour

CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence

CC from an anti-TNFalpha antibody.

XX Sequence 228 AA;

Query Match 72.0%; Score 781; DB 8; Length 228;

Best Local Similarity 71.5%; Pred. No. 66-50; Indels 12; Gaps 2;

Matches 148; Conservative 27; Mismatches 20;

QY 2 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGMNPNNGTGYAQKFGQRTVWNR 61

DB 13 QPGGSLRLSCAASGFTFTSYVNWVRQAPGKLEWVSGISGGGTYTADSVKGRFTISR 72

QY 62 NTSISTAWELSLRSEDATAVYCA-----RGCHGGSFYFYGYMDVWGQGTITVTVSSGS 116

DB 73 DNSMNTLYLQMSLRSEDATAVYCAKDLNRLSGGTF-----DIWGQGTITVTVSSGS 125

QY 117 ASAPTLPFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRG 176

DB 126 ASAPTLPFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRG 185

QY 177 GKAAATSVQLLPKDVMOGTDEHVCK 203

DB 186 GKAAATSVQLLPKDVMOGTDEHVCK 212

RESULT 11

ADM05427

ID ADM05427 standard; protein; 595 AA.

XX ADM05427;

XX 20-MAY-2004 (first entry)

XX Human protein of the invention SEQ ID NO:4112.

XX human; gene therapy; diagnostic marker; pharmaceutical.

XX

OS Homo sapiens.

PN EP1347046-A1.

XX 24-SEP-2003.

XX 12-APR-2002; 2002EP-00008400.

XX 22-MAR-2002; 2002JP-00137785.

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;

PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;

PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

DR WPI; 2003-723558/69.

DR N-PSDB; ADM02984.

XX New polynucleotides and polypeptides are useful in gene therapy, for

PT developing a diagnostic marker or medicines for regulating their

PT expression and activity, or as a target of gene therapy.

PS Claim 1; SEQ ID NO 4112; 305pp; English.

XX The invention relates to a novel human polynucleotide and the encoded

CC polypeptide. A polynucleotide of the invention may have a use in gene

CC therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful

CC as a primer for synthesizing the polynucleotide or as a probe for

CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are

CC useful in gene therapy, for developing a diagnostic marker or medicines

CC for regulating their expression and activity, or as a target of gene

CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides

CC are useful as pharmaceutical agents. The present sequence represents a

CC protein sequence of the invention.

XX Sequence 595 AA;

Query Match 71.5%; Score 775.5; DB 7; Length 595;

Best Local Similarity 71.8%; Pred. No. 4.3e-49;

Matches 145; Conservative 30; Mismatches 24; Indels 3; Gaps 1;

QY 2 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGMNPNNGTGYAQKFGQRTVWNR 61

DB 33 QPGGSLRLSCAASGFTFTSFAMHVRQAPGKLEWVSTISSNGRKQYGESVKGRFTISR 92

QY 62 NTSISTAWELSLRSEDATAVYCA--GCHGGSFYFYGYMDVWGQGTITVTVSSGSASAPT 121

DB 93 DSSKNTLYLQMSLRSEDATAVYCA--GCHGGSFYFYGYMDVWGQGTITVTVSSGSASAPT 149

QY 122 LFPVLSVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGKYAA 181

DB 150 LFPVLSVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGKYAA 209

QY 182 TSQVLLPSKDVMOGTDEHVCK 203

DB 210 TSQVLLPSKDVMOGTDEHVCK 231

RESULT 12

AAW23924

ID AAW23924 standard; protein; 596 AA.

XX AAW23924;

XX 12-OCT-2001 (first entry)

XX Human EST encoded protein SEQ ID NO: 1449.

XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;

XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;

XX diagnostic; forensic test; gene mapping; genetic disorder; biodiversity;

XX gene therapy; nutrition.

```

XX OS Homo sapiens.
XX PN WO200154477-A2.
XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-US002687.
XX PR 25-JAN-2000; 2000US-00491404.
XX FR 17-JUL-2000; 2000US-00617746.
XX PR 03-AUG-2000; 2000US-00631451.
XX PR 15-SEP-2000; 2000US-00663870.
XX XX (HYSE-) HYSEQ INC.
XX XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Aeundi V;
XX PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX DR WPI; 2001-476164/51.
XX DR N-PSDB; AAH98583.
XX XX Isolated polypeptide for treatment of diseases, diagnostics, raising
XX PT antibodies and research use.
XX PS Claim 20; Page 1011-1012; 1275pp; English.
XX CC The present invention provides the protein and coding sequences of novel
XX CC proteins from a variety of organisms, including human, dog, cat, horse,
XX CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
XX CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
XX CC from the organism of interest. They can be used in diagnostics,
XX CC forensics, gene mapping, identification of mutations, to assess
XX CC biodiversity and for nutritional purposes. The present sequence is a
XX CC protein of the invention
XX SQ Sequence 596 AA;

Query Match 70.6%; Score 766.5; DB 4; Length 596;
Best Local Similarity 72.3%; Pred. No. 2e-48; Mismatches 30; Indels 1; Gaps 1;
Matches 146; Conservative 25;

Qy 2 KPGASVKVSKASGYTFTSVDINWVRQATGQGLEWMGMNPNNGNTGYAQKFGQGRVTMNR 61
Db 32 QPGGSLRLSCAASGFTSSYWMHWVRQAPGKGLVWVSRINTDGSSTSYADSVKGRFTISR 91

Qy 62 NTSISTAYMELSSLRSEDTAVYYCARGHGSGSYFYSGMDVWGQGTITVTVSSGSASAPT 121
Db 92 DNAKNTLYLQWNSLRRAEDTAVYYCARADNCSS-TSCYKCFDYWGQGTITVTVSSGSASAPT 150

Qy 122 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAA 181
Db 151 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAA 210

Qy 182 TSQVLLPSKDVWQGTDEHVCK 203
Db 211 TSQVLLPSKDVWQGTDEHVCK 232

RESULT 13
AAy08598
ID AAy08598 standard; protein; 223 AA.
XX AC AAy08598;
XX XX 05-AUG-1999 (first entry)
XX DT Anti-human TNF-alpha monoclonal antibody H-chain protein.
XX DE Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;
XX KW tumour necrosis factor; light chain; L chain.
XX OS Homo sapiens.

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XX PN JP11127855-A.
XX PD 18-MAY-1999.
XX XX 27-OCT-1997; 97JP-00293994.
XX PF 27-OCT-1997; 97JP-00293994.
XX PR 27-OCT-1997; 97JP-00293994.
XX XX (NTHA ) JAPAN ENERGY CORP.
XX PA WPI; 1999-350318/30.
XX DR N-PSDB; AAX77407.
XX XX Recombinant anti-human TNF-alpha human monoclonal antibody - produced
XX PT stably with a high purity, and in large amounts.
XX PT Claim 3; Page 12-13; 22pp; Japanese.
XX PS This invention describes novel recombinant anti-human TNF-alpha human
XX CC monoclonal antibody consisting of a heavy (H) chain and a light (L)
XX CC chain. The recombinant anti-human TNF-alpha human monoclonal antibody can
XX CC be produced stably in a high purity and in a large amount
XX SQ Sequence 223 AA;

Query Match 70.4%; Score 763.5; DB 2; Length 223;
Best Local Similarity 72.3%; Pred. No. 1.1e-48; Mismatches 24; Indels 7; Gaps 2;
Matches 146; Conservative 25;

Qy 2 KPGASVKVSKASGYTFTSVDINWVRQATGQGLEWMGMNPNNGNTGYAQKFGQGRVTMNR 61
Db 13 QPGGSLRLSCAASGFTSSYWMHWVRQAPGKGLVWVSRINTDGSSTSYADSVKGRFTISR 72

Qy 62 NTSISTAYMELSSLRSEDTAVYYCARGHGSGSYFYSGMDVWGQGTITVTVSSGSASAPT 121
Db 73 DNSKNTLYLQWNSLRRAEDTAVYYCAKDS-GDLAF-----DINGQGTMTVTVSSGSASAPT 125

Qy 122 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAA 181
Db 126 LPPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSVLRGGKYAA 185

Qy 182 TSQVLLPSKDVWQGTDEHVCK 203
Db 186 TSQVLLPSKDVWQGTDEHVCK 207

RESULT 14
ADL70773
ID ADL70773 standard; protein; 223 AA.
XX AC ADL70773;
XX XX 03-JUN-2004 (first entry)
XX DT Anti-TNFalpha antibody VH region, SEQ ID 46.
XX DE Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;
XX KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;
XX KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulneryary;
XX KW Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antiatherosclerotic;
XX KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
XX KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFalpha;
XX KW antibody; VH region.
XX OS Unidentified.
XX PN WO2004020588-A2.
XX XX 11-MAR-2004.
XX PD 28-AUG-2003; 2003WO-US026779.
XX PF
XX XX

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Db	13	QPGGSMKLSCAASGFTFS	DAWMDVROSPKGLEWVAEIRSKANNHATYYAESVKGRFTI	72
Qy	60	NRNTSISTAYMELSSLRSEDTAVY	CARGHGGSYFYSGMDYWGOGTTVTUSSGSASA	119
Db	73	SRDVSKSVYLQMNLR	AE DTGIYCTRGG-----YGFYWGOGTTLTV-SGSASA	122
Qy	120	PTLPPLVSCENSPSDTSSVAVGCL	AQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKY	179
Db	123	PTLPPLVSCENSPSDTSSVAVGCL	AQDFLPDSITLSWKYKNSDISSTRGPPSVLRGGKY	182
Qy	180	AATSQVLLP	SKDVMQGTDEHVCK	203
Db	183	AATSQVLLP	SKDVMQGTDEHVCK	206

Search completed: March 8, 2005, 06:17:09
Job time : 95.1163 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM protein - protein search, using sw model
Run on: March 8, 2005, 05:48:12 ; Search time 107.727 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-27
Perfect score: 1085
Sequence: 1 KPGASVKVCKASGYTFTS.....QVLLPSKDVMTQGDHVVCK 203

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5
Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452
Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	894	82.4	627 13 US-10-047-542-47 Sequence 47, Appl
2	775.5	71.5	595 15 US-10-108-260A-4112 Sequence 4112, Ap
3	731.5	67.4	533 15 US-10-104-047-3224 Sequence 3224, Ap
4	638	58.8	476 9 US-09-747-669-3 Sequence 3, Appli
5	638	58.8	476 14 US-10-290-703-3 Sequence 3, Appli
6	596	54.9	470 9 US-09-859-053-28 Sequence 28, Appl
7	596	54.9	470 16 US-10-625-105-28 Sequence 28, Appl
8	592.5	54.6	228 16 US-10-128-520-163 Sequence 163, App
9	584.5	53.9	230 16 US-10-128-520-151 Sequence 151, App
10	583	53.7	221 16 US-10-128-520-174 Sequence 174, App
11	580.5	53.5	471 15 US-10-292-088-46 Sequence 46, Appl
12	559.5	51.6	125 14 US-10-041-860-238 Sequence 238, App
13	559.5	51.6	126 14 US-10-041-860-19 Sequence 19, Appl

14	559.5	51.6	126	14	US-10-041-860-201	Sequence 201, App
15	559.5	51.6	126	14	US-10-041-860-288	Sequence 288, Appl
16	559.5	51.6	126	16	US-10-665-383-18	Sequence 18, Appl
17	559	51.5	125	14	US-10-041-860-38	Sequence 38, Appl
18	559	51.5	125	14	US-10-041-860-203	Sequence 203, App
19	559	51.5	125	14	US-10-041-860-240	Sequence 240, App
20	559	51.5	125	14	US-10-041-860-343	Sequence 343, App
21	559	51.5	125	16	US-10-665-383-54	Sequence 54, Appl
22	543.5	50.1	448	14	US-10-171-452A-42	Sequence 42, Appl
23	543.5	50.1	448	14	US-10-171-452A-48	Sequence 48, Appl
24	543.5	50.1	448	14	US-10-171-452A-54	Sequence 54, Appl
25	543.5	50.1	448	14	US-10-171-452A-60	Sequence 60, Appl
26	543.5	50.1	448	15	US-10-353-708-42	Sequence 42, Appl
27	543.5	50.1	448	15	US-10-353-708-48	Sequence 48, Appl
28	543.5	50.1	448	15	US-10-353-708-54	Sequence 54, Appl
29	543.5	50.1	448	15	US-10-353-708-60	Sequence 60, Appl
30	543.5	50.1	448	16	US-10-731-984-8	Sequence 8, Appli
31	543.5	50.1	448	16	US-10-731-984-16	Sequence 16, Appl
32	543.5	50.1	448	16	US-10-731-984-32	Sequence 32, Appl
33	543.5	50.1	448	16	US-10-731-984-41	Sequence 41, Appl
34	543.5	50.1	467	14	US-10-171-452A-41	Sequence 47, Appl
35	543.5	50.1	467	14	US-10-171-452A-47	Sequence 53, Appl
36	543.5	50.1	467	14	US-10-171-452A-53	Sequence 59, Appl
37	543.5	50.1	467	14	US-10-171-452A-59	Sequence 8, Appli
38	543.5	50.1	467	15	US-10-353-708-41	Sequence 41, Appl
39	543.5	50.1	467	15	US-10-353-708-47	Sequence 47, Appl
40	543.5	50.1	467	15	US-10-353-708-53	Sequence 53, Appl
41	543.5	50.1	467	15	US-10-353-708-59	Sequence 59, Appl
42	543.5	50.1	467	16	US-10-731-984-7	Sequence 7, Appli
43	543.5	50.1	467	16	US-10-731-984-15	Sequence 15, Appl
44	543.5	50.1	467	16	US-10-731-984-23	Sequence 23, Appl
45	543.5	50.1	467	16	US-10-731-984-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-047-542-47
; Sequence 47, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 47
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-47

Query Match 82.4%; Score 894; DB 13; Length 627;
Best Local Similarity 83.4%; Pred. No. 4.5e-58;
Matches 176; Conservative 7; Mismatches 20; Indels 8; Gaps 1;

Qy	1	KPGASVKVCKASGYTFTS	YDINVRQATGGLGELWGMNPN	SGNTGYAQFQGRVTWN	60
Db	31	KKPGSSVKVCKASGGTFTS	VAISWVRQAPGQGLEWMGGII	PIFGTANYAQFQGRVTIT	90
Qy	61	RNTSTSTAMELSSLRSEDT	AVYVCARGHGGSYF	-----YSYGMVDVNGQGT	112
Db	91	ADESTSTAMELSSLRSEDT	AVYCAKTGILGFLPSYSGWPN	SDYYGMDVNGQGT	150


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; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001002
; CURRENT APPLICATION NUMBER: US/10/290,703
; CURRENT FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: US 09/747,669
; PRIOR FILING DATE: 2000-12-21
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: US 60/051,945
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-10-290-703-3

Query Match 58.8%; Score 638; DB 14; Length 476;
Best Local Similarity 62.1%; Pred. No. 2.9e-39;
Matches 126; Conservative 22; Mismatches 47; Indels 8; Gaps 5;

QY 1 KPGASVKVCKASGYTFTSYDINVRQATGCGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 31 KPGASVKVCKASGYTFTSYDINVRQAPGCGLEWGMWNPNSGNTGYAOKFQGRVTMT 90
QY 61 RNTSISTAYMELSLRSEDATVYVCARGHGSGFY---SY--GMDVMGQTTVTVS 115
DB 91 RNTSISTAYMELSLRSEDATVYVCARGHGSGFY---SY--GMDVMGQTTVTVS 145
QY 116 SASAPTLPLVSCNSPDSSTSSVAVGCLAQPLDPSITFSWKYKKNDSISSTRGPPSVLR 175
DB 146 STKGPSVFPPLAPCSRSTSE-STAAALGCLVKDYFPEPTVSM--NSGALTSGVHTTTPAVLIQ 202
QY 176 -GGKYAATSOVLLPSKD 191
DB 203 SSGLYSLSSVVTVPSSN 219

RESULT 7
US-10-625-105-28
; Sequence 28, Application US/10625105
; Publication No. US20040180052A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Takashi
; APPLICANT: Tezuka, Takunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/10/625,105
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-625-105-28

Query Match 54.9%; Score 596; DB 16; Length 470;
Best Local Similarity 59.9%; Pred. No. 3.6e-36;
Matches 118; Conservative 26; Mismatches 39; Indels 14; Gaps 6;

QY 1 KPGASVKVCKASGYTFTSYDINVRQATGCGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 31 KPGASVKVCKASGYTFTSYDINVRQAPGCGLEWGMWNPNSGNTGYAOKFQGRVTMT 90
QY 61 RNTSISTAYMELSLRSEDATVYVCARGHGSGFY---SY--GMDVMGQTTVTVS 115
DB 91 RNTSISTAYMELSLRSEDATVYVCARGHGSGFY---SY--GMDVMGQTTVTVS 145
QY 116 SASAPTLPLVSCNSPDSSTSSVAVGCLAQPLDPSITFSWKYKKNDSISSTRGPPSVLR 175
DB 146 STKGPSVFPPLAPCSRSTSE-STAAALGCLVKDYFPEPTVSM--NSGALTSGVHTTTPAVLIQ 202
QY 176 -GGKYAATSOVLLPSKD 191
DB 203 SSGLYSLSSVVTVPSSN 219

RESULT 8
US-10-128-520-163
; Sequence 163, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
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; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-163

Query Match      54.6%; Score 592.5; DB 16; Length 228;
Best Local Similarity 58.7%; Pred. No. 3.2e-36;
Matches 121; Conservative 24; Mismatches 44; Indels 17; Gaps 6;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 12 KPGASVKVSKASGYTFTSYDMHVRQAPQGGLWGMWNPNSGGTNYAOKFQGRVTMT 71
QY 61 RNTSISTAYMELSSLRSRSDTAVYYCARGHGGSYFYSGM-----DVMGGTITVTYSSG 115
DB 72 RDTSISTAYMELSSLRSRSDTAVYYCAR-----IMWSDYGQLVKGGLIWGGTILVTYSSA 125
QY 116 SASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR 175
DB 126 STKGPSVFLAPSSKSTSG-GTAALGCLVKDYFPEPPTVSW--NSGALTSGVHTFPAVLQ 182
QY 176 -GGKYAATSOVLLPSKDVMOGTDHEV 200
DB 183 SSGLYSLSSVTVTPSSSL--GTQTYI 206

RESULT 9
US-10-128-520-151
; Sequence 151, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 151
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-151

Query Match      53.9%; Score 584.5; DB 16; Length 230;
Best Local Similarity 58.7%; Pred. No. 1.3e-35;
Matches 121; Conservative 22; Mismatches 46; Indels 15; Gaps 6;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 12 KPGASVKVSKASGYTFTSYDMHVRQAPQGGLWGMWNPNSGGTNYAOKFQGRVTMT 71
QY 61 RNTSISTAYMELSSLRSRSDTAVYYCAR-----GHHGGSYFYSGYMDVMGGQTTVTYSSG 115
DB 72 RDTSISTAYMELSSLRSRSDTAVYYCARLVIGIVGKPDSELY----FDVMGGQTLVTYSSA 127
QY 116 SASAPTLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR 175
DB 128 STKGPSVFLAPSSKSTSG-GTAALGCLVKDYFPEPPTVSW--NSGALTSGVHTFPAVLQ 184
QY 176 -GGKYAATSOVLLPSKDVMOGTDHEV 200
DB 185 SSGLYSLSSVTVTPSSSL--GTQTYI 208
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RESULT 10
US-10-128-520-174
; Sequence 174, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-174

Query Match      53.7%; Score 583; DB 16; Length 221;
Best Local Similarity 58.7%; Pred. No. 1.6e-35;
Matches 118; Conservative 24; Mismatches 45; Indels 14; Gaps 5;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 12 KPGSSVKVSKASGGTFSYVAISWVRQAPQGGLWGMWNPNSGGTNYAOKFQGRVTMT 71
QY 61 RNTSISTAYMELSSLRSRSDTAVYYCARGHGGGSFYSGYMDVMGGQTTVTYSSGSASAP 120
DB 72 RDTSISTAYMELSSLRSRSDTAVYYCAR-----ITYGYDFWGGQGLTVTVSSASTKGP 123
QY 121 TLFPLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-GGKY 179
DB 124 SVFPLAPSSKSTSG-GTAALGCLVKDYFPEPPTVSW--NSGALTSGVHTFPAVLQSSGLY 180
QY 180 AATSOVLLPSKDVMOGTDHEV 200
DB 181 SLSSVTVTPSSSL--GTQTYI 199

RESULT 11
US-10-292-088-46
; Sequence 46, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 46
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-46

Query Match      53.5%; Score 580.5; DB 15; Length 471;
Best Local Similarity 59.5%; Pred. No. 5e-35;
Matches 116; Conservative 27; Mismatches 43; Indels 9; Gaps 5;

QY 1 KPGASVKVSKASGYTFTSYDINWVRQATCGGLEWGMWNPNSGNTGYAOKFQGRVTMN 60
DB 31 KPGASVKVSKASGYTFTGYMHVVRQAPQGGLWGMWNPNSGGTNYAOKFQGRVTMT 90
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QY 61 RNTSISTAYMELSSLRSEDATVYYCARG--CHGGSYFYSGYMDVWGQTTVTVSSGSA 117
; LENGTH: 126
; TYPE: PRT
Db 91 RDTISISTAYMELNRLSRDSTAVYCARDOPLGYCTNGVCYSF--DYWGQGLTVTVSSAST 148
; ORGANISM: homo sapiens
; US-10-041-860-19

QY 118 SAPTLFPLVSCNSPDSSTSVAVGCLAODFLDPSITFSWKYKNSDISSTRGFPVLR-G 176
; Query Match 51.6%; Score 559.5; DB 14; Length 126;
; Best Local Similarity 92.2%; Pred. No. 4.9e-34; Indels 3; Gaps 2;
; Matches 107; Conservative 2; Mismatches 4;
Db 149 KCPSPVPLAPCSRSTSE-STALGCLVKDYFPFPTVSW--NSGALTSGVHTFPAVLQSS 205
; Mismatches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

QY 177 SKYAATSQVLLPSKD 191
; Query Match 51.6%; Score 559.5; DB 14; Length 126;
; Best Local Similarity 92.2%; Pred. No. 4.9e-34; Indels 3; Gaps 2;
; Matches 107; Conservative 2; Mismatches 4;
Db 206 GLYLSVVTVPPSSN 220
; Mismatches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

RESULT 12
US-10-041-860-238
; Sequence 238, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-238

Query Match 51.6%; Score 559.5; DB 14; Length 125;
Best Local Similarity 92.2%; Pred. No. 4.9e-34;
Matches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

QY 1 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAOKFQGRVTMN 60
; US-10-041-860-238
Db 11 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAOKFQGRVTMT 70
; US-10-041-860-238

QY 61 RNTSISTAYMELSSLRSEDATVYYCARG--HGSYFYSGYMDVWGQTTVTVSS 114
; US-10-041-860-238
Db 71 RNTSISTAYMELSSLRSEDATVYYCAREGIAVAGTYYY-YGMDVWGQTTVTVSS 125
; US-10-041-860-238

RESULT 13
US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19

Query Match 51.6%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.2%; Pred. No. 4.9e-34;
Matches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

QY 1 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAOKFQGRVTMN 60
; US-10-041-860-19
Db 12 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAOKFQGRVTMT 71
; US-10-041-860-19

QY 61 RNTSISTAYMELSSLRSEDATVYYCARG--HGSYFYSGYMDVWGQTTVTVSS 114
; US-10-041-860-19
Db 72 RNTSISTAYMELSSLRSEDATVYYCAREGIAVAGTYYY-YGMDVWGQTTVTVSS 126
; US-10-041-860-19

RESULT 14
US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-041-860-201

Query Match 51.6%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.2%; Pred. No. 4.9e-34;
Matches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

QY 1 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAOKFQGRVTMN 60
; US-10-041-860-201
Db 12 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNSGNTGYAOKFQGRVTMT 71
; US-10-041-860-201

QY 61 RNTSISTAYMELSSLRSEDATVYYCARG--HGSYFYSGYMDVWGQTTVTVSS 114
; US-10-041-860-201
Db 72 RNTSISTAYMELSSLRSEDATVYYCAREGIAVAGTYYY-YGMDVWGQTTVTVSS 126
; US-10-041-860-201

RESULT 15
US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
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; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288

Query Match      51.6%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.2%; Pred. No. 4.9e-34;
Matches 107; Conservative 2; Mismatches 4; Indels 3; Gaps 2;

Qy 1 KKPGRASVKVCKASGYTFTSYDINWVRQATGQGLEWGMGNPNPNSGNTGYAOKFQGRVTMN 60
Db 12 KKPGRASVKVCKASGYTFTSYDINWVRQATGQGLEWGMGNPNPNSGNTGYAOKFQGRVTMT 71

Qy 61 RNTSISTAYMELSSLRSEDYAVYICARGG--HGGSYFYFYGYGMDVWGQGTITVTVSS 114
Db 72 RNTSISTAYMELSSLRSEDYAVYICAREGLAVAGTYYY-YYGMDVWGQGTITVTVSS 126

Search completed: March 8, 2005, 07:05:50
Job time : 108.727 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 22.3212 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-27

Perfect score: 1085

Sequence: 1 KPGASVKVCKASGYTFTS.....QVLLPSKDVWGQTDHVVCK 203

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap:*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	54.9	470	4	US-09-859-053-28
2	527.5	48.6	279	3	US-08-397-411-13
3	519.5	47.9	462	4	US-09-627-896B-24
4	518.5	47.8	467	2	US-07-916-098A-45
5	512	47.2	468	3	US-09-485-737B-67
6	512	47.2	468	4	US-10-071-485-67
7	512	47.2	711	3	US-09-485-737B-90
8	512	47.2	711	4	US-10-071-485-90
9	502.5	46.3	235	3	US-08-444-644-28
10	502.5	46.3	235	3	US-08-232-246A-28
11	502	46.3	222	1	US-08-458-516-22
12	502	46.3	235	1	US-08-458-516-23
13	502	46.3	449	1	US-08-458-516-13
14	497.5	45.9	235	3	US-08-444-644-42
15	497.5	45.9	235	3	US-08-232-246A-42
16	495	45.6	451	4	US-09-472-087-70
17	495	45.6	472	4	US-09-301-593-43
18	489.5	45.1	235	3	US-08-444-644-19
19	489.5	45.1	235	3	US-08-232-246A-19
20	485.5	44.7	120	3	US-09-025-769B-36
21	485.5	44.7	120	3	US-09-025-769B-59
22	485.5	44.7	120	4	US-09-490-070A-36
23	485.5	44.7	120	4	US-09-490-070A-59
24	485.5	44.7	120	4	US-09-490-153-36
25	485.5	44.7	120	4	US-09-490-153-59
26	485.5	44.7	120	4	US-09-490-324-36
27	485.5	44.7	120	4	US-09-490-324-59

28	485.5	44.7	253	3	US-09-027-449-52	Sequence 52, Appl
29	485.5	44.7	253	3	US-08-804-444A-52	Sequence 52, Appl
30	485.5	44.7	253	3	US-09-026-985-52	Sequence 52, Appl
31	485.5	44.7	253	4	US-09-121-952A-52	Sequence 52, Appl
32	485.5	44.7	253	4	US-09-234-340A-52	Sequence 52, Appl
33	485.5	44.7	256	3	US-09-027-449-70	Sequence 70, Appl
34	485.5	44.7	256	3	US-09-026-985-70	Sequence 70, Appl
35	485.5	44.7	256	4	US-09-121-952A-70	Sequence 70, Appl
36	485.5	44.7	256	4	US-09-234-340A-70	Sequence 70, Appl
37	485.5	44.7	298	3	US-09-027-449-60	Sequence 60, Appl
38	485.5	44.7	298	3	US-08-804-444A-60	Sequence 60, Appl
39	485.5	44.7	298	3	US-09-026-985-60	Sequence 60, Appl
40	485.5	44.7	298	4	US-09-121-952A-60	Sequence 60, Appl
41	485.5	44.7	298	4	US-09-234-340A-60	Sequence 60, Appl
42	485.5	44.7	452	3	US-09-027-449-71	Sequence 71, Appl
43	485.5	44.7	452	3	US-09-026-985-71	Sequence 71, Appl
44	485.5	44.7	452	4	US-09-121-952A-71	Sequence 71, Appl
45	485.5	44.7	452	4	US-09-234-340A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1

US-09-859-053-28

; Sequence 28, Application US/09859053

; Patent No. 6803039

; GENERAL INFORMATION:

; APPLICANT: Tsuji, Takashi

; APPLICANT: Tezuka, Katsunari

; APPLICANT: Hori, No. 6803039uaki

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

; FILE REFERENCE: 06501-079001

; CURRENT APPLICATION NUMBER: US/09/859,053

; CURRENT FILING DATE: 2001-05-16

; PRIOR APPLICATION NUMBER: JP 2001-99508

; PRIOR FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: JP 2000-147116

; PRIOR FILING DATE: 2000-05-18

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 28

; TYPE: PRT

; LENGTH: 470

; ORGANISM: Homo sapiens

US-09-859-053-28

Query Match 54.9%; Score 596; DB 4; Length 470;

Best Local Similarity 59.9%; Pred. No. 5.6e-45;

Matches 118; Conservative 26; Mismatches 39; Indels 14; Gaps 6;

Qy	1	KPGASVKVCKASGYTFTSVDINWVRQATCGGLEMMGMNPNSGNTGYAOKFGQGRVTMN	60
Db	31	KPGASVKVCKASGYTFTGYIMHWVRQAPGQGLEMMGMNPNSGNTGYAOKFGQGRVTMT	90
Qy	61	RNTSISTAYMELSLRSRSEDATVYTCARGHGGSFY---SY- -GMDVWGQGTGTTVTSSG	115
Db	91	RDTSISTAYMELSLRSRSDTAVYTCAR-----TYYDSGGYHDAFDINGQGTMTVTSSA	145
Qy	116	SASAPTLFPLVSCNPSDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR	175
Db	146	STKGPSVFPFLAPCSRSTSE-STAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQ	202
Qy	176	-GGKYAATSOVLLPSKD	191
Db	203	SSGLYSLSVVTVFSSN	219

RESULT 2

US-08-397-411-13

; Sequence 13, Application US/08397411

; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Teo, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/397,411
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 279 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-411-13

Query Match 48.6%; Score 527.5; DB 3; Length 279;
Best Local Similarity 53.7%; Pred. No. 3.6e-39;
Matches 108; Conservative 27; Mismatches 55; Indels 11; Gaps 5;

Qy 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNSGNTGYAQKFGQGRVTMN 60
Db 12 KPGASVKVSKASGYTFTSYDINWVRQAPGQGLEWMGVINPRSGYTHYNQKLDKATLT 71

Qy 61 RNTSISTAYMELSLRSEDATVYYCARGHGGGSFYSYGYMDVMVGQGTVTTVSSGSASAP 120
Db 72 ADKASATAYMELSLRSEDATVYYCAR-----SAYDYDGFAYMGQGTTLTVSSASTKGP 126

Qy 121 TLPFLVSCNSPSTSSVAVCLAQDFLPDSITFSWKYKNSDLSSTRGPPSVLR-GGKY 179
Db 127 SVFPLAPSKSTSG-GTAAAGCLVKDYFPEPTVTSW---NSGALTSGVHTFPAVLQSSGLY 183

Qy 180 AATSOVLLPSKDVMTGTDH 200
Db 184 SLSSVTVTPSSSL-GTQTYI 202

RESULT 3
US-09-627-896B-24
; Sequence 24, Application US/09627896B
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ

; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; TITLE OF INVENTION: OF TREATMENT THEREWITH
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 24
; LENGTH: 462
; TYPE: PRT
; ORGANISM: 3D1 heavy chain
US-09-627-896B-24

Query Match 47.9%; Score 519.5; DB 4; Length 462;
Best Local Similarity 55.7%; Pred. No. 3.5e-38;
Matches 107; Conservative 25; Mismatches 47; Indels 13; Gaps 5;

Qy 1 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNSGNTGYAQKFGQGRVTMN 60
Db 31 KPGSSVKVSKASGYTFTDYAIQWVRQAPGQGLEWGVINYYDNTYNYNQKFKGKATWT 90

Qy 61 RNTSISTAYMELSLRSEDATVYYCARGHGGGSFYSYGYMDVMVGQGTVTTVSSGSASAP 120
Db 91 VKSTSTAYMELSLRSEDATVYYCAR-----AWY-MDYWGQGTTLTVSSASTKGP 141

Qy 121 TLPFLVSCNSPSTSSVAVCLAQDFLPDSITFSWKYKNSDLSSTRGPPSVLR-GGKY 179
Db 142 SVFPLAPCSRSTSE-STAAAGCLVKDYFPEPTVTSW---NSGALTSGVHTFPAVLQSSGLY 198

Qy 180 AATSOVLLPSKD 191
Db 199 SLSSVTVTPSSN 210

RESULT 4
US-07-916-098A-45
; Sequence 45, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843


```
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90
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Query Match 47.2%; Score 512; DB 3; Length 711;
Best Local Similarity 48.8%; Pred. No. 2.7e-37;
Matches 98; Conservative 36; Mismatches 53; Indels 14; Gaps 5;

QY 1 KPGASVKVCKASGYTFTSYDINNVRQATGQGLEWMGMNPNNGNTGYAOKFQGRVTMN 60
DB 32 KPGASVKISKASGYTFTDYGMMWVKQAPGQGLKMMGWINTYTGESTYVDDFKGRFVFS 91
QY 61 RNTSISTAYMELSLRSEDATVYYCARGHGGSFYFYGYGMDVWGQGTITVTVSSGSASAP 120
DB 92 LDTSVSAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQGTITVTVSSASTKGP 143
QY 121 TLPLVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNNDSISSTRGFPSVLR-GGKY 179
DB 144 SVFPLAPSKSTSG-GTAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSSGLY 200

QY 180 AATSOVLLPSKDVMOGTDEHV 200
DB 201 SLSSVTVTPSSSL--GTQTYI 219
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RESULT 8
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match 47.2%; Score 512; DB 4; Length 711;
Best Local Similarity 48.8%; Pred. No. 2.7e-37;
Matches 98; Conservative 36; Mismatches 53; Indels 14; Gaps 5;

QY 1 KPGASVKVCKASGYTFTSYDINNVRQATGQGLEWMGMNPNNGNTGYAOKFQGRVTMN 60
DB 32 KPGASVKISKASGYTFTDYGMMWVKQAPGQGLKMMGWINTYTGESTYVDDFKGRFVFS 91
QY 61 RNTSISTAYMELSLRSEDATVYYCARGHGGSFYFYGYGMDVWGQGTITVTVSSGSASAP 120
DB 92 LDTSVSAAYLQISLKAEDTATYFCARRG-----FYAMDYWGQGTITVTVSSASTKGP 143
QY 121 TLPLVSCENSPDTSVAVGCLAQDFLPSITFSWKYKNNDSISSTRGFPSVLR-GGKY 179
DB 144 SVFPLAPSKSTSG-GTAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSSGLY 200

QY 180 AATSOVLLPSKDVMOGTDEHV 200
DB 201 SLSSVTVTPSSSL--GTQTYI 219

RESULT 9
US-08-444-644-28
; Sequence 28, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
US-08-444-644-28

Query Match 46.3%; Score 502.5; DB 3; Length 235;
Best Local Similarity 50.3%; Pred. No. 4.8e-37;
Matches 96; Conservative 36; Mismatches 48; Indels 11; Gaps 4;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMNR 61
DB 32 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMNR 61
QY 62 NTSISTAYMELSLRSEDYAVYYCARGHGSGSYFYSGMDVWGQGTVTYVSSGSASAPT 121
DB 92 DKSSNTAYMELSLRSEDYAVYYCARGHGSGSYFYSGMDVWGQGTVTYVSSGSASAPT 121
QY 122 LFPLVSCNSPDTSSTVAAGCLADPLDPSITFSWKYKNNSDISSTRGPPSVLR-GGKYA 180
DB 145 VFPLAPCSRSTSE-STAAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYS 201
QY 181 ATSOVLLPSKD 191
DB 202 LSSVTVFPSSN 212

RESULT 10
US-08-232-246A-28
; Sequence 28, Application US/08232246A
; Patent No. 6329508
; GENERAL INFORMATION:
; APPLICANT: Friden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALX88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
US-08-232-246A-28

Query Match 46.3%; Score 502.5; DB 3; Length 235;
Best Local Similarity 50.3%; Pred. No. 4.8e-37;
Matches 96; Conservative 36; Mismatches 48; Indels 11; Gaps 4;

QY 2 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMNR 61
DB 32 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMNR 61
QY 62 NTSISTAYMELSLRSEDYAVYYCARGHGSGSYFYSGMDVWGQGTVTYVSSGSASAPT 121
DB 92 DKSSNTAYMELSLRSEDYAVYYCARGHGSGSYFYSGMDVWGQGTVTYVSSGSASAPT 121
QY 122 LFPLVSCNSPDTSSTVAAGCLADPLDPSITFSWKYKNNSDISSTRGPPSVLR-GGKYA 180
DB 145 VFPLAPCSRSTSE-STAAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYS 201
QY 181 ATSOVLLPSKD 191
DB 202 LSSVTVFPSSN 212

RESULT 11
US-08-458-516-22
; Sequence 22, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPTIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-22

Query Match 46.3%; Score 502; DB 1; Length 222;
Best Local Similarity 52.2%; Pred. No. 5e-37;

Matches	105;	Conservative	30;	Mismatches	54;	Indels	12;	Gaps	67;
Qy	1	KKPCASVKVCKASGYTFTSYDINWVRQATQGGLEWGMWNPNSGNTGYAQKFGQGRVTMN	60						
Db	12	KKPGSSVKVCKASGYAFTNYLIEWVRQA PQQGLEWIGVIYPGSGGTNYNEKFKGRVTLT	71						
Qy	61	RNTSISTAYMELSLSRSEDYAVYICARGHGGSFYFYGGMDVWGQGTITVTVSSGSASAP	120						
Db	72	VDESTNTAYMELSLSRSEDYAVYFCAR - RDGNYGWFAV - - - - -WGQGLTVTVSSASTKGP	125						
Qy	121	TLRPLVSCENSPDTSVAVVCGCLAQDFLPDSITFSPWKYKNNSDISSTRGPPSVLR -GGKY	179						
Db	126	SVFELAPSSKTSG -GTAALGCLVKDYPPEPVTVSW - -NSGALTSGVHTFPAVLQSSGLY	182						
Qy	180	AATSQVLLPSKDVNQGTDEHV	200						
Db	183	SLSSVVTVPSSSL - -GTOTYI	201						

```

RESULT 12
US-08-458-516-23
; Sequence 23, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GP1IB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-458-516-23

```

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Db          72 VDSESTAYMELSLRSEDYAVPCAR--RDNGTGWFA-----WGQGLVTVSSASTKGP 125
QY          121 TLFLPLVSCENSPDTSVAVYGLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLK--GGKY 179
Db          126 SVFPLAPSSKSTG--GTAALGCLVKDYFPEPVTVSW--NSCALTSGVHTFPAVLQSSGLY 182
QY          180 AATSOVLPLPSKDVMOGTDHV 200
Db          183 SLSSWTVPSSSL--GTQTYI 201

RESULT 13
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PS-08-458-516-13

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		Query Match	46.3%	Score 502;	DB 1;	Length 235;	
		Best Local Similarity	52.2%;	Pred. No. 5.4e-37;			
		Matches 105; Conservative	30;	Mismatches 54;	Indels 12;	Gaps 6	
QY	1	KKPGASVKVSKAGSYFTTSYDINWVRQATCGGLEWMGNPNNSGNTGYAQKFGQRVTMN	60				
Db	12	KKPGSSVKVSKAGSYAFTNLIENWRQAQGGLIEWIGVIYPGGSGTNYNEKFGRVLT	71				
QY	61	RNTSISTAYMELSLRSEDYAVYTCARGHGGSFYFYYGMDVMGQQGTIVTVSSGSASP	120				

Qy 181 ATSOVLLPSKDV 192
:|:|:
Db 202 LSSVTVFPSSL 213

Search completed: March 8, 2005, 05:54:05
Job time : 23.3212 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.5893 Seconds
(without alignments)
1953.842 Million cell updates/sec

Title: US-09-784-950-28
Perfect score: 786
Sequence: 1 HSLAVSLGERATINCKSSQS.....VVCLLNFPYPREAKEHQKSP 149

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	617	78.5	216	2 J0241	Ig kappa chain Am3
2	590	75.1	240	2 S06084	Ig kappa chain pre
3	566.5	72.1	215	2 J0242	Ig kappa chain NIG
4	561	71.4	214	2 S68212	Ig kappa chain (Ma
5	553	70.4	220	2 A31790	Ig kappa chain V r
6	544.5	69.3	215	2 J0244	Ig kappa chain NIG
7	534.5	68.0	215	2 A23746	Ig kappa chain V-I
8	527	67.0	120	2 S51147	antibody light cha
9	522	66.4	114	1 K4HULN	Ig kappa chain V-I
10	520	66.2	113	2 S34002	Ig kappa chain V r
11	515	65.5	134	2 S49531	anti-sm antibody V
12	513.5	65.3	215	2 J0243	Ig kappa chain NIG
13	512	65.1	129	2 S40347	Ig kappa chain - h
14	504	64.1	134	1 K4HUI7	Ig kappa chain pre
15	502	63.9	113	2 S30520	Ig kappa chain V r
16	502	63.9	113	2 S34003	Ig kappa chain V r
17	498.5	63.4	133	1 K4HUI1	Ig kappa chain pre
18	496.5	63.2	138	2 A53261	Ig kappa chain pre
19	496	63.1	113	2 S30523	Ig kappa chain V r
20	496	63.1	114	2 S44119	Ig kappa chain V-J
21	493	62.7	114	2 S44116	Ig kappa chain V-J
22	485.5	61.8	219	2 PC4203	Ig kappa chain (no
23	480	61.1	124	2 S40364	Ig kappa chain - h
24	479	60.9	132	2 S46373	Ig kappa chain V-J
25	479	60.9	145	2 PL0014	Ig kappa chain pre
26	476.5	60.6	219	2 S52028	Ig kappa chain - m
27	475.5	60.5	225	2 S37484	Ig kappa chain - m
28	474	60.3	121	1 K4HUI	Ig kappa chain pre
29	473.5	60.2	217	2 S42772	Ig kappa chain - m

30	473	60.2	92	2 S37533	Ig kappa chain V r
31	471	59.9	210	2 A56169	Ig kappa chain V r
32	471	59.9	218	2 J05810	monoclonal antibod
33	470.5	59.9	219	2 S38865	Ig kappa chain - m
34	470	59.8	101	2 PH0869	Ig kappa chain V r
35	468	59.5	92	2 S37532	Ig kappa chain V r
36	468	59.5	92	2 S37534	Ig kappa chain V r
37	468	59.5	218	2 S68241	Ig kappa chain V r
38	467.5	59.5	118	2 PT0356	Ig kappa chain V r
39	467	59.4	92	2 S37535	Ig kappa chain V r
40	467	59.4	92	2 S37529	Ig kappa chain V r
41	467	59.4	230	2 S33161	Ig kappa chain - s
42	465	59.2	92	2 S37530	Ig kappa chain V r
43	464.5	59.1	219	2 S16112	Ig kappa chain V r
44	462	58.8	129	2 S40329	Ig kappa chain V-J
45	459.5	58.5	106	2 A49138	IgA kappa rheumato

ALIGNMENTS

RESULT 1

JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
Submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 78.5%; Score 617; DB 2; Length 216;
Best Local Similarity 86.2%; Pred. NO. 4.2e-45;
Matches 125; Conservative 7; Mismatches 9; Indels 4; Gaps 3;

Qy	3	LAVSLGERATINCKSSQSVLYSFNNKNYLANVYQKQGPQPKLLIYMASTRESGVDPDRFGG	62
Db	11	LAVSLGERATINCKSSQSVLY--NSKNFLAWYQKPGQ-PKLLI-WANVRSGVDPDRFRG	66
Qy	63	SGSGTDFLTITISSLQAEADVAVVYCOQYVSTPRTFGQTKVEIKRTVAAPSVFIFFPSDSQ	122
Db	67	SGVGTDFLTITISNLQAEVLAVVYCOQYVSTPVSFGQGRLEIKRTVAAPSVFIFFPSDSQ	126
Qy	123	LKSGTASVVCLLNFPYPREAKEHQK	147
Db	127	LKSGTASVVCLLNFPYPREAKVQWK	151

RESULT 2

S06084
Ig kappa chain precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C:Accession: S06084
R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.
A:Reference number: S06084; MUID:90016888; PMID:2508067
A:Accession: S06084
A:Molecule type: mRNA
A:Residues: 1-240 <CRO>
A:Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-240/Product: Ig kappa chain #status predicted <MAT>
F:153-222/Domain: immunoglobulin homology <IMM>


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Db 64 GSGSGTDFLTISLSQSEDFALYYCQYNTWPLTFLFGGKTKVEIKRTVAAPSVFIFFPSD 123
Qy 121 EQLKSGTASVCLNNFYPREAKEHOK 147
Db 124 EQLKSGTASVCLNNFYPREAKVQWK 150

RESULT 7
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leon, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 68.0%; Score 534.5; DB 2; Length 215;
Best Local Similarity 74.7%; Pred. No. 3.9e-38;
Matches 109; Conservative 13; Mismatches 19; Indels 5; Gaps 1;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFG 61
Db 10 TLSLSPGERATVLSGASQSV-----SSNYLAWYQKQPPQAPRLLIYDSSRATGIPDRFS 64
Qy 62 GSGSGTDFLTISLSQAEADVAVYQCQYYSTPRTFGQGTKEIKRTVAAPSVFIFFPSDE 121
Db 65 GSGSGTDFLTISRLEPDEFAVYQCQYSGSPLTFGGGTKEIKRTVAAPSVFIFFPSDE 124
Qy 122 QLKSGTASVCLNNFYPREAKEHOK 147
Db 125 QLKSGTASVGLNNFYPREAKVQWK 150

RESULT 8
S51147
antibody light chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S51147
R:de Kruijf, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL data library, January 1995
A:Description: Selection and application of human SCFV antibody fragments from a semi-synthetic library
A:Reference number: S51147
A:Accession: S51147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <DEK>
A:Cross-references: EMBL:X83714; NID:G633227; PIDN:CAA58689.1; PID:G633228
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 67.0%; Score 527; DB 2; Length 120;
Best Local Similarity 93.6%; Pred. No. 9.3e-38;
Matches 102; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFG 61
Db 10 SLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFS 69
Qy 62 GSGSGTDFLTISLSQAEADVAVYQCQYYSTPRTFGQGTKEIKRTVA 110
Db 70 GSGSGTDFLTISLSQAEADVAVYQCQYYSTLWTFGGGTKEIKRTVAAS 118
```

```
RESULT 9
K4HULN
Ig kappa chain V-IV region (Ien) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C:Accession: A01903; F61458
R:Schneider, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 356, 507-557, 1975
A:Title: Die Primaerstruktur einer monoklonalen Immunoglobulin-L-Kette der Subgruppe IV von
A:Reference number: A01903; MUID:76004342; PMID:50995
A:Accession: A01903
A:Molecule type: protein
A:Residues: 1-114 <SCH>
A:Note: this is the first completely sequenced V region of a new kappa chain subgroup, d
A:Note: the C region of this chain has the Inv (3) marker
R:Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associ
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: F61458
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Comment: This is a Bence Jones protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>
F:23-94/Disulfide bonds: #status predicted

Query Match 66.4%; Score 522; DB 1; Length 114;
Best Local Similarity 93.4%; Pred. No. 2.3e-37;
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HSLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRF 60
Db 9 NSLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRF 68
Qy 61 GSGSGTDFLTISLSQAEADVAVYQCQYYSTPRTFGQGTKEIKR 106
Db 69 GSGSGTDFLTISLSQAEADVAVYQCQYYSTPVSFGGTKEIKR 114

RESULT 10
S34002
Ig kappa chain V region - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S34002; S30522
R:Marlette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A:Title: Nucleotide sequence analysis of the variable domains of four human monoclonal I
A:Reference number: S34001; MUID:93209281; PMID:7681398
A:Accession: S34002
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z18328
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 66.2%; Score 520; DB 2; Length 113;
Best Local Similarity 95.2%; Pred. No. 3.4e-37;
Matches 99; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFG 61
Db 10 SLAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFS 69
Qy 62 GSGSGTDFLTISLSQAEADVAVYQCQYYSTPRTFGQGTKEIK 105
```

Db 70 GSGSGTDTLTITISLQAEADVAVYCHQYGIPTFGQTKVEIK 113

RESULT 11

S49531

anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human

C;Species: Homo sapiens (man)

C;Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000

C;Accession: S49531

R;Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.

submitted to the EMBL Data Library, October 1994

A;Description: Molecular characterization of natural human anti-Sm autoantibodies.

A;Reference number: S48797

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-134 <MAH>

A;Cross-references: EMBL:Z46347; NID:g560841; PIDN:CAA86466.1; PID:g560842

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;36-116/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 515; DB 2; Length 134;

Best Local Similarity 94.3%; Pred. No. 1.1e-36;

Matches 99; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61

Db 30 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFS 89

Qy 62 GSGSGTDTLTITISLQAEADVAVYCCQYVSTPRTFGQTKVEIKR 106

Db 90 GSGSGTDTLTITISLQAEADVAVYCCQYVSTAFPGTKVDIKR 134

RESULT 12

JE0243

Ig kappa chain NIG93 precursor - human

C;Species: Homo sapiens (man)

C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C;Accession: JE0243

R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy

A;Reference number: JE0243

A;Accession: JE0243

A;Molecule type: protein

A;Residues: 1-215 <ALI>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 65.3%; Score 513.5; DB 2; Length 215;

Best Local Similarity 71.4%; Pred. No. 2.3e-36;

Matches 105; Conservative 14; Mismatches 21; Indels 7; Gaps 2;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61

Db 10 TLVSVGERATLSCASQSVATN-----VVMYQKLGQAPRLIYDASTGATGVPARFS 63

Qy 62 GSGSGTDTLTITISLQAEADVAVYCCQYVSTPRTFGQTKVEIK-RTVAAPSVFIFFPSD 120

Db 64 GSGSGTEFTLTITISLQSEDAFYICQHNNAWPPFTFGQTKVETKRRRTVAAPSVFIFFPSD 123

Qy 121 EQLKSGTASVVCLNNFYPREAKEHQK 147

Db 124 EQLKSGTASVVCLNNFYPREAKVQWK 150

RESULT 13

S40347

Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S40347

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur. J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: S40312; MUID:94080891; PMID:8258341

A;Accession: S40347

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-129 <KLE>

A;Cross-references: EMBL:X72457; NID:g441382; PIDN:CAA51125.1; PID:g441383

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;33-113/Domain: immunoglobulin homology <IMM>

Query Match 65.1%; Score 512; DB 2; Length 129;

Best Local Similarity 93.2%; Pred. No. 1.8e-36;

Matches 96; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61

Db 27 SLTVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPQLLIYWASTRESGVDPDRFS 86

Qy 62 GSGSGTDTLTITISLQAEADVAVYCCQYVSTPRTFGQTKVEI 104

Db 87 GSGSGTDTLTITISLQAEADVAVYCCQYVSTPLFFGGGTEVEI 129

RESULT 14

K4HUI7

Ig kappa chain precursor V-IV region (B17) - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000

C;Accession: A01905

R;Marsh, P.; Mills, F.; Gould, H.

Nucleic Acids Res. 13, 6531-6544, 1985

A;Title: Detection of a unique human VkappaIV germline gene by a cloned cDNA probe.

A;Reference number: A01905; MUID:86041854; PMID:2997713

A;Accession: A01905

A;Molecule type: mRNA

A;Residues: 1-134 <MAR>

A;Note: the sequence was determined from the differentiated gene

A;Note: the authors translated the codon TGC for residue 76 as trp

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-134/Product: Ig kappa chain V-IV region (B17) #status predicted <MAT>

F;21-43/Region: framework 1

F;36-116/Domain: immunoglobulin homology <IMM>

F;44-60/Region: complementarity-determining 1

F;61-75/Region: framework 2

F;76-82/Region: complementarity-determining 2

F;83-114/Region: framework 3

F;115-121/Region: complementarity-determining 3

F;122-134/Region: framework 4

F;43-114/Disulfide bonds: #status predicted

Query Match 64.1%; Score 504; DB 1; Length 134;

Best Local Similarity 92.4%; Pred. No. 9.1e-36;

Matches 97; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61

Db 30 SLAVSLGERATINCKSSQSVLYSDNKNYLAWYQKPGQPPKLLIYCASTRESGVDPDRFS 89

Qy 62 GSGSGTDTLTITISLQAEADVAVYCCQYVSTPRTFGQTKVEIKR 106

Db 90 GSGSGTDTLTITISLQAEADVAVYCCQYVSTPLFFGGGTEVEIKR 134

RESULT 15

S30520

Ig kappa chain V region - human

C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S30520
F:Marlette, X.
submitted to the EMBL Data Library, October 1992
A:Reference number: S30520
A:Accession: S30520
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <MAR>
A:Cross-references: EMBL:Z18325
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 63.9%; Score 502; DB 2; Length 113;
Best Local Similarity 91.3%; Pred. No. 1.1e-35;
Matches 95; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61
Db 10 SLAVSLGERATINCKSSQSVLYSFNNKYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 69

Qy 62 GSGSGTDFLTITISSLQAEADVAVYCCQYVYTPRTFGQGTKEIK 105
Db 70 GSGSGTDFLTITISSLQAEADVAVYCCQYVYTPRTFGQGTKEIK 113

Search completed: March 8, 2005, 06:39:24
Job time : 11.6393 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 55.644 Seconds
(without alignment)
1371.214 Million cell updates/sec

Title: US-09-784-950-28

Perfect score: 786

Sequence: 1 HSLAVSLGERATINCKSSQS.....VCLLNFPYREAKEHQKSP 149

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	558	71.0	236	2	Q6PIT5	Q6pit5 homo sapien
2	558	71.0	240	2	Q6PIH6	Q6pih6 homo sapien
3	557.5	70.9	239	2	Q8NEK0	Q8nek0 homo sapien
4	556.5	70.8	235	2	Q6GMV9	Q6gmw9 homo sapien
5	554	70.5	234	2	Q72473	Q72473 homo sapien
6	550	70.0	236	2	Q6PIL8	Q6pil8 homo sapien
7	545	69.3	236	2	Q6GMW1	Q6gmw1 homo sapien
8	545	69.3	236	2	Q6PIH7	Q6pih7 homo sapien
9	543.5	69.1	239	2	Q6P491	Q6p491 homo sapien
10	543	69.1	235	2	Q6GMX8	Q6gmx8 homo sapien
11	542.5	69.0	235	2	Q6PJF2	Q6pjf2 homo sapien
12	541	68.8	236	2	Q723Y4	Q723y4 homo sapien
13	536	68.2	236	2	Q6P5S8	Q6p5s8 homo sapien
14	534.5	68.0	235	2	Q6GMW0	Q6gmw0 homo sapien
15	534.5	68.0	239	2	Q8TCD0	Q8tcd0 homo sapien
16	533	67.8	236	2	Q6GMX0	Q6gmx0 homo sapien
17	527	67.0	236	2	Q6GMX9	Q6gmx9 homo sapien
18	521	66.3	114	1	KV4A_HUMAN	P01625 homo sapien
19	520	66.2	236	2	Q6PIH4	Q6pih4 homo sapien
20	517	65.8	134	1	KV4C_HUMAN	P06314 homo sapien
21	498.5	63.4	133	1	KV4B_HUMAN	P06313 homo sapien
22	478	60.8	238	2	Q6GJS7	Q6gjs7 mus musculus
23	474	60.3	121	1	KV4O_HUMAN	P06312 homo sapien
24	474	60.3	241	2	Q632X4	Q632x4 mus musculus
25	470.5	59.9	219	2	Q652C0	Q652c0 mus musculus
26	457	58.1	109	1	KV4D_HUMAN	P83593 homo sapien
27	452	57.5	236	2	Q7TS98	Q7te98 mus musculus
28	448.5	57.1	243	2	Q6NTU5	Q6ntu5 xenopus lae
29	446	56.7	237	2	Q7S236	Q7s236 xenopus lae
30	415	52.8	255	2	Q6KB05	Q6kb05 mus musculus
31	391.5	49.8	129	1	KV3L_HUMAN	P18135 homo sapien

32	383.5	48.8	109	1	KV3B_HUMAN	P01620 homo sapien
33	382.5	48.7	109	1	KV3D_HUMAN	P01622 homo sapien
34	380.5	48.4	109	2	Q9UL78	Q9ul78 homo sapien
35	378.5	48.2	109	1	KV3E_HUMAN	P01623 homo sapien
36	378	48.1	108	2	Q9UL70	Q9ul70 homo sapien
37	376	47.8	108	1	KV1M_HUMAN	P01605 homo sapien
38	374	47.6	108	2	Q9UL79	Q9ul79 homo sapien
39	371.5	47.3	109	1	KV3G_HUMAN	P04206 homo sapien
40	371.5	47.3	129	1	KV3H_HUMAN	P04207 homo sapien
41	371.5	47.3	129	1	KV3M_HUMAN	P18136 homo sapien
42	370.5	47.1	109	1	KV3F_HUMAN	P01624 homo sapien
43	368	46.8	99	2	Q9JL74	Q9jl74 mus musculus
44	366	46.6	149	1	KV5A_MOUSE	P01633 mus musculus
45	363.5	46.2	117	1	KV2E_HUMAN	P06309 homo sapien

ALIGNMENTS

RESULT 1

Q6PIT5 PRELIMINARY; PRT; 236 AA.

AC Q6PIT5; DT 05-JUL-2004 (Tremblrel. 27, Created)

DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)

DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RX MEDLINE=23188257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schestz T.E., Brownstein M.J., Usdin T.B., Toehiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters K.G., Abramson R.D., Mullahy S.J., Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.A.;

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Jones S.J., Marra M.A.;

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smalius D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung;

RA Strausberg R.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC029444; AAH29444.1; -

DR HSSP; P01607; 1AR2.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; C1-set; 1.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; IGv; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FE8E351 CRC64;
Query Match 71.0%; Score 558; DB 2; Length 236;
Best Local Similarity 75.3%; Pred. No. 6.3e-48;
Matches 110; Conservative 10; Mismatches 20; Indels 6; Gaps 1;
Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQKPPKLLIYWASTRESGVPRDFG 61
Db 32 SLASVGERVITTCRASQI-----SSALAWYQKQKPPKLLIYDASTWESGVPRDFG 85
Qy 62 GSGSGTDTLTITISLQAEADVAVYCCQYYSPTFGQGTKEIKRTVAAPSVFIPPPSDE 121
Db 86 GSGSGTDTLTITISLQAEADVAVYCCQYYSPTFGQGTKEIKRTVAAPSVFIPPPSDE 145
Qy 122 QLKSGTASVCLNNFYPREAKEHQK 147
Db 146 QLKSGTASVCLNNFYPREAKEVQWK 171
RESULT 2
Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; --
DR HSSP; P01837; 1KB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188D4DDB8B781EC4 CRC64;
Query Match 71.0%; Score 558; DB 2; Length 240;
Best Local Similarity 75.5%; Pred. No. 6.4e-48;
Matches 111; Conservative 11; Mismatches 23; Indels 2; Gaps 2;
Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQKPPKLLIYWASTRESGVPRDFG 61
Db 30 SLSTVPGEPASISCRSSQSLHS-NGNYFDWYLYQKFGSQPLLIIYGSNRSAGVPRDFG 88
Qy 62 GSGSGTDTLTITISLQAEADVAVYCCQYYSPTFGQGTKEIKRTVAAPSVFIPPPSD 120
Db 89 GSGSGTDTLTISRVEADVGVYCCQALQTPPTFGQGTKEIKRTVAAPSVFIPPPSD 148
Qy 121 EQLKSGTASVCLNNFYPREAKEHQK 147
Db 149 EQLKSGTASVCLNNFYPREAKEVQWK 175
RESULT 3
Q8NEKO PRELIMINARY; PRT; 239 AA.
AC Q8NEKO;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030814; AAH30814.1; --
DR PIR; S23638; S23638.
DR PIR; S34091; S34091.
DR PIR; S40342; S40342.
DR PIR; S40357; S40357.
DR HSSP; P01834; 1I7Z.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552C0A CRC64;

Query Match 70.9%; Score 557.5; DB 2; Length 239;
Best Local Similarity 75.3%; Pred. No. 7.2e-48;
Matches 110; Conservative 12; Mismatches 23; Indels 1; Gaps 1;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKYNLAWYQKQPGPKLLIYWASTRESSGVDPDRFG 61
DQ 30 SLPTVTPGEPASISCHSSQSLHLS-DGYNLYDWLQKPGSQQLLIYLSNRSASGVDPDRFS 88
QY 62 GSGSGTDTFTLTISSLOAEDVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSFIIPPPSDE 121
DQ 89 GSGSGTDTFTLTKISKEAEDVGIIYCMQGLQTPQTFTGQGTKEIKRTVAAPSFIIPPPSDE 148
QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
DQ 149 QKSGTASVVCLLNNFYPREAKVQWK 174

RESULT 4
Q6GMV9 PRELIMINARY; PRT; 235 AA.
AC Q6GMV9;
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGV; 1.
DR PROSITE; PS00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 70.8%; Score 556.5; DB 2; Length 235;
Best Local Similarity 73.3%; Pred. No. 8.9e-48;
Matches 107; Conservative 17; Mismatches 17; Indels 5; Gaps 1;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKYNLAWYQKQPGPKLLIYWASTRESSGVDPDRFG 61
DQ 30 TSLSPGFRALUSCRASQSV-----NSKYLAWYQKQPGAPRLMLYASIRATGIPDRFS 84
QY 62 GSGSGTDTFTLTISSLOAEDVAVYCOQYYSPTPTFGQGTKEIKRTVAAPSFIIPPPSDE 121
DQ 85 GSGSGTDTFTLISRLESEDFALYFCQYGTGTPFTGSGTKEIKRTVAAPSFIIPPPSDE 144
QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
DQ 145 QKSGTASVVCLLNNFYPREAKVQWK 170

RESULT 5
Q7Z473 PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
DR HSSP; F01834; 1HEZ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.c1.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
```

[illegible]

DR SMART; SMO0407; IGC1; 1.
 DR SMART; SMO0406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 2.
 DR PROSITE; PS0290; IG MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25751 MW; 5BFE6A087AFAC437 CRC64;

Query Match 69.3%; Score 545; DB 2; Length 236;
 Best Local Similarity 74.0%; Pred. NO. 1.3e-46;
 Matches 108; Conservative 10; Mismatches 22; Indels 6; Gaps 1

QY 2 SLAVSLGERATINCKSSQSOLVSYFNKNKYLAWYOQQKPQGPPKKLLIYWASTRESGVPDREG 61
 :|::|||::|::|:
 Db 32 SLSASVGDRVITTCRASGGI-----SNDLGWYQQPKGPAPKAPKLLIYAASSLGSQGPSRFS 85
 ||:|||::|::|:
 QY 62 GSGSGTDFTLTISSIQAEDVAIVYYCQQYSYPTRTEGQTKEIKRTVAAPSFIPIPPSPDE 121
 |::::|::|::|:
 Db 86 GSGSGTDFTLTISSLOPEDFATICYLDNYNPWTFGTGKTVEIKRTVAAPSFIPIPPSPDE 145
 |||||||::|::|:
 QY 122 QLKSGTASVVCLLNPFYPREAKEHQK 147
 |||||||
 Db 146 QLKSGTASVVCLLNPNFYPREAKVQWK 171
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RESULT 8

Q6PIH7 ID O6PIH7 PRELIMINARY; PRT; 236 AA.

AC AC O6PIH7;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUN-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DE DE Hypothesical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OM Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

RN SEQUENCE FROM N.A.

RC TISSUE=Lung;
 RP MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Klausner R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuler G.D.,
 RA Straussberg R.L., Collins F.S., Wagner L., Shermen C.M., Schuler K.K.,
 RA Altschul S.F., Zeeberg B., Buotow K.H., Schaefer C.-F., Bhattacharya N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshikiyuki S., Carrincci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Petersen G.J., Abramson R.D., Mullighan S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliyil S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
 RA Krzywicki M.I., Skalska U., Smalls D.E., Schmerer A., Schein J.E.,
 RA Jones S.J., Marra W.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RE and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]

RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RA Straussberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
 RM EMBL; BC034141; AAA34141.1; -.
 RS HSHP; P01607; IAR2.
 DR InterPro; IPRO03599; Ig.
 DR InterPro; IPRO07110; Ig-like.
 DR InterPro; IPRO03597; Ig.c1.
 DR InterPro; IPRO03006; IgMHC.
 DR InterPro; IPRO03596; Ig.v.
 DR Pfam; PF07654; CI-set; I.


```
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_..._KW
SQ SEQUENCE 236 AA; 25702 MW; 7BFE4ED23084BC6 CRC64;

Query Match      69.8%; Score 541; DB 2; Length 236;
Best Local Similarity 72.6%; pred. No. 3.3e-46;
Matches 106; Conservative 12; Mismatches 22; Indels 6; Gaps 1

Qy    2 SLAVSLGERATINCKSSQSVLVYFNKNYLAWYQQKPGPPKLLIYWASTRESGVDPDRFG 61
      |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    32 SLGASVGDTVTITCRASQDI-----SNYLAWFOOKPGKAPKSLIYGASSLQSGVQSKFS 85
      |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy    62 GSGSGTDFTLTISSLQADENVAVYYCQOYSPYTPRTFGQGTVKEIKETVAAPSVFIFPPPSDE 121
      |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db    86 GSGSGTDFTLTISSLQPEDFATYYCQYKSYPTVTFGGTKLEIKETVAAPSVFIFPPSDE 145
      |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Qy   122 QLKSGTASVCLLNNTFYPREAKEHQK 147
      |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db   146 QLKSGTASVCLLNNTFYPREAKQWK 171
      |||::||::||::||::||::||::||::||::||::||::||::||::||::||::||
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RESULT 13	
Q6P5S8	
ID	Q6P5S8
AC	PRELIMINARY; PRT; 236 AA.
Q6P5S8;	
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	03-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
DE	Homo sapiens (Human).
OS	Homo sapiens
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
PN	[1]

RC TTSUUE=Glandular pool- thyroid;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2].
RP SEQUENCE FROM N.A.
RC TTSUUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -;
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig MHC.

DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSP; P01834; I172.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3AB03871D CRC64;

Query Match 68.0%; Score 534.5; DB 2; Length 239;
Best Local Similarity 71.2%; Pred. No. 1.5e-45;
Matches 104; Conservative 17; Mismatches 24; Indels 1; Gaps 1;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNVLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61
DB 30 SLPVTIGQPASISCRSTOSLVYSDGN-TYLNWFQQRPGQSPRLIYKVSNRD SGVDPDRFS 88
QY 62 GSGSGTDFTLTISSLQAEADVAVYCOQYVSTPTFTGGTKVEIKRTVAAPS VFIPPPSDE 121
DB 89 GSGSGTDFTLKLTIRVEADVGVFCWQGTHTPESTFGQGTKEIKRTVAAPS VFIPPPSDE 148
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147
DB 149 QLKSGTASVVCLLNNFYPREAKVQWK 174

Search completed: March 8, 2005, 06:35:49
Job time : 56.644 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 69.0805 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-28

Perfect score: 786

Sequence: 1 HSLAVSLGERATINCKSSQS.....VCLLNFFPREAKHOKSP 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	786	100.0	149	2	AAY34311 IgM antib
2	735	93.5	147	2	AAY34314 IgM antib
3	729	92.7	211	5	Abp43134 Human ova
4	715	91.0	179	8	ADK52434 Human ant
5	709	90.2	240	4	Aau00815 Human Imm
6	708	90.1	163	8	ADK52394 Human ant
7	707	89.9	220	8	ADK52314 Human ant
8	706	89.8	159	8	ADK52406 Human ant
9	703	89.4	173	8	ADK52430 Human ant
10	703	89.4	220	8	ADK52386 Human ant
11	702	89.3	171	8	ADK52422 Human ant
12	702	89.3	220	8	ADK52334 Human ant
13	701	89.2	159	8	ADK52382 Human ant
14	701	89.2	163	8	ADK52310 Human ant
15	699	88.9	154	8	ADK52342 Human ant
16	698	88.8	220	8	ADK52362 Human ant
17	696	88.5	163	8	ADK52346 Human ant
18	696	88.5	163	8	ADK52306 Human ant
19	696	88.5	163	8	ADK52326 Human ant
20	696	88.5	173	8	ADK52438 Human ant
21	695	88.4	149	8	ADK52402 Human ant
22	694	88.3	159	8	ADK52302 Human ant
23	694	88.3	264	5	Abp43142 Human ova
24	693	88.2	158	8	ADK52378 Human ant
25	693	88.2	240	2	AAY50161 Human res

ALIGNMENTS

RESULT 1

AAY34311

ID AAY34311 standard; protein; 149 AA.

AC AAY34311;

XX DT 19-NOV-1999 (first entry)

XX DE IGM antibody CEM 10.12 F3 kappa chain sequence.

XX KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;

XX KW activated B-cell; monocytic; graft versus host disease; therapy; cancer;

XX KW organ transplant rejection disease; lymphoma; pancreatic disease;

XX KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX FN WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX DR WPI; 1999-540816/45.

XX DR N-PSDB; AAZ20412.

XX PT New monoclonal antibody, used for treating e.g. graft versus host

XX PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 61; Fig 26; 245pp; English.

XX CC This sequence represents the kappa chain of an antibody of the invention.

XX CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes

XX CC complement and a variable region that binds to the epitope on CD147 Mab

XX CC by the IGM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab

XX CC can selectively kill activated T-cells, activated B-cells or treating or

XX CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft

XX CC versus host disease (GVHD), organ transplant rejection diseases (e.g.

XX CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
SQ Sequence 149 AA;
Query Match 100.0%; Score 786; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 5.2e-56;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HSLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRF 60
DB 1 HSLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRF 60
QY 61 GSGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQTKVEIKRTVAAPSVFIFFPSD 120
DB 61 GSGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQTKVEIKRTVAAPSVFIFFPSD 120
QY 121 EQLKSGTASVVCLLNNFYPREAKEHQSP 149
DB 121 EQLKSGTASVVCLLNNFYPREAKEHQSP 149
RESULT 2
AAY34314
ID AAY34314 standard; protein; 147 AA.
XX AC AAY34314;
XX DT 19-NOV-1999 (first entry)
XX DE IgM antibody CEM 13.5 kappa chain sequence.
XX KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX OS Homo sapiens.
XX PN WO9945031-A2.
XX PD 10-SEP-1999.
XX PF 03-MAR-1999; 99WO-US004583.
XX PR 03-MAR-1998; 98US-00034607.
XX PR 03-FEB-1999; 99US-00244253.
XX PA (ABGE-) ABGENIX INC.
XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX DR WPI; 1999-540816/45.
XX DR N-PSDB; AA220415.
XX PT New monoclonal antibody, used for treating e.g. graft versus host
XX PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX PS Claim 61; Fig 29; 245pp; English.
XX This sequence represents the kappa chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBLI. The Mab
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

SQ Sequence 147 AA;
Query Match 93.5%; Score 735; DB 2; Length 147;
Best Local Similarity 97.2%; Pred. No. 6.9e-52;
Matches 141; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 62
DB 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 60
QY 63 SSGSTDFTLTISLQAEADVAVYCCQYYSPTPTFGQTKVEIKRTVAAPSVFIFFPSDEQ 122
DB 61 SSGSTDFTLTISLQAEADVAVYCCQYYSPTPTFGQTKVEIKRTVAAPSVFIFFPSDEQ 120
QY 123 LKSGTASVVCLLNNFYPREAKEHQK 147
DB 121 LKSGTASVVCLLNNFYPREAKVQWK 145
RESULT 3
ABP43134
ID ABP43134 standard; protein; 211 AA.
XX AC ABP43134;
XX DT 22-AUG-2002 (first entry)
XX DE Human ovarian antigen HVVBK13, SEQ ID NO:4266.
XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive.
XX OS Homo sapiens.
XX PN WO200200677-A1.
XX PD 03-JAN-2002.
XX PF 07-JUN-2001; 2001WO-US018569.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Birse CE, Rosen CA;
XX DR WPI; 2002-147878/19.
XX DR N-PSDB; ABQ56211.
XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX PT cancer), immune disorders, cardiovascular disorders and neurological
XX PT diseases.
XX PS Claim 11; SEQ ID NO 4266; 2922pp; English.
XX This invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and

CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g., congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 211 AA;

Query Match 92.7%; Score 729; DB 5; Length 211;
 Best Local Similarity 95.2%; Pred. No. 3e-51; 4; Indels 0; Gaps 0;
 Matches 139; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLSPFNKNVLAQYQKPGQPKLLIYWASTREGVDPDRFG 61
 DB 34 SLAVSLGERATINCKSSQSVLSPFNKNVLAQYQKPGQPKLLIYWASTREGVDPDRVG 93
 QY 62 GSGSGTDFLTITSSLAQEDVAVYQCYQYSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
 DB 94 GSGSGTDFLTITSSLAQEDVAVYQCYQYSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 153
 QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
 DB 154 QKSGTASVVCLLNNFYPREAKEHOK 179

RESULT 4
 ADK52434
 ID ADK52434 standard; protein; 179 AA.
 XX
 AC ADK52434;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human anti-MCP-1 variable region light chain #35.
 XX
 KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
 KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
 KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;
 KW anti-MCP-1; heavy chain; light chain.
 XX
 OS Homo sapiens.
 PN WO2004016769-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 19-AUG-2003; 2003WO-US026232.
 XX
 PR 19-AUG-2002; 2002US-0404802P.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
 PI Bhakta S;
 XX
 DR WPI: 2004-203794/19.
 DR N-PSDB; ADK52433.

XX New human monoclonal antibody that binds to monocyte chemo-attractant
 PT protein-1 and is immobilized on an insoluble matrix, useful for
 PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
 PT rheumatoid arthritis or psoriasis.
 PS Claim 2; SEQ ID NO 140; 154pp; English.
 XX
 CC The present invention relates to a human monoclonal antibody that binds
 CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
 CC for the preparation of a medicament useful for treating neoplastic or
 CC inflammatory conditions. The neoplastic disease is selected from breast
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer or prostate cancer. The inflammatory condition is
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
 CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
 CC antibodies are also useful for diagnosing the above diseases. It is also
 CC useful for the determining the level of MCP-1 and MCP-1 family members in
 CC patient samples. The present sequence represents a human anti-MCP-1
 CC variable region light chain sequence.
 XX
 SQ Sequence 179 AA;

Query Match 91.0%; Score 715; DB 8; Length 179;
 Best Local Similarity 93.8%; Pred. No. 3.5e-50;
 Matches 137; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLSPFNKNVLAQYQKPGQPKLLIYWASTREGVDPDRFG 61
 DB 26 SLAVSLGERATINCKSSQSVLSPFNKNVLAQYQKPGQPKLLIYWASTREGVDPDRFS 85
 QY 62 GSGSGTDFLTITSSLAQEDVAVYQCYQYSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
 DB 86 GSGSGTDFLTITSSLAQEDVAVYQCYQYSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 145
 QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
 DB 146 QKSGTASVVCLLNNFYPREAKEHOK 171

RESULT 5
 AAU00815
 ID AAU00815 standard; protein; 240 AA.
 XX
 AC AAU00815;
 XX
 DT 01-JUN-2001 (first entry)
 XX
 DE Human Immunoglobulin superfamily, IgsF, protein #1.
 XX
 KW Human; Immunoglobulin superfamily protein; IgsF; Immune response;
 KW inflammatory response; cell-cell interaction; cell-surface recognition;
 KW neural disorder; immune system disorder; muscular disorder;
 KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
 KW cardiovascular disorder; renal disorder; proliferative disorder; cancer;
 KW common variable deficiency syndrome; AIDS; SCID;
 KW acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis;
 KW Alzheimer's disease; Crohn's disease; liver cancer; leukaemia;
 KW Hodgkin's lymphoma; Parkinson's disease; Huntington's disease;
 KW arteriosclerosis; stroke; diabetes mellitus; Addison's disease;
 KW urticaria; severe combined immunodeficiency; antibody.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Region 52..58 /label= Immunogenic_epitope
 FT Region 63..70 /label= Immunogenic_epitope
 FT Region 79..90 /label= Immunogenic_epitope
 FT Region 118..126 /label= Immunogenic_epitope

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FT Region /label= Immunogenic_epitope
FT 146..154
FT /label= Immunogenic_epitope
FT Domain 160..240
FT /label= Immunoglobulin_like_domain
FT Region 183..199
FT /label= Immunogenic_epitope
FT Region 209..215
FT /label= Immunogenic_epitope
FT Region 233..240
FT /label= Immunogenic_epitope
XX
XX WO200118176-A1.
XX
XX 15-MAR-2001.
XX
XX 29-AUG-2000; 2000WO-US023662.
XX
XX 03-SEP-1999; 99US-0152248P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX (NIJ/) NI J.
XX
XX Young PE, Ruben SM, Shi Y;
XX
XX WPI; 2001-203084/20.
XX
XX N-PSDB; AAS00145.
XX
XX Isolated nucleic acid molecule encoding a human secreted protein is used
XX in preventing, treating or ameliorating a medical condition.
XX
XX Claim 11; Page 237; 247pp; English.
XX
XX The sequence is a Human Immunoglobulin superfamily, IgSF, protein, a
XX diverse family of proteins involved in cell-cell interactions, cell-
XX surface recognition, intercellular communication and immune and
XX inflammatory responses. Polypeptides and antibodies directed to
XX polypeptides of the present invention are useful to provide immunological
XX probes for differential identification of tissues. Antibodies can be used
XX to assay levels of polypeptides encoded by polynucleotides of the
XX invention. Polypeptides of the present invention can be used to treat or
XX prevent diseases or conditions such as neural disorders, immune system
XX disorders, muscular disorders, reproductive disorders, gastrointestinal
XX disorders, pulmonary disorders, cardiovascular disorders, renal
XX disorders, proliferative disorders, and/or cancerous diseases and
XX conditions. Polynucleotides of the invention are also useful in treating
XX the above disorders. Examples of the disorders include common variable
XX adhesion deficiency syndrome, acquired immunodeficiency syndrome (AIDS),
XX anaemia, rheumatoid arthritis, Alzheimer's disease, Crohn's disease,
XX liver cancer, leukaemia, Hodgkin's lymphoma, Parkinson's disease,
XX Huntington's disease, dementia, arterosclerosis, stroke, diabetes
XX mellitus, Addison's disease, urticaria, severe combined immunodeficiency
XX (SCID). Many more examples of diseases and disorders are given in the
XX specification
XX
XX SQ Sequence 240 AA;
XX
XX Query Match 90.2%; Score 709; DB 4; Length 240;
XX Best Local Similarity 93.2%; Pred. No. 1.4e-49;
XX Matches 136; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61
XX Db 30 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFS 89
XX
XX QY 62 GSGSGTDFTLTISSLQAEDVAVYCCQYYSYTPRTFGQTKVEIKRTVAAPSVFIPPPSDE 121
XX Db 90 GSGSGTDFTLTISSLQAEDVAVYCCQYYSYTPSYSPGQTKLEIKRTVAAPSVFIPPPSDE 149
XX
XX QY 122 QKSGTASVWCLNNFYPREAKEHOK 147
XX Db 150 QKSGTASVWCLNNFYPREAKVQWK 175
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RESULT 6
ADK52394
ID ADK52394 standard; protein; 163 AA.
XX
XX AC ADK52394;
XX
XX 20-MAY-2004 (first entry)
XX
XX Human anti-MCP-1 variable region light chain #25.
XX
XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
XX Antirheumatic; Nephrotropic; Antiartherosclerotic; Antiporiatic;
XX Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
XX inflammatory condition; cancer; arthritis; multiple sclerosis;
XX anti-MCP-1; heavy chain; light chain.
XX
XX Homo sapiens.
XX
XX WO2004016769-A2.
XX
XX 26-FEB-2004.
XX
XX 19-AUG-2003; 2003WO-US026232.
XX
XX 19-AUG-2002; 2002US-0404802P.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
XX Bhakta S;
XX
XX WPI; 2004-203794/19.
XX
XX N-PSDB; ADK52393.
XX
XX New human monoclonal antibody that binds to monocyte chemo-attractant
XX protein-1 and is immobilized on an insoluble matrix, useful for
XX diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
XX rheumatoid arthritis or psoriasis.
XX
XX Claim 2; SEQ ID NO 100; 154pp; English.
XX
XX The present invention relates to a human monoclonal antibody that binds
XX to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
XX for the preparation of a medicament useful for treating neoplastic or
XX inflammatory conditions. The neoplastic disease is selected from breast
XX cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
XX stomach cancer, endometrial cancer, kidney cancer, colon cancer,
XX pancreatic cancer or prostate cancer. The inflammatory condition is
XX selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
XX psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
XX antibodies are also useful for diagnosing the above diseases. It is also
XX useful for the determining the level of MCP-1 and MCP-1 family members in
XX patient samples. The present sequence represents a human anti-MCP-1
XX variable region light chain sequence.
XX
XX SQ Sequence 163 AA;
XX
XX Query Match 90.1%; Score 708; DB 8; Length 163;
XX Best Local Similarity 93.2%; Pred. No. 1.2e-49;
XX Matches 136; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
XX
XX QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61
XX Db 10 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFS 69
XX
XX QY 62 GSGSGTDFTLTISSLQAEDVAVYCCQYYSYTPRTFGQTKVEIKRTVAAPSVFIPPPSDE 121
XX Db 70 GSGSGTDFTLTISSLQAEDVAVYCCQYYSYTPWTFGQTKVEIKRTVAAPSVFIPPPSDE 129
XX
XX QY 122 QKSGTASVWCLNNFYPREAKEHOK 147
XX Db 130 QKSGTASVWCLNNFYPREAKVQWK 155
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RESULT 7

ADK52314
ID ADK52314 standard; protein; 220 AA.
XX AC ADK52314;
XX DT 20-MAY-2004 (first entry)
XX DE Human anti-MCP-1 variable region light chain #5.
XX KW monocytic chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX OS Homo sapiens.
XX PN WO2004016769-A2.
XX PD 26-FEB-2004.
XX PF 19-AUG-2003; 2003WO-US026232.
XX PR 19-AUG-2002; 2002US-0404802P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX DR WPI; 2004-203794/19.
XX DR N-PSDB; ADK52313.
XX PT New human monoclonal antibody that binds to monocytic chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX PS Claim 2; SEQ ID NO 20; 154pp; English.
XX CC The present invention relates to a human monoclonal antibody that binds
CC to monocytic chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX SQ Sequence 220 AA;

Query Match 89.9%; Score 707; DB 8; Length 220;
Best Local Similarity 93.8%; Pred. No. 1.9e-49;
Matches 137; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESSGVDPDRFG 61
DB 10 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESSGVDPDRFS 69
QY 62 GSGSGTDFLTITSSLAQEDVAVYQCYYSYTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
DB 70 GSGSGTDFLTITSSLAQEDVAVYQCYYSYTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 129
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147

Db 130 QLKSGTASVVCLLNNFYPREAKEHOK 155

RESULT 8

ADK52406
ID ADK52406 standard; protein; 159 AA.
XX AC ADK52406;
XX DT 20-MAY-2004 (first entry)
XX DE Human anti-MCP-1 variable region light chain #28.
XX KW monocytic chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX OS Homo sapiens.
XX PN WO2004016769-A2.
XX PD 26-FEB-2004.
XX PF 19-AUG-2003; 2003WO-US026232.
XX PR 19-AUG-2002; 2002US-0404802P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX DR WPI; 2004-203794/19.
XX DR N-PSDB; ADK52405.
XX PT New human monoclonal antibody that binds to monocytic chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX PS Claim 2; SEQ ID NO 112; 154pp; English.
XX CC The present invention relates to a human monoclonal antibody that binds
CC to monocytic chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX SQ Sequence 159 AA;

Query Match 89.8%; Score 706; DB 8; Length 159;
Best Local Similarity 93.8%; Pred. No. 1.7e-49;
Matches 137; Conservative 1; Mismatches 8; Indels 0; Gaps 0;
QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESSGVDPDRFG 61
DB 10 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESSGVDPDRFS 69
QY 62 GSGSGTDFLTITSSLAQEDVAVYQCYYSYTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
DB 70 GSGSGTDFLTITSSLAQEDVAVYQCYYSYTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 129
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147

Db 130 QKSGTASVCLNNFYPREAKVQWK 155
|||||

RESULT 9
ADK52430
ID ADK52430 standard; protein; 173 AA.

AC ADK52430;

DT 20-MAY-2004 (first entry)

DE Human anti-MCP-1 variable region light chain #34.

KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antiporiatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; Neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.

OS Homo sapiens.

XX WO2004016769-A2.

XX 26-FEB-2004.

XX 19-AUG-2003; 2003WO-US026232.

XX 19-AUG-2002; 2002US-0404802P.

XX (ABGE-) ABGENIX INC.

PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;

DR WPI; 2004-203794/19.

DR N-PSDB; ADK52429.

XX New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.

XX Claim 2; SEQ ID NO 136; 154pp; English.

XX The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.

XX Sequence 173 AA;

Query Match 89.4%; Score 703; DB 8; Length 173;
Best Local Similarity 92.5%; Pred. No. 3.2e-49;
Matches 135; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPCKLLIYWASTRESGVDPDRFG 61

Db 25 SLAVSLGERAAINCKSSQTVLYSSNNKNYLVWYQKQGPCKLLIYWASTRESGVDPDRFS 84

QY 62 GSGSGTDFTLTSSLOAEDVAVYCOQYVSPRTFGQTKVEIKRTVAAPSVFIIPPSDE 121

Db 85 GSGSGTDFTLTSSLOAEDVAVYCOQYKSPWTFGQTKVEIKRTVAAPSVFIIPPSDE 144

QY 122 QKSGTASVCLNNFYPREAKEHQK 147
|||||
Db 145 QKSGTASVCLNNFYPREAKVQWK 170

RESULT 10

ADK52386

ID ADK52386 standard; protein; 220 AA.

XX ADK52386;

XX 20-MAY-2004 (first entry)

DE Human anti-MCP-1 variable region light chain #23.

XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antiporiatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; Neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.

OS Homo sapiens.

XX WO2004016769-A2.

XX 26-FEB-2004.

XX 19-AUG-2003; 2003WO-US026232.

XX 19-AUG-2002; 2002US-0404802P.

XX (ABGE-) ABGENIX INC.

PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;

DR WPI; 2004-203794/19.

DR N-PSDB; ADK52385.

XX New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.

XX Claim 2; SEQ ID NO 92; 154pp; English.

XX The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.

XX Sequence 220 AA;

Query Match 89.4%; Score 703; DB 8; Length 220;
Best Local Similarity 92.5%; Pred. No. 4e-49;
Matches 135; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQGPCKLLIYWASTRESGVDPDRFG 61

Db 10 SLAVSLGERATINCKSSQSVLYSSNNKNYLVWYQKQGPCKLLIYWASTRESGVDPDRFS 69

QY 62 GSGSGTDFTLTSSLOAEDVAVYCOQYVSPRTFGQTKVEIKRTVAAPSVFIIPPSDE 121

Db 70 GSGSGTDFTLTSSLOAEDVAVYCOQYVSPWTFGQTKVEIKRTVAAPSVFIIPPSDE 129

QY 122 QKSGTASVCLNNFYPREAKEHOK 147
 DB 130 QKSGTASVCLNNFYPREAKVQWK 155
 RESULT 11
 ADK52422
 ID ADK52422 standard; protein; 171 AA.
 XX AC ADK52422;
 XX DT 20-MAY-2004 (first entry)
 XX DE Human anti-MCP-1 variable region light chain #32.
 XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
 KW Antiheumatic; Nephrotropic; Antiartherosclerotic; Antiporiatic;
 KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;
 KW anti-MCP-1; heavy chain; light chain.
 XX OS Homo sapiens.
 XX PN WO2004016769-A2.
 XX PD 26-FEB-2004.
 XX PF 19-AUG-2003; 2003WO-US026232.
 XX PR 19-AUG-2002; 2002US-0404802P.
 XX PA (ABGE-) ABGENIX INC.
 XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
 XX PI Bhakta S;
 XX DR WPI; 2004-203794/19.
 XX DR N-PSDB; ADK52421.
 XX PT New human monoclonal antibody that binds to monocyte chemo-attractant
 PT protein-1 and is immobilized on an insoluble matrix, useful for
 PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
 PT rheumatoid arthritis or psoriasis.
 XX PS Claim 2; SEQ ID NO 128; 154pp; English.
 CC The present invention relates to a human monoclonal antibody that binds
 CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
 CC for the preparation of a medicament useful for treating neoplastic or
 CC inflammatory conditions. The neoplastic disease is selected from breast
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer or prostate cancer. The inflammatory condition is
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
 CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
 CC antibodies are also useful for diagnosing the above diseases. It is also
 CC useful for the determining the level of MCP-1 and MCP-1 family members in
 CC patient samples. The present sequence represents a human anti-MCP-1
 CC variable region light chain sequence.
 XX SQ Sequence 171 AA;
 Query Match 89.3%; Score 702; DB 8; Length 171;
 Best Local Similarity 91.8%; Pred. No. 3.8e-49;
 Matches 134; Conservative 4; Mismatches 8; Indels 0; Gaps 0;
 QY 2 SLAVSLGERATINCKSSQVLYSFNNKNLYAWYQKPGPPKLLIYWASTRESGVDPFRG 61
 DB 24 SLAVSLGERATINCKSSQVLYSSNNKNLYVYQKPGPPKLLIYWASTRESGVDPFRS 83
 QY 62 GSGSGTDFLTITSSLOAEDVAVYQCYQYVSTPRFTGQGTKEIKRTVAAPSVFIIPPSDE 121
 DB 84 GSGSGTDFLTITSSLOAEDVAVYQCYQYVSTPRFTGQGTKEIKRTVAAPSVFIIPPSDE 147
 QY 122 QKSGTASVCLNNFYPREAKEHOK 147
 DB 144 QKSGTASVCLNNFYPREAKVQWK 169
 RESULT 12
 ADK52334
 ID ADK52334 standard; protein; 220 AA.
 XX AC ADK52334;
 XX DT 20-MAY-2004 (first entry)
 XX DE Human anti-MCP-1 variable region light chain #10.
 XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
 KW Antihematic; Nephrotropic; Antiartherosclerotic; Antiporiatic;
 KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;
 KW anti-MCP-1; heavy chain; light chain.
 XX OS Homo sapiens.
 XX PN WO2004016769-A2.
 XX PD 26-FEB-2004.
 XX PF 19-AUG-2003; 2003WO-US026232.
 XX PR 19-AUG-2002; 2002US-0404802P.
 XX PA (ABGE-) ABGENIX INC.
 XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
 XX PI Bhakta S;
 XX DR WPI; 2004-203794/19.
 XX DR N-PSDB; ADK52333.
 XX PT New human monoclonal antibody that binds to monocyte chemo-attractant
 PT protein-1 and is immobilized on an insoluble matrix, useful for
 PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
 PT rheumatoid arthritis or psoriasis.
 XX PS Claim 2; SEQ ID NO 40; 154pp; English.
 CC The present invention relates to a human monoclonal antibody that binds
 CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
 CC for the preparation of a medicament useful for treating neoplastic or
 CC inflammatory conditions. The neoplastic disease is selected from breast
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer or prostate cancer. The inflammatory condition is
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
 CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
 CC antibodies are also useful for diagnosing the above diseases. It is also
 CC useful for the determining the level of MCP-1 and MCP-1 family members in
 CC patient samples. The present sequence represents a human anti-MCP-1
 CC variable region light chain sequence.
 XX SQ Sequence 220 AA;
 Query Match 89.3%; Score 702; DB 8; Length 220;
 Best Local Similarity 92.5%; Pred. No. 4.8e-49;
 Matches 135; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
 QY 2 SLAVSLGERATINCKSSQVLYSFNNKNLYAWYQKPGPPKLLIYWASTRESGVDPFRG 61
 DB 10 SLAVSLGERATINCKSSQVLYSSNNKNLYVYQKPGPPKLLIYWASTRESGVDPFRS 69
 QY 62 GSGSGTDFLTITSSLOAEDVAVYQCYQYVSTPRFTGQGTKEIKRTVAAPSVFIIPPSDE 121

Db 70 GSGGTDFTLTISLQAEADVAVYYCQYYSPTFTGQGTKEIKRTVAAPSVFIIPPSDE 129
QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
Db 130 QKSGTASVVCLLNNFYPREAKVQWK 155

RESULT 13
ADKS2382
ID ADK52382 standard; protein; 159 AA.
AC ADK52382;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #22.
XX
KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neoprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52381.
XX
New human monoclonal antibody that binds to monocyte chemo-attractant protein-1 and is immobilized on an insoluble matrix, useful for diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer, rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 88; 154pp; English.
XX
The present invention relates to a human monoclonal antibody that binds to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful for the preparation of a medicament useful for treating neoplastic or inflammatory conditions. The neoplastic disease is selected from breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, kidney cancer, colon cancer, pancreatic cancer or prostate cancer. The inflammatory condition is selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease or multiple sclerosis. The antibodies are also useful for diagnosing the above diseases. It is also useful for the determining the level of MCP-1 and MCP-1 family members in patient samples. The present sequence represents a human anti-MCP-1 variable region light chain sequence.
XX
SQ Sequence 159 AA;

Query Match 89.2%; Score 701; DB 8; Length 159;
Best Local Similarity 93.2%; Pred. No. 4.2e-49;
Matches 136; Conservative 1; Mismatches 9; Indels 0; Gaps 0;
QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRG 61
Db 10 SLAVSLGERATINCKSSQSVLYSFNNKNYLVWYQKPGQPPKLLIYWASTRESGVDPDRFS 69

QY 62 GSGGTDFTLTISLQAEADVAVYYCQYYSPTFTGQGTKEIKRTVAAPSVFIIPPSDE 121
Db 70 GSGGTDFTLTISLQAEADVAVYYCQYYSPTFTGQGTKEIKRTVAAPSVFIIPPSDE 129
QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
Db 130 QKSGTASVVCLLNNFYPREAKVQWK 155

RESULT 14
ADKS2310
ID ADK52310 standard; protein; 163 AA.
AC ADK52310;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #4.
XX
KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neoprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52309.
XX
New human monoclonal antibody that binds to monocyte chemo-attractant protein-1 and is immobilized on an insoluble matrix, useful for diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer, rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 16; 154pp; English.
XX
The present invention relates to a human monoclonal antibody that binds to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful for the preparation of a medicament useful for treating neoplastic or inflammatory conditions. The neoplastic disease is selected from breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma, stomach cancer, endometrial cancer, kidney cancer, colon cancer, pancreatic cancer or prostate cancer. The inflammatory condition is selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis, psoriasis, restenosis, autoimmune disease or multiple sclerosis. The antibodies are also useful for diagnosing the above diseases. It is also useful for the determining the level of MCP-1 and MCP-1 family members in patient samples. The present sequence represents a human anti-MCP-1 variable region light chain sequence.
XX
SQ Sequence 163 AA;

Query Match 89.2%; Score 701; DB 8; Length 163;
Best Local Similarity 92.5%; Pred. No. 4.3e-49;
Matches 135; Conservative 3; Mismatches 8; Indels 0; Gaps 0;
QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRG 61
Db 10 SLAVSLGERATINCKSSQSVLYSFNNKNFLVWYQKPGQPPKLLIYWASTRESGVDPDRFS 69

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 79.0704 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-28

Perfect score: 786

Sequence: 1 HSLAVSLGERATINCKSSQS.....VCLLNFFPREAKHQKSP 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	729	92.7	211	15	US-10-264-049-4266	Sequence 4266, Ap
2	709	90.2	240	9	US-09-799-514-8	Sequence 8, Appli
3	694	88.3	264	15	US-10-264-049-4274	Sequence 4274, Ap
4	693	88.2	240	9	US-09-301-593-36	Sequence 36, Appl
5	693	88.2	240	14	US-10-159-006-36	Sequence 36, Appl
6	668.5	85.1	165	15	US-10-364-743-26	Sequence 26, Appl
7	661	84.1	153	9	US-09-187-693-62	Sequence 62, Appl
8	660	84.0	240	16	US-10-630-406-8	Sequence 8, Appli
9	649.5	82.6	239	9	US-09-249-011A-22	Sequence 22, Appl
10	646	82.2	239	9	US-09-825-012-9	Sequence 9, Appli
11	646	82.2	242	10	US-09-819-266-26	Sequence 26, Appl
12	640	81.4	220	9	US-09-993-693-1	Sequence 1, Appli
13	640	81.4	220	14	US-10-232-408-1	Sequence 1, Appli

14	629	80.0	220	9	US-09-301-593-17	Sequence 17, Appl
15	629	80.0	220	14	US-10-159-006-17	Sequence 17, Appl
16	629	80.0	240	9	US-09-301-593-28	Sequence 28, Appl
17	629	80.0	240	14	US-10-159-006-28	Sequence 28, Appl
18	624	79.4	220	9	US-09-917-410-5	Sequence 5, Appli
19	617	78.5	218	15	US-10-449-566-102	Sequence 102, App
20	613	78.0	218	15	US-10-449-566-119	Sequence 119, App
21	610	77.6	218	14	US-10-171-452A-39	Sequence 39, Appl
22	610	77.6	218	14	US-10-171-452A-57	Sequence 57, Appl
23	610	77.6	218	15	US-10-353-708-39	Sequence 39, Appl
24	610	77.6	218	15	US-10-353-708-57	Sequence 57, Appl
25	610	77.6	218	16	US-10-731-984-4	Sequence 4, Appli
26	610	77.6	218	16	US-10-731-984-28	Sequence 28, Appl
27	610	77.6	238	14	US-10-171-452A-38	Sequence 38, Appl
28	610	77.6	238	14	US-10-171-452A-56	Sequence 56, Appl
29	610	77.6	238	15	US-10-353-708-38	Sequence 38, Appl
30	610	77.6	238	15	US-10-353-708-56	Sequence 56, Appl
31	610	77.6	238	16	US-10-731-984-3	Sequence 3, Appli
32	610	77.6	238	16	US-10-731-984-27	Sequence 27, Appl
33	609	77.5	218	15	US-10-449-566-98	Sequence 98, Appl
34	600	76.3	218	14	US-10-171-452A-45	Sequence 45, Appl
35	600	76.3	218	14	US-10-171-452A-51	Sequence 51, Appl
36	600	76.3	218	15	US-10-353-708-45	Sequence 45, Appl
37	600	76.3	218	15	US-10-353-708-51	Sequence 51, Appl
38	600	76.3	218	16	US-10-731-984-12	Sequence 12, Appl
39	600	76.3	218	16	US-10-731-984-20	Sequence 20, Appl
40	600	76.3	238	14	US-10-171-452A-44	Sequence 44, Appl
41	600	76.3	238	14	US-10-171-452A-50	Sequence 50, Appl
42	600	76.3	238	15	US-10-353-708-44	Sequence 44, Appl
43	600	76.3	238	15	US-10-353-708-50	Sequence 50, Appl
44	600	76.3	238	16	US-10-731-984-11	Sequence 11, Appl
45	600	76.3	238	16	US-10-731-984-19	Sequence 19, Appl

ALIGNMENTS

RESULT 1
US-10-264-049-4266
; Sequence 4266, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PAL33P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4266
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4266

Query Match 92.7%; Score 729; DB 15; Length 211;
Best Local Similarity 95.2%; Pred. No. 4e-49;
Matches 139; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKYLAWYQQPGPPKLLIYWASTRESGVPDRFG 61
Db 34 SLAVSLGERATINCKSSQSVLYSPDNKYLAWYQQPGHPKLLIYWASTRESGVPDRYG 93
Qy 62 GSGSGTDTLTISSLOAEDVAVYQQYVPTRTGGTQKVEIKETVAAPSFIIPPSDE 121
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; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match      88.2%; Score 693; DB 9; Length 240;
Best Local Similarity 91.8%; Pred. No. 2.8e-46;
Matches 134; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFG 61
Db 30 SLAVSLGERATINCKSSOSVLYSRNQKNYLAWYQKPGPPKLLIFWASTRESGVDPDRFS 89
QY 62 GSGGTDFTLTISLQAEADVAVYCOQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSDE 121
Db 90 GSGGTDFTLTISLQAEADVAVYCOQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSDE 149
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147
Db 150 QLKSGTASVVCLLNNFYPREAKEHOK 175

RESULT 5
US-10-159-006-36
; Sequence 36, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John B.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-36

Query Match      88.2%; Score 693; DB 14; Length 240;
Best Local Similarity 91.8%; Pred. No. 2.8e-46;
Matches 134; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFG 61
Db 30 SLAVSLGERATINCKSSOSVLYSRNQKNYLAWYQKPGPPKLLIFWASTRESGVDPDRFS 89
QY 62 GSGGTDFTLTISLQAEADVAVYCOQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSDE 121
Db 90 GSGGTDFTLTISLQAEADVAVYCOQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSDE 149
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147
Db 150 QLKSGTASVVCLLNNFYPREAKEHOK 175

RESULT 6
US-10-364-743-26
; Sequence 26, Application US/10364743
; Publication No. US20040009178A1

; GENERAL INFORMATION:
; APPLICANT: Bowditch, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 26
; LENGTH: 165
; TYPE: PRT
; ORGANISM: human
US-10-364-743-26

Query Match      85.1%; Score 668.5; DB 15; Length 165;
Best Local Similarity 88.4%; Pred. No. 1.6e-44;
Matches 129; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFG 61
Db 12 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFS 70
QY 62 GSGGTDFTLTISLQAEADVAVYCOQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSDE 121
Db 71 GSGGTDFTLTISLQAEADVAVYCOQYVSTPRTFGQGTKEIKRTVAAPSFIIPPSDE 130
QY 122 QLKSGTASVVCLLNNFYPREAKEHOK 147
Db 131 QLKSGTASVVCLLNNFYPREAKEHOK 156

RESULT 7
US-09-187-693-62
; Sequence 62, Application US/09187693
; Patent No. US20020173629A1
; GENERAL INFORMATION:
; APPLICANT: Jakobovits, Aya
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Gallo, Michael
; APPLICANT: Jia, Xiao-Chi
; TITLE OF INVENTION: Human Monoclonal Antibodies to Epidermal
; FILE REFERENCE: Cell 4.20 CIP2
; CURRENT APPLICATION NUMBER: US/09/187,693
; CURRENT FILING DATE: 1998-11-05
; PRIOR APPLICATION NUMBER: 09/162,280
; PRIOR FILING DATE: 1998-09-29
; PRIOR APPLICATION NUMBER: 08/851,362
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 153
; TYPE: PRT
; ORGANISM: human
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(153)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-187-693-62

Query Match      84.1%; Score 661; DB 9; Length 153;
Best Local Similarity 90.3%; Pred. No. 5.7e-44;
Matches 130; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDPDRFG 61
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Db 6 SLAVSLGERATINCKSSQSVLYSGKNQYLAWYQKQGPCKLLIYWASTRESGVDPDRF 65
Qy 62 GSGSGTDFLTLSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 66 GSGSGTDFLTLSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 125
Qy 122 QKSGTASVCLNNFY--PREAK 143
Db 126 QKSGTASVCLNNFYRKPRTRK 149

RESULT 8
US-10-630-406-8
; Sequence 8, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Ganguly, Subinay
; APPLICANT: Abraham, Ralph
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Rillema, Jill
; APPLICANT: Thorne, Barbara
; APPLICANT: Shuford, Walter W.
; APPLICANT: Mittler, Robert S.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: D0288 NP
; CURRENT APPLICATION NUMBER: US/10/630,406
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,646
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-630-406-8

Query Match 84.0%; Score 660; DB 16; Length 240;
Best Local Similarity 89.0%; Pred. No. 1e-43;
Matches 130; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKYLAWYQKQGPCKLLIYWASTRESGVDPDRFG 61
Db 30 SLAVSLGERATINCKSSQSVLYSGKNQYLAWYQKQGPCKLLIYASTRQSGVDPDRFS 89
Qy 62 GSGSGTDFLTLSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 90 GSGSGTDFLTLSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 149
Qy 122 QKSGTASVCLNNFYPREAKEHOK 147
Db 150 QKSGTASVCLNNFYPREAKVQWK 175

RESULT 9
US-09-249-011A-22
; Sequence 22, Application US/09249011A
; Patent No. US20020176855A1
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GERTTRUIDA M.

; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-00000
; CURRENT APPLICATION NUMBER: US/09/249,011A
; CURRENT FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-249-011A-22

Query Match 82.6%; Score 649.5; DB 9; Length 239;
Best Local Similarity 88.4%; Pred. No. 6.8e-43;
Matches 129; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKYLAWYQKQGPCKLLIYWASTRESGVDPDRFG 61
Db 30 SLAVSLGERATINCKSSQSVLYSGKNQYLAWYQKQGPCKLLIYWASTRESGVDPDRFS 89
Qy 62 GSGSGTDFLTLSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 90 GSGSGTDFLTLSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 148
Qy 122 QKSGTASVCLNNFYPREAKEHOK 147
Db 149 QKSGTASVCLNNFYPREAKVQWK 174

RESULT 10
US-09-825-012-9
; Sequence 9, Application US/09825012
; Patent No. US20020122798A1
; GENERAL INFORMATION:
; APPLICANT: Young, Robert
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: 43191-256808
; CURRENT APPLICATION NUMBER: US/09/825,012
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/237,159
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: GB 0008049.9
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 9
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised HMFG-1 light chain
US-09-825-012-9

Query Match 82.2%; Score 646; DB 9; Length 239;
Best Local Similarity 84.2%; Pred. No. 1.3e-42;
Matches 123; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKYLAWYQKQGPCKLLIYWASTRESGVDPDRFG 61
Db 29 SLSASVGDVRVTICKSSQSVLYSGKNQYLAWYQKQGPCKLLIYWASTRESGVPSRFS 88
Qy 62 GSGSGTDFLTLSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 121
Db 89 GSGSGTDFLTLSLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFI PPPSDE 148
Qy 122 QKSGTASVCLNNFYPREAKEHOK 147
Db 149 QKSGTASVCLNNFYPREAKVQWK 174

RESULT 11
US-09-819-266-26
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; Sequence 26, Application US/09819266
; Publication No. US20030017163A1
; GENERAL INFORMATION:
; APPLICANT: Antisoma Research limited
; TITLE OF INVENTION: Compounds for Targeting
; FILE REFERENCE: JG-EPC-4955/500563-20013
; CURRENT APPLICATION NUMBER: US/09/819,266
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/193,156
; PRIOR FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: SeqWin99
; SEQ ID NO 26
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HMG1 Fab/Caespase-3 fusion protein light chain
US-09-819-266-26

Query Match 82.2%; Score 646; DB 10; Length 242;
Best Local Similarity 84.2%; Pred. No. 1.3e-42;
Matches 123; Conservative 6; Mismatches 17; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 61
DB 32 SLASVGDVTTITCKSSQSLLYSSNQKIYLAWYQKPGKAPKLLIYWASTRESGVPSRFS 91
QY 62 GSGSGTDFTLTITSSLOAEDVAVYCCQYVSTPRFTGGTKVEIKRTVAAPSVFIFFPSDE 121
DB 92 GSGSGTDFTLTITSSLOPEDIATYVCCQYRYRPTFGGTKVEIKRTVAAPSVFIFFPSDE 151
QY 122 QLKSGTASVVCLLNNFYPREAKEHQK 147
DB 152 QLKSGTASVVCLLNNFYPREAKVQWK 177

RESULT 12
US-09-995-693-1
; Sequence 1, Application US/0995693
; Patent No. US20020136721A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,693
; FILING DATE: 29-No. US20020136721A1-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,235
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-5416
; TELEFAX: 650/952-9881

US-10-232-408-1
; Sequence 1, Application US/10232408
; Publication No. US20030118587A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; Tabor, Kelly H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/232,408
; FILING DATE: 03-Sep-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/669,971
; FILING DATE: 05-Jul-2001
; APPLICATION NUMBER: US/08/952,235
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-232-408-1

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Query Match 81.4%; Score 640; DB 14; Length 220;
Best Local Similarity 82.2%; Pred. No. 3.4e-42;
Matches 120; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFG 61
Db 10 SLTVSVGEKVTMSCKSSQSLLYTSQKNYLAWYQKQPSKLLIYWASTRESGVDPDRFT 69

Qy 62 GSGSGTDFTLTISLQAEADVAVYVCOQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDE 121
Db 70 GSGSGTDFTLTISVQAEADVAVYVCOQYVSTPRTFGGKLEIKRTVAAPSVFIPPPSDE 129

Qy 122 QKSGTASVCLNNFYPREAKEHOK 147
Db 130 QKSGTASVCLNNFYPREAKVQWK 155

RESULT 14
US-09-301-593-17
; Sequence 17, Application US/09301593A
; Publication No. US20020052480A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-17

Query Match 80.0%; Score 629; DB 9; Length 220;
Best Local Similarity 82.2%; Pred. No. 2.5e-41;
Matches 120; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFG 61
Db 10 SLAVSVGEKVTMSCKSSQSLLYSRNQKNYLAWFQKQSPKLLIFWASTRESGVDPDRFT 69

Qy 62 GSGSGTDFTLTISLQAEADVAVYVCOQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDE 121
Db 70 GSGGTFDNLTISVQAEADVAVYVCOQYVSTPRTFGAGTKLEKRTVAAPSVFIPPPSDE 129

Qy 122 QKSGTASVCLNNFYPREAKEHOK 147
Db 130 QKSGTASVCLNNFYPREAKVQWK 155

RESULT 15
US-10-159-006-17
; Sequence 17, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility

; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159.006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-17

Query Match 80.0%; Score 629; DB 14; Length 220;
Best Local Similarity 82.2%; Pred. No. 2.5e-41;
Matches 120; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDPDRFG 61
Db 10 SLAVSVGEKVTMSCKSSQSLLYSRNQKNYLAWFQKQSPKLLIFWASTRESGVDPDRFT 69

Qy 62 GSGSGTDFTLTISLQAEADVAVYVCOQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDE 121
Db 70 GSGGTFDNLTISVQAEADVAVYVCOQYVSTPRTFGAGTKLEKRTVAAPSVFIPPPSDE 129

Qy 122 QKSGTASVCLNNFYPREAKEHOK 147
Db 130 QKSGTASVCLNNFYPREAKVQWK 155

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Job time : 79.0704 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.3835 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-28

Perfect score: 786

Sequence: 1 HSLAVSLGERATINCKSSQS.....VVCLLNFFPREAKEHQSP 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PTCUTS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693	88.2	240	4	US-09-301-593-36
2	683.5	87.0	241	2	US-07-916-098A-56
3	649.5	82.6	239	4	US-09-627-898B-22
4	640	81.4	220	3	US-08-952-235-1
5	629	80.0	220	4	US-09-301-593-17
6	629	80.0	240	4	US-09-301-593-28
7	607	77.2	239	3	US-08-812-586-29
8	607	77.2	239	4	US-09-535-832A-30
9	581	73.9	120	1	US-08-026-320A-4
10	573	72.9	214	4	US-09-472-087-71
11	572	72.8	139	4	US-09-472-087-22
12	572	72.8	139	4	US-09-472-087-96
13	567.5	72.2	235	4	US-09-472-087-14
14	567.5	72.2	235	4	US-09-472-087-65
15	566.5	72.1	141	4	US-09-472-087-88
16	566	72.0	226	4	US-09-456-090A-74
17	566	72.0	226	4	US-09-453-234-74
18	565	71.9	226	4	US-09-456-090A-86
19	565	71.9	226	4	US-09-453-234-86
20	564	71.8	224	4	US-09-456-090A-82
21	564	71.8	224	4	US-09-456-090A-88
22	564	71.8	224	4	US-09-456-090A-90
23	564	71.8	224	4	US-09-453-234-82
24	564	71.8	224	4	US-09-453-234-88
25	564	71.8	224	4	US-09-453-234-90
26	564	71.8	224	4	US-09-453-234-90
27	564	71.8	226	4	US-09-456-090A-50

28	564	71.8	226	4	US-09-456-090A-80	Sequence 80, Appl
29	564	71.8	226	4	US-09-453-234-50	Sequence 50, Appl
30	564	71.8	226	4	US-09-453-234-80	Sequence 80, Appl
31	562	71.5	146	4	US-09-472-087-21	Sequence 21, Appl
32	562	71.5	146	4	US-09-472-087-93	Sequence 93, Appl
33	561	71.4	139	4	US-09-472-087-16	Sequence 16, Appl
34	561	71.4	139	4	US-09-472-087-90	Sequence 90, Appl
35	560	71.2	218	2	US-08-887-352B-13	Sequence 13, Appl
36	560	71.2	218	3	US-08-466-151-9	Sequence 9, Appl
37	560	71.2	218	3	US-09-109-207C-13	Sequence 13, Appl
38	560	71.2	218	3	US-09-296-005-13	Sequence 13, Appl
39	560	71.2	218	3	US-08-466-163B-9	Sequence 9, Appl
40	560	71.2	218	4	US-09-920-171-13	Sequence 13, Appl
41	560	71.2	218	4	US-09-802-056-9	Sequence 9, Appl
42	560	71.2	218	4	US-09-802-077-9	Sequence 9, Appl
43	560	71.2	218	4	US-09-716-028-13	Sequence 13, Appl
44	560	71.2	218	4	US-10-113-996-13	Sequence 13, Appl
45	560	71.2	224	4	US-09-456-090A-36	Sequence 36, Appl

ALIGNMENTS

RESULT 1

US-09-301-593-36

; Sequence 36, Application US/09301593A

; Patent No. 6455677

; GENERAL INFORMATION:

; APPLICANT: Park, John E.

; APPLICANT: Garin-Chesa, Pilar

; APPLICANT: Bamberger, Uwe

; APPLICANT: Leger, Olivier

; APPLICANT: Saldanha, Jose W.

; APPLICANT: Rettig, Wolfgang J.

; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility

; FILE REFERENCE: 0652.1890001

; CURRENT APPLICATION NUMBER: US/09/301,593A

; CURRENT FILING DATE: 1999-04-29

; EARLIER APPLICATION NUMBER: EP 98107925.4

; EARLIER FILING DATE: 1998-04-30

; EARLIER APPLICATION NUMBER: US 60/086,049

; EARLIER FILING DATE: 1998-05-18

; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: Patent in Ver. 2.0

; SEQ ID NO 36

; LENGTH: 240

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-301-593-36

Query Match 88.2%; Score 693; DB 4; Length 240;

Best Local Similarity 91.8%; Pred. No. 7.9e-62;

Matches 134; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSQS...VLFNNKYLAWYQKQPPKLLIYWA...TRESGVDPDRG 61

DB 30 SLAVSLGERATINCKSSQS...VLFNNKYLAWYQKQPPKLLIYWA...TRESGVDPDRG 89

QY 62 GSGGTDTFTLTSSLOAEDVAVYQCYSTPTFGQGTKEIKRTVAAPS...VFIPPSDE 121

DB 90 GSGGTDTFTLTSSLOAEDVAVYQCYSTPTFGQGTKEIKRTVAAPS...VFIPPSDE 149

QY 122 QKSGTASVCLNFFPREAKEHQK 147

DB 150 QKSGTASVCLNFFPREAKEVQWK 175

RESULT 2

US-07-916-098A-56

; Sequence 56, Application US/07916098A

; Patent No. 5871732

; GENERAL INFORMATION:

; APPLICANT: BURKLY, LINDA C.

APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,098A
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-916-098A-56

Query Match 87.0%; Score 683.5; DB 2; Length 241;
Best Local Similarity 91.8%; Pred. No. 7.1e-61;
Matches 134; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAUWYQKPGQPKLLIYWASTRESGVDPDRFG 61
Db 32 SLAVSLGERATINCKSSQSVLYSFNNKNYLAUWYQKPGQPKLLIYWASTRESGVDPDRFS 91

QY 62 GSGSGTDTFTLTISSLQAEADVAVYQYQYVSTPRTFGQGTKEIKRTVAAPSVFIFPPSDE 121
Db 92 GSGSGTDTFTLTISSLQAEADVAVYQYQYVSTPRTFGQGTKEIKRTVAAPSVFIFPPSDE 150

QY 122 QKSGTASVCLNNFYPREAKEHOK 147
Db 151 QKSGTASVCLNNFYPREAKEHOK 176

RESULT 3
US-09-627-896B-22
Sequence 22, Application US/09627896B
Patent No. 6827934
GENERAL INFORMATION:
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
APPLICANT: CARENNO, BEATRIZ
APPLICANT: CELNIKER, ABBIE CHERYL
APPLICANT: COLLINS, MARY

APPLICANT: GOLDMAN, SAMUEL
APPLICANT: GRAY, GARY S.
APPLICANT: KNIGHT, ANDREA
APPLICANT: O'HARA, DENISE
APPLICANT: RUP, BONITA
APPLICANT: VELDMAN, GEBTRUIDA M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
TITLE OF INVENTION: OF TREATMENT THEREWITH
FILE REFERENCE: 08702.0081-01000
CURRENT APPLICATION NUMBER: US/09/627,896B
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 239
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: 3d1 light chain
US-09-627-896B-22

Query Match 82.6%; Score 649.5; DB 4; Length 239;
Best Local Similarity 88.4%; Pred. No. 1.8e-57;
Matches 129; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

QY 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAUWYQKPGQPKLLIYWASTRESGVDPDRFG 61
Db 30 SLAVSLGERATINCKSSQSVLYSFNNKNYLAUWYQKPGQPKLLIYWASTRESGVDPDRFS 89

QY 62 GSGSGTDTFTLTISSLQAEADVAVYQYQYVSTPRTFGQGTKEIKRTVAAPSVFIFPPSDE 121
Db 90 GSGSGTDTFTLTISSLQAEADVAVYQYQYVSTPRTFGQGTKEIKRTVAAPSVFIFPPSDE 148

QY 122 QKSGTASVCLNNFYPREAKEHOK 147
Db 149 QKSGTASVCLNNFYPREAKEHOK 174

RESULT 4
US-08-952-235-1
Sequence 1, Application US/08952235
Patent No. 6207152
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
APPLICANT: Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
TITLE OF INVENTION: Antagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460368
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416


```

; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-952-235-1

Query Match      81.4%; Score 640; DB 3; Length 220;
Best Local Similarity 82.2%; Pred. No. 1.5e-56;
Matches 120; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 61
Db 10 SLTVSVGEKVTVCSSQSLLYTSQKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFT 69

QY 62 GSGGTDFTLTITSSIQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
Db 70 GSGGTDFTLTITSSVKADDLAVYCCQYYAYPTWTFGGGTKEIKRTVAAPSFIIPPSPDE 129

QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
Db 130 QKSGTASVVCLLNNFYPREAKVQWK 155

RESULT 5
US-09-669-971-1
; Sequence 1, Application US/09669971
; Patent No. 6468529
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/669,971
; FILING DATE: 05-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/952,235
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/460368
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-669-971-1

Query Match      81.4%; Score 640; DB 4; Length 220;
Best Local Similarity 82.2%; Pred. No. 1.5e-56;
Matches 120; Conservative 14; Mismatches 12; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 61
Db 10 SLTVSVGEKVTVCSSQSLLYTSQKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFT 69

QY 62 GSGGTDFTLTITSSIQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
Db 70 GSGGTDFTLTITSSVKADDLAVYCCQYYAYPTWTFGGGTKEIKRTVAAPSFIIPPSPDE 129

QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
Db 130 QKSGTASVVCLLNNFYPREAKVQWK 155

RESULT 6
US-09-301-593-17
; Sequence 17, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-17

Query Match      80.0%; Score 629; DB 4; Length 220;
Best Local Similarity 82.2%; Pred. No. 1.9e-55;
Matches 120; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

QY 2 SLAVSLGERATINCKSSOSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 61
Db 10 SLAVSVGEKVTVCSSQSLLYSRNKNYLAWFOQKPGQPKLLIYWASTRESGVDPDRFT 69

QY 62 GSGGTDFTLTITSSIQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSFIIPPSPDE 121
Db 70 GSGGTDFTLTITSSVQAEADVAVYCCQYYSTPRTFGAGTKLEIKRTVAAPSFIIPPSPDE 129

QY 122 QKSGTASVVCLLNNFYPREAKEHOK 147
Db 130 QKSGTASVVCLLNNFYPREAKVQWK 155

RESULT 7
US-09-301-593-28
; Sequence 28, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
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; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026.320A
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/609803
; FILING DATE: 05-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29421
; REFERENCE/DOCKET NUMBER: 94268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3107885046
; TELEFAX: 3102771297
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-026-320A-4

Query Match      73.9%; Score 581; DB 1; Length 120;
Best Local Similarity 97.4%; Pred. No. 6e-51;
Matches 112; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFG 61
Db 6 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFS 65

Qy 62 GSGSGTDTFTLTSSLSQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSVFIF 116
Db 66 GSGSGTDTFTLTSSLSQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSVFIF 120

RESULT 11
US-09-472-087-71
; Sequence 71, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 71
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-71

Query Match      72.9%; Score 573; DB 4; Length 214;
Best Local Similarity 76.7%; Pred. No. 7.7e-50;
Matches 112; Conservative 10; Mismatches 18; Indels 6; Gaps 1;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFG 61
Db 10 SLSASVGRVITCRASQSI-----NSYLDWYQKPGKAPKLLIYAASSLSQSGVPSRFS 63

Qy 62 GSGSGTDTFTLTSSLSQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSVFIF 121
Db 64 GSGSGTDTFTLTSSLSQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSVFIF 123

; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/026.320A
; FILING DATE: 26-FEB-1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/609803
; FILING DATE: 05-NOV-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oldenkamp, David J.
; REGISTRATION NUMBER: 29421
; REFERENCE/DOCKET NUMBER: 94268
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 3107885046
; TELEFAX: 3102771297
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 120 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-026-320A-4

Query Match      72.8%; Score 572; DB 4; Length 139;
Best Local Similarity 78.2%; Pred. No. 5.7e-50;
Matches 111; Conservative 10; Mismatches 15; Indels 6; Gaps 1;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFG 61
Db 3 SLSASVGRVITCRASQSI-----NSYLDWYQKPGKAPKLLIYAASSLSQSGVPSRFS 56

Qy 62 GSGSGTDTFTLTSSLSQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSVFIF 121
Db 57 GSGSGTDTFTLTSSLSQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSVFIF 116

Qy 122 QKSGTASVWCLNNFYPREAK 143
Db 117 QKSGTASVWCLNNFYPREAK 138

RESULT 12
US-09-472-087-22
; Sequence 22, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-22

Query Match      72.8%; Score 572; DB 4; Length 139;
Best Local Similarity 78.2%; Pred. No. 5.7e-50;
Matches 111; Conservative 10; Mismatches 15; Indels 6; Gaps 1;

Qy 2 SLAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFG 61
Db 3 SLSASVGRVITCRASQSI-----NSYLDWYQKPGKAPKLLIYAASSLSQSGVPSRFS 56

Qy 62 GSGSGTDTFTLTSSLSQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSVFIF 121
Db 57 GSGSGTDTFTLTSSLSQAEADVAVYCCQYYSTPRTFGQGTKEIKRTVAAPSVFIF 116

Qy 122 QKSGTASVWCLNNFYPREAK 143
Db 117 QKSGTASVWCLNNFYPREAK 138

RESULT 13
US-09-472-087-96
; Sequence 96, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-96
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.1428 Seconds
(without alignment)
1353.842 Million cell updates/sec

Title: US-09-784-950-29

Perfect score: 1054

Sequence: 1 EVKPGASVKVCKASGYTF.....TSQVLLPSKDVMOGTDEHKV 199

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	870	82.5	627	2	S14683
2	663.5	63.0	231	2	B23746
3	590	56.0	288	2	S29690
4	526.5	50.0	136	2	S31600
5	524	49.7	127	2	S34014
6	506.5	48.1	110	2	PH1670
7	500	47.4	160	2	PL0105
8	497.5	47.2	132	2	S31596
9	495.5	47.0	246	2	S38950
10	495.5	47.0	446	2	S40295
11	492	46.7	469	2	S37483
12	491	46.6	171	2	S23623
13	476.5	45.2	118	2	PH1666
14	476	45.2	98	2	S26918
15	474	45.0	142	2	A32483
16	473	44.9	129	2	S46393
17	470.5	44.6	241	2	S69131
18	467.5	44.4	118	2	S36265
19	466.5	44.3	568	2	A34891
20	466	44.2	592	2	S25705
21	463.5	44.0	114	2	PH1667
22	462.5	43.9	135	2	S49530
23	458	43.5	129	2	S36260
24	458	43.5	475	2	S01321
25	454	43.1	109	2	PH1668
26	454	43.1	123	2	D33548
27	451.5	42.8	474	1	G2MS11
28	451	42.8	214	2	PC4202
29	447.5	42.5	110	2	PH1669

RESULT 1
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <PRI>
A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin; membrane protein
F:1-15/Domain: signal sequence #status predicted <SIG>
F:16-627/Product: Ig mu chain #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match	82.5%	Score	870	DB	2	Length	627
Best Local Similarity	82.0%	Pred. No.	7.5e-62				
Matches	173	Conservative	7	Mismatches	19	Indels	12
Gaps	2						
Qy	1	EVKPGASVKVCKASGYTFTSYDINWVRQATGCGLEWGMWNPNSGNTGYAQKFGQGRVT	60				
Db	29	EVKPGSSVKVCKASGTFSSYAIISWVRQAPGGGLEWGGIIPIFGTANYAQKFGQGRVT	88				
Qy	61	MTRNTSISTAYMELSSLRSEDTAVYYCAR-----EEWLVR---YGMQVMOGQTTV	108				
Db	89	ITADESTSTAYMELSSLRSEDTAVYYCAKTIIGFYSSGMYPNSDYYYYGMDVMQGGTTV	148				
Qy	109	TVSSGSASAPTLPLVSCNSPSTSSVAVCCLAQDFLPDSITFSWKYKNNSDISSTRGF	168				
Db	149	TVSSGSASAPTLPLVSCNSPSTSSVAVCCLAQDFLPDSITFSWKYKNNSDISSTRGF	208				
Qy	169	PSVLRGKGYAATSOVLLPSKDVMOGTDEHKV	199				
Db	209	PSVLRGKGYAATSOVLLPSKDVMOGTDEHVV	239				
RESULT 2							
B23746							
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)							
C:Species: Homo sapiens (man)							
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000							
C:Accession: B23746							
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.							
J. Biol. Chem. 266, 2836-2842, 1991							
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin							
A:Reference number: A23746; MUID:91131575; PMID:1993660							
A:Accession: B23746							

Ig mu chain C regi
Ig mu chain C regi
Ig mu chain C regi
Ig heavy chain - h
Ig heavy chain pre
Ig heavy chain v r
Ig heavy chain v r
Ig heavy chain v r
Ig heavy chain v r
Ig heavy chain v r
Ig heavy chain v-1
Ig heavy chain v r
Ig heavy chain pre
Ig heavy chain v r

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-231 <LBO>

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;140-209/Domain: immunoglobulin homology <IMM>

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Query Match      63.0%; Score 663.5; DB 2; Length 231;
Best Local Similarity 67.3%; Pred. No. 7.4e-46;
Matches 132; Conservative 24; Mismatches 39; Indels 1; Gaps 1;

Qy      4  KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVTWTR 63
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      12  KPSTLSLTGAVYGGSDYVSWIRPPGKLEWIGEIN-HSGSTYNPLSKSRVTSV 70
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      64  NTSISTAYMELSLRSEDATVYVCAREEWLVRYGMDVWGQGTVTVTSSGSASAPTLPPL 123
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      71  DTSKNQPSLKLSSVTAADTAVYCARPHDTSGHYVWVGQGLTVTVSSGSASAPTLPPL 130
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      124  VSCNSPDTSSVAVGCLAQDFLPSDITFSWKYKKNSDISSTRGFPSPVLRGGKYAATSOV 183
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      131  VSCNSPDTSSVAVGCLAQDFLPSDITFSWKYKKNSDISSTRGFPSPVLRGGKYAATSOV 190
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      184  LLPSKDVMOGTDDEHKV 199
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      191  LLPSKDVMOGTDDEHV 206
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 3

S29690

Ig heavy chain VDJ region - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000

C;Accession: S29690

R;Dammers, P.M.; Bos, N.A.; Kroese, F.G.M.

submitted to the EMBL Data Library, October 1992

A;Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.

A;Reference number: S29690

A;Accession number: S29690

A;Molecule type: mRNA

A;Residues: 1-288 <DAM>

A;Cross-references: EMBL:X68782; NID:g56442; PID:g1334294

A;Experimental source: strain D2B

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;12-95/Domain: immunoglobulin homology <IMM>

```
Query Match      56.0%; Score 590; DB 2; Length 288;
Best Local Similarity 56.5%; Pred. No. 6.9e-40;
Matches 113; Conservative 38; Mismatches 45; Indels 4; Gaps 2;
```

```
Qy      1  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 60
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      7  ELVRGSSVKISKASGYTFTDYMHVVKQRPQGLWIGRINPANGNTEYAEKPKSRAT 66
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      61  MTRNTSISTAYMELSLRSEDATVYVCAREEWLVRYGMDVWGQGTVTVTSSGSASAPT 120
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      67  LTADKSSNTAYMQLSLTSEDATYFCTITGTVVFPF---DYWGQGVYVTVSSSESQSPTV 123
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      121  PLVSCNSPDTSSVAVGCLAQDFLPSDITFSWKYKKNSDI-SSTRGFPSPVLRGGKYAA 179
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      124  LPLVSCSPSLDENLVAMCLARDFLPSSISFSWYQNNTIEVWQGVRFPTLTGDKYTA 183
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      180  TSQVLLPSKDVMOGTDDEHKV 199
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      184  TSQVLLSAKNVLEGSDEYLV 203
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 4

S31600

Ig heavy chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C;Accession: S31600

R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.

submitted to the EMBL Data Library, June 1992

A;Description: Mechanisms that generate human immunoglobulin diversity operate from the

A;Reference number: S31585

A;Accession: S31600

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-136 <CUI>

A;Cross-references: EMBL:Z14165; NID:g30994; PIDN:CAA78534.1; PID:g30995

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-117/Domain: immunoglobulin homology <IMM>

```
Query Match      50.0%; Score 526.5; DB 2; Length 136;
Best Local Similarity 89.4%; Pred. No. 3.5e-35;
Matches 101; Conservative 3; Mismatches 4; Indels 5; Gaps 2;

Qy      1  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 60
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      29  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 88
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      61  MTRNTSISTAYMELSLRSEDATVYVCAREEWLVRYGMDVWGQGTVTVTSSG 113
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      89  MTRNTSISTAYMELSLRSEDATVYVCAR--WRDAF---DIWGQGTMTVTSSG 136
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 5

S34014

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-1996

C;Accession: S34014; S30535

R;Mariette, X.; Tsapis, A.; Brouet, J.C.

Eur. J. Immunol. 23, 846-851, 1993

A;Title: Nucleotide sequence analysis of the variable domains of four human monoclonal

A;Reference number: S34001; MUID:93209281; PMID:7681398

A;Accession: S34014

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-127 <MAR>

A;Cross-references: EMBL:Z18321

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

```
Query Match      49.7%; Score 524; DB 2; Length 127;
Best Local Similarity 85.6%; Pred. No. 5.2e-35;
Matches 101; Conservative 7; Mismatches 4; Indels 6; Gaps 2;
```

```
Qy      1  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 60
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      10  EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMWNPNSGNTGYAQKFGQGRVT 69
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Qy      61  MTRNTSISTAYMELSLRSEDATVYVCARE---EWLVR---YGMVDVWGQGTVTTVSS 112
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      70  MTRNTSISTAYMELSLRSEDATVYFCARALSIGVAVIRGYVYALDVWGQGTVTTVSS 127
      |||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
```

RESULT 6

PH1670

Ig heavy chain V region (clone 2A12) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 16-Aug-1996

C;Accession: PH1670

R;Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.

J. Exp. Med. 178, 331-336, 1993

A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococ

A;Reference number: PH1642; MUID:93301610; PMID:8315388

A;Accession: PH1670

A;Molecule type: mRNA

A;Residues: 1-110 <HIL>

A;Experimental source: B cell

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 48.1%; Score 506.5; DB 2; Length 110;
Best Local Similarity 84.6%; Pred. No. 1.1e-33;
Matches 99; Conservative 2; Mismatches 3; Indels 13; Gaps 2;
QY 1 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 60
DB 2 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 61
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYG-----MDVWGQGTITVTVSS 112
DB 62 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYG-----GKGGEFDINGQGTITVTVSS 110

RESULT 7

PL0105
anti-PR2 erythrocyte autoantibody heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 26-Apr-1996
C:Accession: PL0105
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma secretory cell line to the human B cell lymphoma secretory cell line
A:Reference number: PL0106; MUID:89235583; PMID:2541221
A:Accession: PL0105
A:Molecule type: mRNA
A:Residues: 1-160 <SIL>
A:Note: The authors translated the codon GAC for residues 108 and 109 as Glu
C:Comment: The antibody is one of the cold agglutinins that preferentially bind red blood cells
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: autoantibody; hemagglutinin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:34-117/Domain: immunoglobulin homology <IMM>
F:49-54/Region: complementarity-determining 1
F:69-84/Region: complementarity-determining 2
F:118-131/Domain: D region <DRG>
F:132-144/Domain: J4 segment <JSG>
F:145-160/Domain: C region <CRG>

Query Match 47.4%; Score 500; DB 2; Length 160;
Best Local Similarity 74.2%; Pred. No. 5.5e-33;
Matches 98; Conservative 8; Mismatches 22; Indels 4; Gaps 1;
QY 1 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 60
DB 29 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 88
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYG-----YGMVWGQGTITVTVSSGSAS 116
DB 89 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYG-----YGMVWGQGTITVTVSSGSAS 148
QY 117 APTLPPLVSCEN 128
DB 149 APTLPPLVSCEN 160

RESULT 8

S31596
Ig heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S31596
R:Cuissinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnel, C.
submitted to the EMBL Data Library, June 1992
A:Description: Mechanisms that generate human immunoglobulin diversity operate from the V region
A:Reference number: S31585
A:Accession: S31596
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-132 <CUI>
A:Cross-references: EMBL:Z14166; NID:G30996; PIDN:CAA78535.1; PID:G30997

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 47.2%; Score 497.5; DB 2; Length 132;
Best Local Similarity 85.0%; Pred. No. 7e-33;
Matches 96; Conservative 3; Mismatches 5; Indels 9; Gaps 1;
QY 1 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 60
DB 29 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 88
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTITVTVSS 113
DB 89 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTITVTVSS 132

RESULT 9

S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bitzan, C.
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(2) macroglobulin
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLS>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 47.0%; Score 495.5; DB 2; Length 246;
Best Local Similarity 51.8%; Pred. No. 2e-32;
Matches 99; Conservative 34; Mismatches 43; Indels 15; Gaps 6;
QY 1 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 60
DB 10 ELVRPGASVKVSKASGYFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTITVTVSSGSASAPTL 120
DB 70 LTVDTSSSTAYMQLSLTSEDSAVYFCARG----GKFMDYWGQGTITVTVSSAKTTAPSV 125
QY 121 PLVLS-CENSPSDT--SSVAVGCLAQDFLPDSITFSWKYKNSDLS--TRGFPSVLRGCK 176
DB 126 YPLAPVC---GDTTSSVTLGCLVGFPEPVTITW---NSGSLSSGVHTTFAVLQSDL 178
QY 177 YAATSQVLLPS 187
DB 179 YTLSSSVTVTS 189

RESULT 10

S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
C:Accession: S40295
R:Kleber, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bitzan, C.
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(2) macroglobulin
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLS>
A:Cross-references: UNIPROT:Q99L25
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology


```
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26918
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26918
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <IOM>
A:Cross-references: EMBL:Z12317; NID:g32857; PIDN:CAA78187.1; PID:g32858
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 45.2%; Score 476; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 2.6e-31;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEGWGMWNPNSGNTGYAQKFGQGRVT 60
Db 10 EVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEGWGMWNPNSGNTGYAQKFGQGRVT 69

QY 61 MTRNTSISTAYMELSLRSEDVAVYYCAR 89
Db 70 MTRNTSISTAYMELSLRSEDVAVYYCAR 98

RESULT 15
A32483
IG heavy chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 16-Aug-1996
C:Accession: A32483
R:Larrick, J.W.; Danielsson, L.; Brenner, C.A.; Abrahamson, M.; Fry, K.E.; Borrebaeck, C
Biochem. Biophys. Res. Commun. 160, 1250-1256, 1989
A:Title: Rapid cloning of rearranged immunoglobulin genes from human hybridoma cells usi
A:Reference number: A32483; MUID:89273586; PMID:2499327
A:Accession: A32483
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-142 <LAR>
A:Cross-references: GB:M26463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-108/Domain: immunoglobulin homology <IMM>

Query Match 45.0%; Score 474; DB 2; Length 142;
Best Local Similarity 75.6%; Pred. No. 5.7e-31;
Matches 93; Conservative 9; Mismatches 15; Indels 6; Gaps 1;

QY 1 EVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEGWGMWNPNSGNTGYAQKFGQGRVT 60
Db 20 EVKKPGASVKVSKASGYTFTSYDINWVRQATQGLEGWGMWNPNSGNTGYAQKFGQGRVT 79

QY 61 MTRNTSISTAYMELSLRSEDVAVYYCAR 117
Db 80 MTRDTSTVYMEYELSLRSEDVAVYYCAR 139

QY 115 ASA 117
Db 140 ASA 142

Search completed: March 8, 2005, 06:39:24
Job time : 14.1928 secs
```

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 74.3165 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-29

Perfect score: 1054

Sequence: 1 EVKPGASVKVSKASGYTF.....TSQVLLPSKDVMOGTDEHKV 199

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	778.5	73.9	606	Q6GMV2	Q6gmv2 homo sapien
2	754.5	71.6	613	Q8WUK1	Q8wuk1 homo sapien
3	749	71.1	597	Q96BB9	Q96bb9 homo sapien
4	702	66.6	595	Q8WUX4	Q8wux4 homo sapien
5	702	66.6	597	Q6GMK5	Q6gmk5 homo sapien
6	702	66.6	597	Q9BU10	Q9bu10 homo sapien
7	702	66.6	625	Q96A6	Q96a6 homo sapien
8	698	66.2	597	Q9BQB8	Q9bqb8 homo sapien
9	692.5	65.7	620	Q96EY0	Q96ey0 homo sapien
10	625	59.3	613	Q8VCX7	Q8vcx7 mus musculus
11	586.5	55.6	614	Q7TWT6	Q7twt6 mus musculus
12	544.5	51.7	518	Q6N030	Q6n030 homo sapien
13	518.5	49.2	497	Q8WZ24	Q8wz24 homo sapien
14	512.5	48.6	469	Q7Z7P5	Q7z7p5 homo sapien
15	511	48.5	500	Q9BRV0	Q9brv0 homo sapien
16	508.5	48.2	475	Q6N095	Q6n095 homo sapien
17	505	47.9	498	Q6N041	Q6n041 homo sapien
18	503.5	47.8	470	Q7TWK1	Q7twk1 mus musculus
19	497.5	47.2	500	Q6N091	Q6n091 homo sapien
20	484.5	46.0	480	Q6P089	Q6p089 homo sapien
21	484	45.9	480	Q6PJF1	Q6pjf1 homo sapien
22	481	45.6	481	Q91WT1	Q91wt1 mus musculus
23	480.5	45.6	482	Q8K172	Q8k172 mus musculus
24	480	45.5	463	Q991C4	Q991c4 mus musculus
25	478	45.4	484	Q99LA6	Q99la6 mus musculus
26	475	45.1	465	Q6PJB2	Q6pjb2 mus musculus
27	474.5	45.0	473	Q9D8L4	Q9d8l4 mus musculus
28	468.5	44.4	472	Q6PJA7	Q6pia7 mus musculus
29	465	44.1	480	Q8K0Z4	Q8k0z4 mus musculus
30	462	43.8	244	Q65ZC8	Q65zc8 homo sapien
31	461	43.7	489	Q8VCX4	Q8vcx4 mus musculus

32	460.5	43.7	593	2	Q6INM5	Q6imn5 xenopus lae
33	457.5	43.4	488	2	Q8K0F2	Q8k0f2 mus musculus
34	456.5	43.3	488	2	Q91WR1	Q91wr1 mus musculus
35	456	43.3	208	2	Q6ZP87	Q6zpb7 homo sapien
36	455	43.2	125	2	Q9UL95	Q9ul95 homo sapien
37	454.5	43.1	159	2	Q96Q80	Q96q80 homo sapien
38	450	42.7	472	2	Q6N089	Q6n089 homo sapien
39	448.5	42.6	464	2	Q6PF95	Q6pf95 mus musculus
40	448	42.5	573	2	Q8WU38	Q8wu38 homo sapien
41	446.5	42.4	145	2	Q924Q6	Q924q6 mus musculus
42	445	42.2	119	2	Q9UL94	Q9ul94 homo sapien
43	444.5	42.2	145	2	Q924Q9	Q924q9 mus musculus
44	444	42.1	142	2	Q924Q1	Q924q1 mus musculus
45	443.5	42.1	124	2	Q9UL92	Q9ul92 homo sapien

ALIGNMENTS

RESULT 1
Q6GMV2 PRELIMINARY; PRT; 606 AA.
ID Q6GMV2
AC Q6GMV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Srausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udgin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skaleka U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Srausberg R.;
DR Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC073758; AAH73758.1; -;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.

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KW Hypothetical protein.
SQ SEQUENCE 606 AA; 66184 MW; B6B38B51114E4C55 CRC64;

Query Match 73.9%; Score 778.5; DB 2; Length 606;
Best Local Similarity 70.3%; Pred. No. 9.7e-62;
Matches 147; Conservative 26; Mismatches 23; Indels 13; Gaps 1;

QY 4 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTMTR 63
DQ |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::
Db 32 KPGSIRLSCAASGFTFSYDYNMSWIRQAPGKLEWVSISSSSYTNVADSVKGRFTISR 91
QY 64 NTSISTAYMELSLRSEDVAVYYCAR-----EVLVRYGMDVMGQGTVTTV 110
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 92 DNKNSLYLQMSLRAEDTAVYCARGGNGIAAGRVVVAEYVYVYGGMDVMGQGTVTTV 151
QY 111 SSGSASAPTLFPLVSCENSPDTSVAVGCLAQDPLPSITFSWKYKNNSDISSRGPFS 170
DQ |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 152 SSGSASAPTLFPLVSCENSPDTSVAVGCLAQDPLPSITFSWKYKNNSDISSRGPFS 211
QY 171 VLRRGGKYAATSOVLLPSKDVMOGTDEHKV 199
DQ |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 212 VLRRGGKYAATSOVLLPSKDVMOGTDEHKV 240

RESULT 2
Q8WUK1 PRELIMINARY; PRT; 613 AA.
AC Q8WUK1
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; F36005; F36005.
DR PIR; G36005; G36005.
DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PH0098; PH0098.

Query Match 71.6%; Score 754.5; DB 2; Length 613;
Best Local Similarity 72.2%; Pred. No. 1.4e-59;
Matches 143; Conservative 26; Mismatches 28; Indels 1; Gaps 1;

QY 2 VKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVTM 61
DQ |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 30 VVQGRSIRLSCAASGFTFSYDYNMSWIRQAPGKLEWVSISSSSYTNVADSVKGRFTI 89
QY 62 TRNTSISTAYMELSLRSEDVAVYYCAREEVLVRYGMDVMGQGTVTTVSSGSASAPTLF 121
DQ : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 90 SRDNSKNTLYLQMSLRAEDTAVYYCAK-DHSEGVETFDIMQGTMTVTTVSSGSASAPTLF 148
QY 122 PLVSCENSPDTSVAVGCLAQDPLPSITFSWKYKNNSDISSRGPFSVLRRGGKYAATS 181
DQ |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 149 PLVSCENSPDTSVAVGCLAQDPLPSITFSWKYKNNSDISSRGPFSVLRRGGKYAATS 208
QY 182 QVLLPSKDVMOGTDEHKV 199
DQ |||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||:::|||||
Db 209 QVLLPSKDVMOGTDEHKV 226

RESULT 3
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whitling M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; F36005; F36005.
DR PIR; G36005; G36005.
DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PH0098; PH0098.

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RL Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC015760; AAH15760.1; -.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 597 AA; 65039 MW; 4FC3AD8ECE263D9 CRC64;

Query Match 71.1%; Score 749; DB 2; Length 597;
Best Local Similarity 70.9%; Pred. No. 4.4e-59;
Matches 144; Conservative 25; Mismatches 24; Indels 10; Gaps 2;

QY 4 KPGASVKVSKASGYTFTSYDINWVRQATGGGLEWMGMNPNNGTGYAQKFGQRTVWTR 63
Db 32 QFGGSLRLSCAASGFSFSGYAMNWRQAPGKLEWVSAISGGSGTYYADSVKGRFTISR 91
QY 64 NTSISTAYMELSSLRSEDATVYCYAREEWLYRYCM-----DYWGQGTTVTVSSGSAS 116
Db 92 DNSRDRLYLQNSLRADATVYICAKP---RGYSAGNYTREDYWGQGTTLTVTVSSGSAS 148
QY 117 APTLFPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNSDISSTRGPPSVLRGK 176
Db 149 APTLFPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNSDISSTRGPPSVLRGK 208
QY 177 YAATSQVLLPSKDVNQGTDEHKV 199
Db 209 YAATSQVLLPSKDVNQGTDEHV 231

RESULT 4
Q8WUX4 PRELIMINARY; PRT; 595 AA.
ID Q8WUX4 AC Q8WUX4 Q6GMX5 Q6GMX5
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR PIR; G34964; G34964.
DR HSP; P01861; 1ADQ.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 4.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Query Match 66.6%; Score 702; DB 2; Length 595;
Best Local Similarity 69.0%; Pred. No. 7.7e-55;
Matches 140; Conservative 22; Mismatches 31; Indels 10; Gaps 3;

QY 4 KPGASVKVSKASGYTFTSYDINWVRQATGGGLEWMGMNPNNGTGYAQKFGQRTVWTR 63
Db 39 KPSETLSLTGCVGSGFSGYWMIQPPGKLEWIGBIN-HSGSTNYPNPSLKSRTISV 97
QY 64 NTSISTAYMELSSLRSEDATVYCYAREEWLYR-----YYGMDVWGQGTTVTVSSGSAS 116
Db 98 DTSKKQLSLKLSLSSNAADATVYICARV--ITRASPGTDGRYGMVWGQGTTVTVSSGSAS 155
QY 117 APTLFPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNSDISSTRGPPSVLRGK 176
Db 156 APTLFPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNSDISSTRGPPSVLRGK 215
QY 177 YAATSQVLLPSKDVNQGTDEHKV 199
Db 216 YAATSQVLLPSKDVNQGTDEHV 238

RESULT 5
Q6GMX5 PRELIMINARY; PRT; 597 AA.
ID Q6GMX5 AC Q6GMX5 Q6GMX5 Q6GMX5
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
```

```

RN  SEQUENCE FROM N.A.
RP  TISSUE=Lymph;
RA  Strausberg R.;
RL  Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC073767; AAH73767.1; -.
DR  InterPro; IPR003599; IG.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG cl.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF07654; Cl-set; 4.
DR  SMART; SM00407; IGc1; 4.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS00835; IG LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW  Hypothetical protein.
SQ  SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 66.6%; Score 702; DB 2; Length 597;
Best Local Similarity 69.0%; Pred. No. 7.7e-55;
Matches 140; Conservative 22; Mismatches 31; Indels 10; Gaps 3;

Qy 4 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGNPNSGNTGYAQKFGQGRVTMTR 63
Db 32 KPSETLSITCGVYGGSFSGYYSWIRQPPGKLEWIGEIN-HSGSTNYPNLSKSRVTISV 90
Qy 64 NTSISTAYMELSSLRSEDTAVYICAREEWLVR-----YYGMDVWGQGTITVTVSSGSGS 116
Db 91 DTSKKQLSLKSSVNAADTAVYICARV--ITRASPGTDGRYGMVWGQGTITVTVSSGSGS 148
Qy 117 APTLFPVLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNDISSTRGFPSPVLRGCK 176
Db 149 APTLFPVLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNDISSTRGFPSPVLRGCK 208
Qy 177 YAATSQVLLPSKDVWQGTDEHKV 199
Db 209 YAATSQVLLPSKDVWQGTDEHV 231

RESULT 6
Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
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RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; BC002963; AAH02963.1; -.
DR  HSSP; P01861; 1ADQ.
DR  InterPro; IPR007110; IG-like.
DR  InterPro; IPR003597; IG cl.
DR  InterPro; IPR003006; IG_MHC.
DR  InterPro; IPR003596; IG_v.
DR  Pfam; PF07654; Cl-set; 4.
DR  SMART; SM00406; IGv; 1.
DR  PROSITE; PS00835; IG LIKE; 5.
DR  PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ  SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 66.6%; Score 702; DB 2; Length 597;
Best Local Similarity 69.0%; Pred. No. 7.7e-55;
Matches 140; Conservative 22; Mismatches 31; Indels 10; Gaps 3;

Qy 4 KPGASVKVCKASGYTFTSYDINVRQATGQGLEWMGNPNSGNTGYAQKFGQGRVTMTR 63
Db 32 KPSETLSITCGVYGGSFSGYYSWIRQPPGKLEWIGEIN-HSGSTNYPNLSKSRVTISV 90
Qy 64 NTSISTAYMELSSLRSEDTAVYICAREEWLVR-----YYGMDVWGQGTITVTVSSGSGS 116
Db 91 DTSKKQLSLKSSVNAADTAVYICARV--ITRASPGTDGRYGMVWGQGTITVTVSSGSGS 148
Qy 117 APTLFPVLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNDISSTRGFPSPVLRGCK 176
Db 149 APTLFPVLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKKNNDISSTRGFPSPVLRGCK 208
Qy 177 YAATSQVLLPSKDVWQGTDEHKV 199
Db 209 YAATSQVLLPSKDVWQGTDEHV 231

RESULT 7
Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
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RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.2; -
DR PIR; S15590; S15590.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBFE CRC64;

Query Match 66.6%; Score 702; DB 2; Length 625;
Best Local Similarity 69.0%; Pred. No. 8.2e-55;
Matches 140; Conservative 22; Mismatches 31; Indels 10; Gaps 3;
QY 4 KPGASVKVCASGVTFTSYDINVRQATGQGLEWMGNPNNGTGYAQKFGQRTVTR 63
DB 39 KPSSETLSLTCTGVYGSFGYWSWIROPKGLWIGIN-HSGSTNPNLSKSRVTISV 97
QY 64 NTSISTAYMELSSLRSEDTAVVYCARBEWLVR-----YGMVWGOGTTVTYSSGSAS 116
DB 98 DTSKKQLSLSSVNAADTAVVYCARV--ITRASPGTGRYGMVWGOGTTVTYSSGSAS 155
QY 117 APTLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGPPSVLRGK 176
DB 156 APTLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGPPSVLRGK 215
QY 177 YAATSQVLLPSKDVNQGTDEHKV 199
DB 216 YAATSQVLLPSKDVNQGTDEHV 238

RESULT 8
Q9BQ88 PRELIMINARY; PRT; 597 AA.
AC Q9BQ88; (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McKernan K.J., Mckernan K.J., Mckernan K.J., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madao A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madao A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
Query Match 66.2%; Score 698; DB 2; Length 597;
Best Local Similarity 69.0%; Pred. No. 1.8e-54;
Matches 140; Conservative 21; Mismatches 32; Indels 10; Gaps 3;
QY 4 KPGASVKVCASGVTFTSYDINVRQATGQGLEWMGNPNNGTGYAQKFGQRTVTR 63
DB 32 KPSSETLSLTCTGVYGSFGYWSWIROPKGLWIGIN-HSGITNPNLSKSRVTISV 90
QY 64 NTSISTAYMELSSLRSEDTAVVYCARBEWLVR-----YGMVWGOGTTVTYSSGSAS 116
DB 91 DTSKKQLSLSSVNAADTAVVYCARV--ITRASPGTGRYGMVWGOGTTVTYSSGSAS 148
QY 117 APTLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGPPSVLRGK 176
DB 149 APTLPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGPPSVLRGK 208
QY 177 YAATSQVLLPSKDVNQGTDEHKV 199
DB 209 YAATSQVLLPSKDVNQGTDEHV 231

RESULT 9
Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0; (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

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RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01820; 1G7J.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.C1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.V.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS0290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match 65.7%; Score 692.5; DB 2; Length 620;
Best Local Similarity 68.9%; Pred. No. 5.9e-54;
Matches 135; Conservative 23; Mismatches 37; Indels 1; Gaps 1;

Qy 4 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNGTGYAQKFGQRTVWTR 63
Db 39 KPSETLSITCTVSGGSISSYWIQAPAGKLEWIGRIY-TSGSTNNYPSLKSRTVMSV 97

Qy 64 NTSISTAYMELSLRSEDTAVVYCAREBWLVRVYGMVWGQGTVTTVSSGASAPTLFPL 123
Db 98 DTSKNQFSLKLSVTAADTAVVYCASQWELPTVGLFYWGQGLTVTVSSGASAPTLFPL 157

Qy 124 VSCNSPSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKYAATSOV 183
Db 158 VSCNSPSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKYAATSOV 217

Qy 184 LLPKDVVMQGTDEHKV 199
Db 218 LLPKDVVMQGTDEHV 233

RESULT 10
Q8VCX7 PRELIMINARY; PRT; 613 AA.
ID Q8VCX7;
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
GN Name=Igh-6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaeetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAH18315.1; -.
DR PIR; C30562; C30562.
DR HSSP; P01751; 1A6W.
DR MGD; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B-cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; F:antigen binding; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.
DR GO; GO:0030890; P:positive regulation of B-cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS0290; IG MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 59.3%; Score 625; DB 2; Length 613;
Best Local Similarity 60.5%; Pred. No. 7.2e-48;
Matches 121; Conservative 34; Mismatches 41; Indels 4; Gaps 3;

Qy 1 EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNGTGYAQKFGQRTV 60
Db 29 ELMKPGASVKISCKATGYTFSSYWIWVKQRPQGHLEWIGILPFGSGSTNYNEKFKGRAT 88

Qy 61 MTRNTSISTAYMELSLRSEDTAVVYCAREBWLVRVYGMVWGQGTVTTVSSGASAPTL 120
Db 89 FTADTSSNTAYMQLSSLTSEDSAVVYCARR--LGRWY-FDVWGAGTTVTVSSSQSFNV 145

Qy 121 PPLVSCNSPSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKYAA 179
Db 146 PPLVSCNSPSPDTSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKYAA 205

Qy 180 TSQVLLPSKDVVMQGTDEHKV 199
Db 206 TSQVLLPSKDVVMQGTDEHKV 225

RESULT 11
Q7TWT6 PRELIMINARY; PRT; 614 AA.
ID Q7TWT6;
AC Q7TWT6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MGC60843 protein.
OS Mus musculus (Mouse).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
 RA Diatchenko L., Marusan K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.K., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6NCr; TISSUE=Hematopoietic Stem Cell;
 RA Strausberg R.;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC053409; AAH53409.1; --
 DR HSSP; P01820; 1G7J.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
 SQ SEQUENCE 614 AA; 67746 MW; 835BAF3B8D124F89 CRC64;
 Query Match 55.6%; Score 586.5; DB 2; Length 614;
 Best Local Similarity 55.9%; Pred. No. 2.2e-44;
 Matches 114; Conservative 36; Mismatches 43; Indels 11; Gaps 3;
 QY 1 EVKKGASVKVSKASGYFTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 60
 Db 29 ELVKGASVKVSKASGYAFSSWMNVKQRPKGLEWIGRVYPGDGTNYNGKFKGKAT 88
 QY 61 MTRNTSISTAYMELSSLRSEDFAVYVCAREEVLVRYGMD---VWGQTTVTYVSSGSAS 116
 Db 89 LTADKSSSTAYMQLSSLRSEDFAVYFCARD-----YGSYRFPATWGQTLTVTSABSQS 142
 QY 117 APTLPPLVSCNSPSTSSVAVGCLAQDPLPDSITFSWKYKNSD-ISTRGFPSPVLRGG 175
 Db 143 FNVFPLVSCSPSLSDKNLVAMGCLARDPLPDSITFSWYQNAEVIQIRFTFPLRTGG 202
 QY 176 KYAATSOVLPLPSKDVMOGTDHVKV 199
 Db 203 KYLATSOVLPLPSKLSLEGSDYLIV 226
 RESULT 12
 QN030 PRELIMINARY; PRT; 518 AA.
 ID Q6N030
 AC Q6N030;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686i15212.

GN Name=DKFZp686i15212;
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human cDNA Consortium;
 RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
 RA Mewes H.W., Weil B., Amlid C., Osanger A., Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640724; CAE45841.1; --
 DR HSSP; P01861; 1ADQ.
 DR InterPro; IPR000005; HTHARAC.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF07654; CI-set; 3.
 DR SMART; SM00409; IG; 3.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00041; HTH ARAC_FAMILY_1; UNKNOWN_1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 518 AA; 57019 MW; 93B5F98613BF6382 CRC64;
 Query Match 51.7%; Score 544.5; DB 2; Length 518;
 Best Local Similarity 55.5%; Pred. No. 1.1e-40;
 Matches 111; Conservative 30; Mismatches 50; Indels 9; Gaps 6;
 QY 1 EVKKGASVKVSKASGYFTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 60
 Db 29 EVKKGASVKVSKASGYFTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQRTV 88
 QY 61 MTRNTSISTAYMELSSLRSEDFAVYVCARE--EMLVRYGMDVWGQTTVTYVSSGSASAP 118
 Db 89 ITRDTWTTTAYMDLSSLRSEDFAVYWCARDAPQGVTTTY-FDYWGQGLTVTVSSASTKGP 147
 QY 119 TLPVLVSCNSPSTSSVAVGCLAQDPLPDSITFSWKYKNSDISSTRGFPSPVLR-GGKY 177
 Db 148 SVFPLAPCSRSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLY 204
 QY 178 AATSOVLPLPSKDVMOGTDH 197
 Db 205 SLSSVTVPSSSL--GTQTY 222
 RESULT 13
 QN030 PRELIMINARY; PRT; 497 AA.
 ID Q8WY24
 AC Q8WY24;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE SMC66 protein.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng S., Shao X., Cao J., Geng L., Fang Y., Dong Q.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF283666; AAL36987.1; --
 DR HSSP; P01876; 1OWO.
 DR Pfam; PF07654; CI-set; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

```
SQ SEQUENCE 497 AA; 53665 MW; F24D08DFA5A663E5 CRC64;
Query Match 49.2%; Score 518.5; DB 2; Length 497;
Best Local Similarity 52.5%; Pred. No. 2.4e-38; Indels 15; Gaps 6;
Matches 106; Conservative 25; Mismatches 56;
Qy 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNGTGYAQKFGQGRVT 60
Db 29 EVTPFGASVKVSKASGYTFTSYDINWVRQAPGGQGLEWMGMNPNQGTGNTPEAQKFGQRLT 88
Qy 61 MTRNTSISTAYMELSSLRSEDTAVYICAREBWLVR-----YGMVDVWGQTTVTSSGS 114
Db 89 FSRDTSINTAYMVLSSLTSDSAIYFCARGN--LRGGRGFGYNFDPFMWGHGTLVTSSAS 146
Qy 115 ASAPTLPVSCNSPDSSTSVAVGCLAQDFLP--DSITFSWKYKNNSDISSTRGFP--SV 171
Db 147 PTNPKVPLSLCSCTQPD--GNVVIACLVQGFPOEPLSVTWSGQG--VTARNFPSPQD 202
Qy 172 LRGGKYAATSQVLLPSKDVMOG 193
Db 203 ASGDLTYTSSQLTLPATQCLAG 224

RESULT 14
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
DT 01-OCT-2003 (TremBrel. 25, Created)
DT 01-OCT-2003 (TremBrel. 25, Last sequence update)
DT 01-MAR-2004 (TremBrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_Like; 4.
```

```
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;
Query Match 48.6%; Score 512.5; DB 2; Length 469;
Best Local Similarity 52.0%; Pred. No. 7.7e-39; Indels 7; Gaps 5;
Matches 103; Conservative 34; Mismatches 54;
Qy 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGMNPNNGTGYAQKFGQGRVT 60
Db 29 EVKPGASVKVSKASGYTFTSYDINWVRQAPGGQGLEWMGMNPNQGTGNTPEAQKFGQRLT 88
Qy 61 MTRNTSISTAYMELSSLRSEDTAVYICAREBWLVR-----YGMVDVWGQTTVTSSGSAPT 120
Db 89 MTTDTSATTSYMEPRLSLRSDTALFYCATKS--RQVGVDFDSWGQGLTVTVSSASTKGPSV 147
Qy 121 FPLVSCNSPDSSTSVAVGCLAQDFLP--DSITFSWKYKNNSDISSTRGFP--SV 179
Db 148 FPLAPSKSTSG--GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSL 204
Qy 180 TSOVLLPSKDVMOGTDH 197
Db 205 SSVTVFSSSL--GTQTY 220

RESULT 15
Q9BRV0 PRELIMINARY; PRT; 500 AA.
AC Q9BRV0;
DT 01-JUN-2001 (TremBrel. 17, Created)
DT 01-JUN-2001 (TremBrel. 17, Last sequence update)
DT 01-MAR-2004 (TremBrel. 26, Last annotation update)
DE MGC27165 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RX MEDLINE=242388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wortley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickson M.C.,
RA Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Prostate;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005951; AAH05951.1; -.
DR HSSP; P01876; 1OWO.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 2.
DR Pfam; PF00047; IG; 1.
```

```
DR SMART: SM00406; IGv: 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 500 AA; 54154 MW; 0A9BF43F2A3CC6D9 CRC64;

Query Match      48.5%; Score 511; DB 2; Length 500;
Best Local Similarity 51.2%; Pred. No. 1,1e-37;
Matches 104; Conservative 25; Mismatches 60; Indels 14; Gaps 5;

Qy 1 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWGMNPNNGNTGYAQKFQGRVT 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
29 EVMSPGASVRVSKTSGYAFHTYSIIWVRQAPGQGLEWGMWISPSDNTREFAKKFQGRVT 88
Qy 61 MTRNTSISTAYMELSLRSEDYAVYYCAREEWLVR-----YIGMDYWGQGTITVVS 113
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
89 LTDTSTSTVMELSLRSDDTAVYCYARRYSYSSCQNDYIIYYMDYWGKGTITVVS 148
Qy 114 SASAPFLPLVSCNSPDSSTSSVAVGCLAQDFLP--DSITPSWKYKNNSDISSTRGFP--S 170
Db ||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
149 SPTSPKVPFLSLCSTQPD--GNVVIACLIVQGFPOEPLSVTWSESGQG--VTARNFP 204
Qy 171 VLRGGKYAATSQVLLPSKDVMOG 193
Db ||:|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
205 DASGDLTTSSQLTLPATQCLAG 227
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Search completed: March 8, 2005, 06:35:50
Job time : 75.3165 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 92.2618 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-29

Perfect score: 1054

Sequence: 1 EVKKGASVKYVSCRASGYTF.....TSQVLLPSKDVMOGTDEHKV 199

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1990s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1054	100.0	199	2 AAY34302	Aay34302 IgM antib
2	985	93.5	203	2 AAY34301	Aay34301 IgM antib
3	873.5	82.9	588	2 AAW71880	Aaw71880 Anti-huma
4	873.5	82.9	588	3 AAB12917	Aab12917 Anti-huma
5	870	82.5	627	7 ADE97370	Ade97370 Human Imm
6	859.5	81.5	588	2 AAW71881	Aaw71881 Anti-huma
7	859.5	81.5	588	3 AAB12918	Aab12918 Anti-huma
8	803	76.2	266	8 ADF69305	Adf69305 Human lun
9	766.5	72.7	571	8 ADL70776	Adl70776 Chimeric
10	755	71.6	228	8 ADP84970	Adp84970 Anti-TNFA
11	750.5	71.2	223	2 AAY08598	Aay08598 Anti-huma
12	749.5	71.1	595	7 ADM05427	Adm05427 Human pro
13	744.5	70.6	223	8 ADL70773	Adl70773 Anti-TNFA
14	742.5	70.4	596	4 AAM23924	Aam23924 Human EST
15	707.5	67.1	205	2 AAY34299	Aay34299 IgM antib
16	707.5	67.1	533	7 ADB65070	Adb65070 Human pro
17	702	66.6	570	8 ADR19329	Adr19329 Chimeric
18	701.5	66.6	569	8 ADR19330	Adr19330 Chimeric
19	698	66.2	197	2 AAY34300	Aay34300 IgM antib
20	682.5	64.8	202	2 AAY34303	Aay34303 IgM antib
21	673.5	63.9	190	2 AAY34304	Aay34304 IgM antib
22	643	61.0	476	2 AAW88464	Aaw88464 Monoclonal
23	635	60.2	590	2 AAW31751	Aaw31751 H chain s
24	635	60.2	590	2 AAW71888	Aaw71888 Anti-huma
25	635	60.2	590	3 AAB12908	Aab12908 Anti-huma

25	609.5	57.8	228	6 ABR01526	AbR01526 Human ant
26	602.5	57.2	230	6 ABR01514	AbR01514 Human ant
27	600	56.9	470	5 AAD74296	AaU74296 Anti-huma
28	598	56.7	221	6 ABR01537	AbR01537 Human ant
29	594.5	56.4	471	7 ADE28427	Ade28427 Human ant
30	592	56.2	576	8 ADF69325	Adf69325 Human lun
31	592	56.2	576	8 ADP84967	Adp84967 Murine an
32	586	55.6	571	8 ADP84968	Adp84968 Murine an
33	582	55.2	573	8 ADR23348	Adr23348 Human CD7
34	574	54.5	451	8 ADR23350	Adr23350 Human CD7
35	571	54.2	451	8 ADK18814	Adk18814 Anti-huma
36	559.5	53.1	125	7 ADK18864	Adk18864 Anti-huma
37	559.5	53.1	126	7 ADK18595	Adk18595 Anti-huma
38	559.5	53.1	126	7 ADK18777	Adk18777 Anti-huma
39	559.5	53.1	126	7 ADL25408	AdL25408 Human mAb
40	559.5	53.1	126	8 ADK18597	Adk18597 Anti-huma
41	553.5	52.5	126	7 ADK18870	Adk18870 Anti-huma
42	553.5	52.5	126	7 ADK18812	Adk18812 Anti-huma
43	553.5	52.5	126	7 ADK18775	Adk18775 Anti-huma
44	553.5	52.5	126	7 ADL25412	AdL25412 Human mAb
45	553.5	52.5	126	8	

ALIGNMENTS

RESULT 1
AAY34302
ID AAY34302 standard; protein; 199 AA.

XX AAY34302;

XX 19-NOV-1999 (first entry)

XX IgM antibody CEM 10.12 G5 heavy chain sequence.

XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

XX activated B-cell; monocyte; graft versus host disease; therapy; cancer;

XX organ transplant rejection disease; lymphoma; pancreatic disease;

XX autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

XX 03-MAR-1998; 98US-00034607.

XX 03-FEB-1999; 99US-00244253.

XX (ABGE-) ABGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
XX Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX N-PSDB; AAZ20403.

XX New monoclonal antibody, used for treating e.g. graft versus host

XX disease, cancers, autoimmune diseases and inflammatory diseases.

XX Claim 60; Fig 27; 245pp; English.

XX This sequence represents the heavy chain of an antibody of the invention.
XX The antibody is a monoclonal antibody (mAb) with an isotype that fixes
XX complement and a variable region that binds to the epitope on CD147 bound
XX by the IgM mAb ABX-CBL, providing that the antibody is not CBL1. The mAb
XX can selectively kill activated T-cells, activated B-cells or resting or
XX activated monocytes. The products and methods can be used for treating
XX diseases involving activated T-cells or B-cells or monocytes, e.g. graft
XX versus host disease (GVHD), organ transplant rejection diseases (e.g.
XX renal transplant, ocular transplant), cancers (e.g. cancers of the blood

XX WPI: 1998-482965/42.
 DR N-PSDB; AAV61363.
 XX
 PT Production of anti-Fas protein humanised antibodies - for use in inducing
 PT apoptosis on Fas expressing cells in the treatment of auto:immune
 PT diseases, especially rheumatoid arthritis.
 XX
 PS Claim 21; Page 105-107; 187pp; English.
 XX
 CC This is the amino acid sequence of a humanised anti-Fas antibody CH11
 CC heavy chain, designated HmuH. HmuH is based on the heavy chain (see
 CC AAW71889) of murine anti-human Fas monoclonal antibody CH11. The
 CC humanised sequence was designed following selection of donor residues
 CC from CH11 to be grafted onto acceptor molecule 21.28.Cu. 2 Heavy chain
 CC sequences (see AAW71880-81) have been designed, and each can be used in
 CC combination with any of 4 light chain sequences (see AAW71876-79) to
 CC provide novel, claimed humanised CH11 IgM antibodies that lack a J chain.
 CC These humanised anti-human Fas antibodies are capable of inducing
 CC apoptosis in cells expressing Fas (e.g. synoviocytes) and are useful in
 CC the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA
 CC sequences encoding the humanised antibodies are claimed, as are vectors
 CC such as pMuH5-1 including the HmuH nucleotide sequence (see AAV61363),
 CC and host cells such as Escherichia coli pMuH5-1 (FERM BP-5863)
 XX
 SQ Sequence 588 AA;
 Query Match 82.9%; Score 873.5; DB 2; Length 588;
 Best Local Similarity 84.4%; Pred. No. 6.2e-55;
 Matches 168; Conservative 10; Mismatches 16; Indels 5; Gaps 1;
 QY 1 EVKPGASVKVSKCKAGSYFTTSDINWVRQATCGGLEWGWNPNSGNTGYAQKFGQRTV 60
 DB 29 EVKPGASVKVSKCKAGSYFTTSDINWVRQATCGGLEWGWNPNSGNTGYAQKFGKSKAT 88
 QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEMLVRYGMDVWGQGTITVTVSSGSASAPTL 120
 DB 89 LTVDSASTAYMELSLRSEDVAVYCARAEMLVRYGMDVWGQGTITVTVSSGSASAPTL 143
 QY 121 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 180
 DB 144 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 203
 QY 181 SQVLLPSKDVMOGTDHVKV 199
 DB 204 SQVLLPSKDVMOGTDHVV 222
 RESULT 4
 AAB12917
 ID AAB12917 standard; protein; 588 AA.
 XX
 AC AAB12917;
 XX
 DT 16-NOV-2000 (first entry)
 DE
 DE Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #86.
 XX
 KW Antirheumatic agent; immunoglobulin M; IGM; apoptosis inducer;
 KW immunosuppression; autoimmune disease; treatment; rheumatism;
 KW anti-Fas antibody.
 OS
 OS Synthetic.
 PN JP2000154149-A.
 XX
 PD 06-JUN-2000.
 PF 17-SEP-1999; 99JP-00263984.
 PR 18-SEP-1998; 98JP-00264598.
 XX
 PA (SANY) SANKYO CO LTD.

XX WPI: 2000-454476/40.
 DR N-PSDB; AAA78271.
 XX
 PT Anti-human Fas humanizing antibody-containing antirheumatic agents.
 PS Claim 1; Page 75-77; 109pp; Japanese.
 XX
 CC The present invention relates to antirheumatic agents which comprise as
 CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
 CC does not include a J segment, has apoptosis inducing activity, and
 CC consists of a light and heavy chain polypeptide produced synthetically.
 CC The agents of the invention exhibit antirheumatic and immunosuppressive
 CC activity and can be used to treat autoimmune diseases, especially
 CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
 CC binding properties. Included in the invention are nucleotide sequences of
 CC the IgM light and heavy chains (see AAA78267-A78272) and the
 CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
 CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
 CC AAA78202-A78206) and protein sequences (see AAB12908-B12910). Also
 CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
 CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
 CC chains used in the invention are represented by sequences AAA78213-
 CC A78266. Primers used for sequencing the human Ig DNA used in the
 CC invention are represented by sequences AAA78277-A78318 and AAA78335-
 CC A78337, while humanised anti-Fas Ig DNA sequencing primers are
 CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer
 CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in
 CC the production of the agent of the invention
 XX
 SQ Sequence 588 AA;
 Query Match 82.9%; Score 873.5; DB 3; Length 588;
 Best Local Similarity 84.4%; Pred. No. 6.2e-55;
 Matches 168; Conservative 10; Mismatches 16; Indels 5; Gaps 1;
 QY 1 EVKPGASVKVSKCKAGSYFTTSDINWVRQATCGGLEWGWNPNSGNTGYAQKFGQRTV 60
 DB 29 EVKPGASVKVSKCKAGSYFTTSDINWVRQATCGGLEWGWNPNSGNTGYAQKFGKSKAT 88
 QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEMLVRYGMDVWGQGTITVTVSSGSASAPTL 120
 DB 89 LTVDSASTAYMELSLRSEDVAVYCARAEMLVRYGMDVWGQGTITVTVSSGSASAPTL 143
 QY 121 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 180
 DB 144 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAAT 203
 QY 181 SQVLLPSKDVMOGTDHVKV 199
 DB 204 SQVLLPSKDVMOGTDHVV 222
 RESULT 5
 ADE97370
 ID ADE97370 standard; protein; 627 AA.
 XX
 AC ADE97370;
 XX
 DT 12-FEB-2004 (first entry)
 DE
 DE Human immunoadhesin-related protein - SEQ ID 47.
 XX
 KW immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;
 KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;
 KW intercellular adhesion molecule; ICAM-1; human.
 OS
 OS Homo sapiens.
 XX
 PN WO2003064992-A2.
 XX
 PD 07-AUG-2003.
 XX

PF 25-OCT-2002; 2002WO-US034197.
 XX
 PR 26-OCT-2001; 2001US-00047542.
 XX
 XX (PLAN-) PLANET BIOTECHNOLOGY INC.
 PA (LARR/) LARRICK J W.
 XX (WYCO/) WYCOFF K L.
 PI Larrick JW, Wycoff KL;
 XX WPI; 2003-636816/60.
 DR
 XX New immunoadhesin, useful for treating anthrax and rhinovirus, comprises
 PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and
 PT J chain and secretory component associated with the chimeric toxin
 PT receptor protein.
 XX
 XX Disclosure; SEQ ID NO 47; 288pp; English.
 PS
 XX The invention relates to a novel immunoadhesin comprising a chimeric
 CC toxin receptor protein consisting of a toxin receptor protein linked to
 CC at least a portion of an immunoglobulin heavy chain with a J (joining)
 CC chain and secretory component (SC) associated with the chimeric toxin
 CC receptor protein. The immunoadhesin comprises a chimeric bacterial or
 CC viral toxin receptor protein and the immunoadhesin has plant-specific
 CC glycosylation. The immunoadhesin of the invention demonstrates virucide
 CC and antibacterial activities and may be useful for reducing the binding
 CC of a viral or bacterial antigen to a host cell and thus for treating or
 CC preventing anthrax, as well as human rhinovirus infection which results
 CC in the common cold. The current sequence is that of the human
 CC immunoadhesin-related protein of the invention.
 XX
 XX Sequence 627 AA;

Query Match 82.5%; Score 870; DB 7; Length 627;
 Best Local Similarity 82.0%; Pred. No. 1.2e-54;
 Matches 173; Conservative 7; Mismatches 19; Indels 12; Gaps 2;
 QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGTNGVAQKFGGRVT 60
 DB 29 EVKPGSSVKVSKASGTFSSYALSWVRQAPGQGLEWMGGIPIFGTANYAQKFGGRVT 88
 QY 61 MTRNTSISTAYMELSLRSEDFAVYICAR-----BEWLYR-----YGMQVWQGGTIV 108
 DB 89 ITADESTAYMELSLRSEDFAVYICAKTGLGPYSSGWYSPNSDYIYGMQVWQGGTIV 148
 QY 109 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGF 168
 DB 149 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGF 208
 QY 169 PSVLGGKYAATSVQLLPKSDVMQGTDEHKV 199
 DB 209 PSVLGGKYAATSVQLLPKSDVMQGTDEHV 239

RESULT 6
 ID AAW71881
 XX AAW71881 standard; protein; 588 AA.
 AC AAW71881;
 XX
 XX 18-JAN-1999 (first entry)
 DT
 XX Anti-human Fas humanised antibody CH11 heavy chain HmuM.
 XX
 DE Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
 KW autoimmune disease; rheumatoid arthritis; therapy; human;
 KW antibody engineering.
 XX
 XX Homo sapiens.
 OS Synthetic.
 XX
 .FH Key Location/Qualifiers

FT Peptide 1..19
 FT /label= Sig_peptide
 FT Protein 20..588
 FT /label= Mat_protein
 FT Region 50..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1 from CH11
 FT heavy chain"
 FT 69..84
 FT /label= CDR2
 FT /note= "complementarity determining region 2 from CH11
 FT heavy chain"
 FT 118..124
 FT /label= CDR3
 FT /note= "complementarity determining region 3 from CH11
 FT heavy chain"
 FT
 XX EP866131-A2.
 PN
 XX 23-SEP-1998.
 PD
 XX 20-MAR-1998; 98EP-00302113.
 PF
 XX 21-MAR-1997; 97JP-00067938.
 PR
 XX (SANY) SANKYO CO LTD.
 PA
 PI Serizawa N, Haruyama H, Takahaei T, Nakahara K, Yonehara S;
 XX WPI; 1998-482965/42.
 DR N-PSDB; AAV61364.
 DR
 XX Production of anti-Fas protein humanised antibodies - for use in inducing
 PT apoptosis on Fas expressing cells in the treatment of auto-immune
 PT diseases, especially rheumatoid arthritis.
 PT
 XX Claim 22; Page 111-113; 187pp; English.
 PS
 XX This is the amino acid sequence of a humanised anti-Fas antibody CH11
 CC heavy chain, designated HmuM. HmuM is based on the heavy chain (see
 CC AAW71888) of murine anti-human Fas monoclonal antibody CH11. The
 CC humanised sequence was designed following selection of donor residues
 CC from CH11 to be grafted onto acceptor molecule 21.28'Cl. 2 Heavy chain
 CC sequences (see AAW71880-81) have been designed, and each can be used in
 CC combination with any of 4 light chain sequences (see AAW71876-79) to
 CC provide novel, claimed humanised CH11 IGM antibodies that lack a J chain.
 CC These humanised anti-human Fas antibodies are capable of inducing
 CC apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in
 CC the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA
 CC sequences encoding the humanised antibodies are claimed, as are vectors
 CC such as pHmuM1-1 including the HmuM nucleotide sequence (see AAV61364),
 CC and host cells such as Escherichia coli pHmuM1-1 (FERM BP-5864)
 XX
 SQ Sequence 588 AA;

Query Match 81.5%; Score 859.5; DB 2; Length 588;
 Best Local Similarity 82.9%; Pred. No. 6.4e-54;
 Matches 165; Conservative 12; Mismatches 17; Indels 5; Gaps 1;
 QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNNGTNGVAQKFGGRVT 60
 DB 29 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGGIPIFGTANYAQKFGGRVT 88
 QY 61 MTRNTSISTAYMELSLRSEDFAVYICAREEVLVYGYGMDVMQGTFTTVSSGSASAPTL 120
 DB 89 LTVDSASTAYMELSLRSEDFAVYICARS-----YYAMDYMGQGTFTTVSSGSASAPTL 143
 QY 121 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAAT 180
 DB 144 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAAT 203
 QY 181 SQVLLPSKDVMOGTDEHKV 199
 |||||


```
Db      204 SQVLLPSKDVMOGTDEHVV 222
RESULT 7
ID      AAB12918
AA      AAB12918 standard; protein; 588 AA.
XX
XX      AAB12918;
AC
DT      16-NOV-2000 (first entry)
XX
XX      Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #88.
DE
DE      Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW      immunosuppression; autoimmune disease; treatment; rheumatism;
KW      anti-Fas antibody.
XX
XX      Synthetic.
OS
XX      JP2000154149-A.
FN
XX      06-JUN-2000.
PD
PD      17-SEP-1999; 99JP-00263984.
PF
XX      18-SEP-1998; 98JP-00264598.
PR
XX      (SANY ) SANKYO CO LTD.
PA
XX      WPI; 2000-454476/40.
DR      N-PSDB; AAB78272.
XX
XX      Anti-human Fas humanizing antibody-containing antirheumatic agents.
FT
XX      Claim 1; Page 80-81; 109pp; Japanese.
XX
XX      The present invention relates to antirheumatic agents which comprise as
CC      active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC      does not include a J segment, has apoptosis inducing activity, and
CC      consists of a light and heavy chain polypeptide produced synthetically.
CC      The agents of the invention exhibit antirheumatic and immunosuppressive
CC      activity and can be used to treat autoimmune diseases, especially
CC      rheumatism. The IgM molecule used in the invention has human Fas antigen
CC      binding properties. Included in the invention are nucleotide sequences of
CC      the IgM light and heavy chains (see AAB78267-A78272) and the
CC      corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC      nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC      AAB78202-A78206) and protein sequences (see AAB12908-B12910). Also
CC      included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC      Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC      chains used in the invention are represented by sequences AAB78213-
CC      A78266. Primers used for sequencing the human Ig DNA used in the
CC      invention are represented by sequences AAB78277-A78318 and AAB78335-
CC      A78337, while humanised anti-Fas Ig DNA sequencing primers are
CC      represented by sequences AAB78321-A78334 and AAB78338-A78367. Primer
CC      sequences AAB78207-A78212 are specific for murine Ig DNA, and are used in
CC      the production of the agent of the invention
XX      Sequence 588 AA;
SQ
Query Match      81.5%; Score 859.5; DB 3; Length 588;
Best Local Similarity 82.9%; Pred. No. 6.4e-54;
Matches 165; Conservative 12; Mismatches 17; Indels 5; Gaps 1;

QY      1 EVKPGASVKYCKASGYTFTSYDINWVROATGCGLEWGMWNPNSGNTGYAQKFGQRYT 60
Db      29 EVKPGASVKYCKASGYTFTSYDINWVROATGCGLEWGMWNPNSGNTGYAQKFGKAT 88
QY      61 MTRNTSISTAYMELSLRSEDTAVYICAREEWLVRYGYMDVMOGTITTVSSGSASAPTL 120
Db      89 LTVDSASTAYMELSLRSEDTAVYICARS-----YYANDYDYGQGTITTVSSGSASAPTL 143
QY      121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLRGGKYAAT 180

Db      144 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFVLRGGKYAAT 203
QY      181 SQVLLPSKDVMOGTDEHVK 199
Db      204 SQVLLPSKDVMOGTDEHVV 222
RESULT 8
ADF69305
ID      ADF69305 standard; protein; 266 AA.
XX
XX      ADF69305;
AC
DT      26-FEB-2004 (first entry)
XX
XX      Human lung specific protein sequence SEQ ID NO:62.
DE
DE      human; lung specific nucleic acid; lung specific protein; lung cancer;
KW      cytostatic; gene therapy.
XX
XX      Homo sapiens.
OS
XX      WO2003102137-A2.
FN
XX      11-DEC-2003.
PD
PD      30-MAY-2003; 2003WO-US016810.
PF
XX      31-MAY-2002; 2002US-0385301P.
PR
XX      (DIAD-) DIADEXUS INC.
PA
XX      Chen S, Macina RA, Sun Y, Liu C, Turner LR;
PI      WPI; 2004-053457/05.
XX
XX      New human lung specific nucleic acid, useful for preparing a composition
FT      for diagnosing or treating lung cancer.
PT
XX      Claim 11; SEQ ID NO 62; 221pp; English.
XX
XX      The present invention describes a human lung specific nucleic acid
CC      molecule. Also described: (1) a method for determining the presence of a
CC      lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising
CC      the nucleic acid molecule; (3) a host cell comprising the vector; (4) a
CC      method for producing a polypeptide encoded by the nucleic acid molecule;
CC      (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody
CC      or its fragment that specifically binds to the polypeptide; (7) a method
CC      for determining the presence of a lung specific protein in a sample; (8)
CC      a method for diagnosing and monitoring the presence and metastases of
CC      lung cancer in a patient; (9) a kit for detecting a risk of cancer or
CC      presence of cancer in a patient comprising a means for determining the
CC      presence the nucleic acid molecule or polypeptide in a sample of a
CC      patient; (10) a method of treating a patient with lung cancer; and (11) a
CC      vaccine comprising the polypeptide or the nucleic acid encoding the
CC      polypeptide. Human LSNA molecules and related proteins have cytostatic
CC      activity, and can be used in gene therapy. They are useful for preparing
CC      a composition for diagnosing or treating lung cancer. The present
CC      sequence represents a human lung specific protein, which is used in the
CC      exemplification of the present invention.
XX      Sequence 266 AA;
SQ
Query Match      76.2%; Score 803; DB 8; Length 266;
Best Local Similarity 76.9%; Pred. No. 3.4e-50;
Matches 153; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY      1 EVKPGASVKYCKASGYTFTSYDINWVROATGCGLEWGMWNPNSGNTGYAQKFGQRYT 60
Db      21 EVKPGESLKLCKSGSGYSFTSYWIGVROQMPGKLEWNGIYPGDSIDTRYSPFQGGY 80
QY      61 MTRNTSISTAYMELSLRSEDTAVYICAREEWLVRYGYMDVMOGTITTVSSGSASAPTL 120
```

Db 81 ISADKSTSTAYLQWSSLSKASDTAMVYCARPTAVAGHYFYDVMGQGLTVTVSSGSASAPTL 140
Qy 121 FPLVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSRGPSPVLRGGKYAAT 180
Db 141 FPLVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSRGPSPVLRGGKYAAT 200
Qy 181 SQVLLPSKDVMOGTDDEHKV 199
Db 201 SQVLLPSKDVMOGTDDEHV 219

RESULT 9
ADP84970
ID ADP84970 standard; protein; 571 AA.
XX
AC ADP84970;
XX
DT 09-SEP-2004 (first entry)
XX
DE Chimeric antibody cIGM-Kar04.
XX
KW antibody; Core-1 antigen; framework region; immunoglobulin superfamily;
KW protease inhibitor; lectin; helix-bundle protein; lipocalin;
KW variable heavy chain; VH; variable light chain; VL; vaccine; diagnosis;
KW alleviation; treatment; tumour; breast; colon; stomach; pancreas;
KW large/small intestine; ovary; cervix; lung; prostate; kidney; liver;
KW metastasis.
XX
OS Mus musculus.
XX
FN WO2004050707-A2.
XX
PD 17-JUN-2004.
XX
PF 01-DEC-2003; 2003WO-DE003994.
XX
PR 29-NOV-2002; 2002DE-01056900.
XX
PA (NEMO-) NEMOD BIOTHERAPEUTICS GMBH & CO KG.
XX
PI Goletz S, Danielczyk A, Karsten U, Ravn P, Stahn R;
PI Christensen PA;
XX
XX WPI; 2004-461095/43.
XX
PT New recognition molecules, e.g. antibodies (and nucleic acids) that bind
PT specifically to Core-1 antigens, useful for diagnosis, treatment and
PT prevention of tumors and metastases.
XX
PS Claim 26; SEQ ID NO 112; 136pp; German.
XX

CC This invention describes novel recognition molecules, especially
CC antibodies that bind specifically to the Core-1 antigen. The recognition
CC molecules are used to make constructs containing the framework regions
CC that separate, include and/or flank the specified sequences, especially
CC where the framework regions are from the immunoglobulin (Ig) superfamily,
CC protease inhibitors, lectins, helix-bundle proteins and/or lipocalins.
CC Most especially the framework regions are from antibodies, particularly
CC the variable heavy chain (VH) and the variable light chain (VL) of human
CC and/or murine origin. The constructs may also include a His or myc tag, a
CC lysine-rich region and/or a multimerisation domain, most particularly it
CC is a single-chain antibody fragment, multibody, Fab fragment, fusion
CC protein of an antibody fragment with peptide or protein, and/or an Ig of
CC types G, M, A, E or D and/or their subclasses. It may be human,
CC humanised, murine or chimeric, e.g. IgM without the J chain. The
CC additional sequences/structures in the constructs are Ig domains of
CC various species, interacting or stabilising domains, signal sequences,
CC fluorescent dyes, toxins, antibodies with catalytic activity or other
CC specificities, cytolytic agents, enzymes, immuno-modulators or -
CC effectors, MHC molecules, antigens, chelators for radioactive labels,
CC liposomes, transmembrane domains, viruses and/or cells, specifically
CC macrophages. The antibodies, also constructs containing them, nucleic

CC acid encoding them, and related vectors and host cells, are useful for
CC prevention (e.g. as vaccine), diagnosis, alleviation, treatment,
CC monitoring and/or secondary treatment of tumours (specifically of breast,
CC colon, stomach, pancreas, large/small intestine, ovary, cervix, lung,
CC prostate, kidney and/or liver) and/or metastases (particularly to liver),
CC specifically where these are positive for the CI antigen. The products of
CC the invention provide simple, reliable and efficient detection of
CC tumours. They are specific for carcinoma and show almost no binding to
CC healthy tissue.
XX
SQ Sequence 571 AA;

Query Match 72.7%; Score 766.5; DB 8; Length 571;
Best Local Similarity 74.0%; Pred. No. 3.2e-47;
Matches 151; Conservative 16; Mismatches 24; Indels 13; Gaps 3;
Qy 1 EVKKPGASVKYCKASGYTPTSYDINWVROATGQGLEWMGNPNPNSGNTGYAQKFGQRTV 60
Db 10 ELVRPGTSVKISCKASGYTFYTNWLGWVKQRPQGHLEWIGDIYPGGGTYNNEKFGKAT 69
Qy 61 MTRNTSISTAYMELSSLRSEDTAVVYCARAEWLVRYYG-----MDVMGQGITTVTVSSGSA 115
Db 70 LTADTSSSTAMQQLSSLTSEDSAVYFCA-----YYDAAGPWFAYWGQITTVTV-SGSA 121
Qy 116 SAPTLFPLVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSRGPSPVLRGG 175
Db 122 SAPTLFPLVSCENSPDSTSSVAVGCLAQDFLPDSITLSWKYKNNSDISSRGPSPVLRGG 181
Qy 176 KYATTSQVLLPSKDVMOGTDDEHKV 199
Db 182 KYAATTSQVLLPSKDVMOGTDDEHV 205

RESULT 10
ADL70776
ID ADL70776 standard; protein; 228 AA.
XX
AC ADL70776;
XX
DT 03-JUN-2004 (first entry)
XX
DE Anti-TNFalpha antibody VH region, SEQ ID 49.
XX
KW Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;
KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;
KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnerary;
KW Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antiatherosclerotic;
KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFalpha;
KW antibody; VH region.
XX
OS Unidentified.
XX
FN WO2004020588-A2.
XX
PD 11-MAR-2004.
XX
PF 28-AUG-2003; 2003WO-US026779.
XX
PR 30-AUG-2002; 2002US-0406977P.
PR 10-MAR-2003; 2003US-00384060.
PR 09-JUL-2003; 2003US-0485404P.
XX
PA (BIOR-) BIOREXIS PHARM CORP.
XX
PI Prior CP, Turner AJ, Sadeghi H;
XX
XX WPI; 2004-239175/22.
XX
PT Novel library containing several fusion proteins each of which comprises
PT first transferrin polypeptide fused to at least one second peptide,
PT useful for screening for transferrin fusion protein having the particular
PT activity.

XX Example 8; SEQ ID NO 49; 243pp; English.

XX The present invention relates to a library (I) of modified fusion

CC proteins of transferrin (Tf) and therapeutic proteins with increased

CC serum half-life or serum stability. Preferred fusion proteins include

CC those modified so that the Tf moiety exhibits no or reduced

CC glycosylation, iron binding and/or Tf receptor binding. The transferrin

CC fusion proteins are useful for treating, preventing or ameliorating

CC disorders or diseases of endocrine system, nervous system, immune system,

CC respiratory system, cardiovascular system, diseases and/or disorders

CC relating to cell proliferation, and/or diseases or disorders relating to

CC blood. The modified fusion proteins are useful in diagnosis, prognosis,

CC prevention and/or treatment of autoimmune disorders, diseases and

CC disorders of haematopoietic cells (e.g., leucopenia, neutropenia, anaemia

CC and thrombocytopenia); allergic reactions such as allergic rhinitis and

CC anaphylaxis, IgE-mediated allergic reactions such as asthma, asthma and

CC eczema; inflammatory conditions e.g., inflammation associated with

CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,

CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders

CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel

CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders

CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative

CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The

CC fusion protein is also useful as an adjuvant to enhance antibacterial or

CC antifungal immune responses, antiparasitic immune responses, etc. The

CC fusion protein is also useful for treating monoclonal gammopathy of

CC undetermined significance (MGUS), Waldenstrom's disease, plasmacytomas,

CC adult respiratory distress syndrome, for stimulating wound repair, for

CC preventing or treating infections of joints, bones, skin, etc. The fusion

CC protein is also useful for treating or preventing thrombosis, myocardial

CC infarction, cancers, thrombocytopenia, sickle cell anaemia,

CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,

CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf

CC and a specific example of a SCA that can be fused to Tf is anti-tumour

CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence

CC from an anti-TNFalpha antibody.

XX

XX Sequence 228 AA;

Query Match 71.6%; Score 755; DB 8; Length 228;

Best Local Similarity 72.4%; Pred. No. 8.4e-47;

Matches 144; Conservative 27; Mismatches 24; Indels 4; Gaps 2;

QY 4 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNGNTGYAQKQGRVTMTR 63

DB 13 QFGSLRLSCAASGFTFTSYVNWVRQAPGKGLEWVSGISGGGTYIYADSVKGRFTISR 72

QY 64 NTSISTAYMELSLRSEDVAVYICAREEWLVRYG---MDVWQGGTTVTVSSGSASAPTL 120

DB 73 DNSMNTLYLQMNLSRAEDTAVYICAK-DLSNRLSLGGGTFDIWQGGTTVTVSSGSASAPTL 131

QY 121 PFLVSCNSPSTSSVAVGCLAQDFLPDSITTSWKYKNNSDISSTRGPPSVLRGGKYAAT 180

DB 132 PFLVSCNSPSTSSVAVGCLAQDFLPDSITTSWKYKNNSDISSTRGPPSVLRGGKYAAT 191

QY 181 SQVLLPSKDVMOGTDDEHKV 199

DB 192 SQVLLPSKDVMOGTDDEHV 210

RESULT 11

AAV08598

ID AAV08598 standard; protein; 223 AA.

XX

AC AAV08598;

XX

XX 05-AUG-1999 (first entry)

DE

DE Anti-human TNF-alpha monoclonal antibody H-chain protein.

XX

XX Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;

KW tumour necrosis factor; light chain; L chain.

XX OS Homo sapiens.

XX JP11127855-A.

PN

PD 18-MAY-1999.

XX

PF 27-OCT-1997; 97JP-00293994.

XX

PR 27-OCT-1997; 97JP-00293994.

XX

PA (NIHA) JAPAN ENERGY CORP.

XX

XX WPI; 1999-350318/30.

DR N-PSDB; AAX77407.

XX

PT Recombinant anti-human TNF-alpha human monoclonal antibody - produced

PT stably with a high purity, and in large amounts.

XX

PS Claim 3; Page 12-13; 22pp; Japanese.

XX

CC This invention describes novel recombinant anti-human TNF-alpha human

CC monoclonal antibody consisting of a heavy (H) chain and a light (L)

CC chain. The recombinant anti-human TNF-alpha human monoclonal antibody can

CC be produced stably in a high purity and in a large amount

XX

XX Sequence 223 AA;

Query Match 71.2%; Score 750.5; DB 2; Length 223;

Best Local Similarity 71.7%; Pred. No. 1.7e-46;

Matches 142; Conservative 28; Mismatches 25; Indels 3; Gaps 1;

QY 2 VKKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGMNPNNGNTGYAQKQGRVTM 61

DB 11 VVQPGSLRLSCAASGFTFTSYVGMHWVRQAPGKGLEWVAVISYDGSNKKYIADSVKGRFTI 70

QY 62 TRNTSISTAYMELSLRSEDVAVYICAREEWLVRYGMDVWQGGTTVTVSSGSASAPTLF 121

DB 71 SRDMSKNTLYLQMNLSRAEDTAVYICAKDSDGLAF---DIWQGGTMVTVSSGSASAPTLF 127

QY 122 PFLVSCNSPSTSSVAVGCLAQDFLPDSITTSWKYKNNSDISSTRGPPSVLRGGKYAATS 181

DB 128 PFLVSCNSPSTSSVAVGCLAQDFLPDSITTSWKYKNNSDISSTRGPPSVLRGGKYAATS 187

QY 182 QVLLPSKDVMOGTDDEHKV 199

DB 188 QVLLPSKDVMOGTDDEHV 205

RESULT 12

ADM05427

ID ADM05427 standard; protein; 595 AA.

XX

AC ADM05427;

XX

XX 20-MAY-2004 (first entry)

DT

DE Human protein of the invention SEQ ID NO:4112.

XX

XX human; gene therapy; diagnostic marker; pharmaceutical.

XX

OS Homo sapiens.

XX

PN EP1347046-A1.

XX

PD 24-SEP-2003.

XX

XX 12-APR-2002; 2002EP-00008400.

PF

XX

PR 22-MAR-2002; 2002JP-00137785.

XX

XX (REAS-) RES ASSOC BIOTECHNOLOGY.

XX

PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hiro Y, Otsuka K, Nagai K, Irle R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahara K, Masuo Y;
XX
DR WPI; 2003-723558/69.
DR N-PSDB; ADM02984.
XX
PT New polynucleotides and polypeptides are useful in gene therapy, for
PT developing a diagnostic marker or medicines for regulating their
PT expression and activity, or as a target of gene therapy.

XX PS Claim 1; SEQ ID NO 4112; 305pp; English.
XX

CC The invention relates to a novel human polynucleotide and the encoded
CC polypeptide. A polynucleotide of the invention may have a use in gene
CC therapy. An oligonucleotide of the invention ADM06203-ADM06773 is useful
CC as a primer for synthesizing the polynucleotide or as a probe for
CC detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are
CC useful in gene therapy, for developing a diagnostic marker or medicines
CC for regulating their expression and activity, or as a target of gene
CC therapy. The proteins ADM03759-ADM06201 encoded by the polynucleotides
CC are useful as pharmaceutical agents. The present sequence represents a
CC protein sequence of the invention.

XX SQ Sequence 595 AA;

Query Match 71.1%; Score 749.5; DB 7; Length 595;
Best Local Similarity 71.6%; Pred. No. 5.7e-46;
Matches 141; Conservative 29; Mismatches 26; Indels 1; Gaps 1

OY 4 KPQASVKVCKAGYTTSVDINWVRQTGGGLEWMGMNPNNGTVAQKFGQRVTMTTR 63
Db :|:::||:|::||::||::||::||::||::||::||::||::||::||::||:
33 QPGGSLRLSCAASGFTSFNFAMHWVRQAPEGKLEGVSTISSNGRQKYGESVKGRFTISR 92

OY 64 NTISITAYMELSSLRSEDTAVYYCAREEWLVRY-YGMDVMQGCTTVTVSSGSASAPTLFP 122
Db :|:::||:~::~||::||::||::||::||::||::||::||::||::||:
93 DSKNTLFLQMSLRSDTAIVYCARGHSIDNYHGYDVMVGQGTTVTVSSGSASAPTLFP 152

OY 123 LVSCNSPSPDTSVVAVGLAQDFLPDSITFSWKYNKNSDISSTRGFPSVLRGKKYAATSQ 182
Db ||||||||||||||||||||||||||||||||||||||||||||||||||
153 LVSCNSPSPDTSVVAVGLAQDFLPDSITFSWKYNKNSDISSTRGFPSVLRGKKYAATSQ 212

OY 183 VLLPSKDVMQGTDEHKV 199
Db |||||||||||||||

Dbl 213 VLLPSKDVMQGTDEHV 229

RESULT 13
ADL70773
ID ADL70773 standard; protein; 223 AA.
XX
AC ADL70773;
XT
DT 03-JUN-2004 (first entry)
XX
DE Anti-TNFalpha antibody VH region, SEQ ID 46.
XX

KW Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;
KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;
KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnerary;
KW Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antiatherosclerotic;
KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
KW Tf; transferlin fusion protein; Tf fusion protein; anti-TNFalpha;
KW antibody, VH region.
XX Unidentified.
OS
XX WC2004020588-A2.
PN
PD 11-MAR-2004.
XX
PF 28-AUG-2003; 2003WO-USO26779.
XX

```
RESULT 14
AAM23924
ID AAM23924 standard; protein; 596 AA.
XX
AC AAM23924;
XX
DT 12-OCT-2001 (first entry)
XX
DE Human EST encoded protein SEQ ID NO: 1449.
XX
KW Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
KW tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
KW diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
KW gene therapy; nutrition.
XX
OS Homo sapiens.
XX
PN WO200154477-A2.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-US002687.
XX
PR 25-JAN-2000; 2000US-00491404.
PR 17-JUL-2000; 2000US-00617746.
PR 03-AUG-2000; 2000US-00631451.
PR 15-SEP-2000; 2000US-00663870.
XX
PA (HYSE-) HYSEQ INC.
XX
Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX
DR WPI; 2001-476164/51.
DR N-PSDB; AAM98583.
XX
Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
PS Claim 20; Page 1011-1012; 1275pp; English.
XX
CC The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
Sequence 596 AA;
Query Match 70.4%; Score 742.5; DB 4; Length 596;
Best Local Similarity 71.4%; Pred. No. 1.8e-45;
Matches 142; Conservative 25; Mismatches 29; Indels 3; Gaps 1;
QY 4 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMNPNNGTGYAQKFGQRTVMT 63
DB 32 QPGSURLSCASGFTFSYWMHWVQAPQKGLVWVSRINTDGSSTSYADSVKGRFTISR 91
QY 64 NTSISTAYMELSLRSEDATVYYCAR--YYGMDVMGQGTVTTVSSGSASAPTL 120
DB 92 DNAKNTLYLQMSLRAEDTAVYYCARADNCSSFTSCYKCPDYMGQGLTVTVSSGSASAPTL 151
QY 121 PFLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFFSVLRGGKYAT 180
DB 152 PFLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFFSVLRGGKYAT 211
QY 181 SQVLLPSKDVMOGTDEHKV 199
DB 212 SQVLLPSKDVMOGTDEHV 230
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```
RESULT 15
AAY34299
ID AAY34299 standard; protein; 205 AA.
XX
AC AAY34299;
XX
DT 19-NOV-1999 (first entry)
XX
DE IgM antibody CEM 10.1 C3 heavy chain sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 150
FT /label= unknown
FT /note= "encoded by TYC"
XX
PN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VB, Lipani JA, Liu Q, Weber RP, Yang X;
XX
DR WPI; 1999-540816/45.
DR N-PSDB; AAZ20400.
XX
New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 60; Fig 24; 245pp; English.
XX
CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
Sequence 205 AA;
Query Match 67.1%; Score 707.5; DB 2; Length 205;
Best Local Similarity 70.7%; Pred. No. 2e-43;
Matches 140; Conservative 23; Mismatches 32; Indels 3; Gaps 2;
QY 4 KPGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMNPNNGTGYAQKFGQRTVMT 63
DB 4 KSETLSLTCVYGGSGFGYYSWIRQPPKGLWLGIBIN-HSGSTNYNPSLSKRTISV 62
QY 64 NTSISTAYMELSLRSEDATVYYCAR--EEWLVRYGMDVMGQGTVTTVSSGSASAPTL 121
DB 63 DTSKNQPSLKLSSVTAADTAVYYCARGTTEYYYYYGMVDMVGQGTVTTVSSGSASAPTL 122
QY 122 PFLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFFSVLRGGKYAATS 181
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Db 123 PLVSCENSPDTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPSVLRGGKYAATS 182
Qy 182 QVLLPSKDVMOGTDEHKV 199
Db 183 QVLLPSKDVMOGTDEHV 200

Search completed: March 8, 2005, 06:17:12
Job time : 93.2618 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 105.604 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-29

Perfect score: 1054

Sequence: 1 EVKPGASVKVSKASGYTF.....TSQVLLPSKDVNQGTDEHKV 199

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCT05_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	82.5	627	13	US-10-047-542-47 Sequence 47, Appl
2	749.5	71.1	595	15	US-10-108-260A-4112 Sequence 4112, Ap
3	707.5	67.1	533	15	US-10-104-047-3224 Sequence 3224, Ap
4	643	61.0	476	9	US-09-747-669-3 Sequence 3, Appli
5	643	61.0	476	14	US-10-290-703-3 Sequence 3, Appli
6	609.5	57.8	228	16	US-10-128-520-163 Sequence 163, App
7	602.5	57.2	230	16	US-10-128-520-151 Sequence 151, App
8	600	56.9	470	9	US-09-859-053-28 Sequence 28, Appl
9	600	56.9	470	16	US-10-625-105-28 Sequence 28, Appl
10	598	56.7	221	16	US-10-128-520-174 Sequence 174, App
11	594.5	56.4	471	15	US-10-292-088-45 Sequence 46, Appl
12	559.5	53.1	125	14	US-10-041-860-238 Sequence 238, Appl
13	559.5	53.1	126	14	US-10-041-860-19 Sequence 19, Appl

14	559.5	53.1	126	14	US-10-041-860-201 Sequence 201, App
15	559.5	53.1	126	14	US-10-041-860-288 Sequence 288, App
16	559.5	53.1	126	16	US-10-665-383-18 Sequence 18, Appl
17	559	53.0	448	9	US-09-917-410-6 Sequence 6, Appli
18	553.5	52.5	126	14	US-10-041-860-21 Sequence 21, Appl
19	553.5	52.5	126	14	US-10-041-860-199 Sequence 199, App
20	553.5	52.5	126	14	US-10-041-860-236 Sequence 236, App
21	553.5	52.5	126	14	US-10-041-860-294 Sequence 294, App
22	553.5	52.5	126	16	US-10-665-383-22 Sequence 22, Appl
23	549.5	52.1	126	14	US-10-041-860-40 Sequence 40, Appl
24	549.5	52.1	126	14	US-10-041-860-204 Sequence 204, App
25	549.5	52.1	126	14	US-10-041-860-241 Sequence 241, App
26	549.5	52.1	126	14	US-10-041-860-349 Sequence 349, App
27	549.5	52.1	126	16	US-10-665-383-58 Sequence 58, Appl
28	549	52.1	125	14	US-10-041-860-38 Sequence 38, Appl
29	549	52.1	125	14	US-10-041-860-203 Sequence 203, App
30	549	52.1	125	14	US-10-041-860-240 Sequence 240, App
31	549	52.1	125	14	US-10-041-860-343 Sequence 343, App
32	549	52.1	125	16	US-10-665-383-54 Sequence 54, Appl
33	546.5	51.9	122	14	US-10-269-805-61 Sequence 61, Appl
34	545.5	51.8	230	10	US-09-791-153A-53 Sequence 53, Appl
35	545.5	51.8	230	10	US-09-791-153A-55 Sequence 55, Appl
36	545	51.7	470	14	US-10-216-484-157 Sequence 157, App
37	545	51.7	470	14	US-10-384-933-157 Sequence 157, App
38	544.5	51.7	461	9	US-09-249-011A-24 Sequence 24, Appl
39	544.5	51.7	1052	17	US-10-856-272-21 Sequence 21, Appl
40	544.5	51.7	1342	17	US-10-856-272-14 Sequence 14, Appl
41	543.5	51.6	126	14	US-10-041-860-37 Sequence 37, Appl
42	543.5	51.6	126	14	US-10-041-860-202 Sequence 202, App
43	543.5	51.6	126	14	US-10-041-860-239 Sequence 239, App
44	543.5	51.6	126	16	US-10-665-383-74 Sequence 74, Appl
45	543.5	51.6	220	16	US-10-128-520-175 Sequence 175, App

ALIGNMENTS

RESULT 1

US-10-047-542-47
; Sequence 47, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIPI
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-47

Query Match 82.5%; Score 870; DB 13; Length 627;
Best Local Similarity 82.0%; Pred. No. 3.6e-56;
Matches 173; Conservative 7; Mismatches 19; Indels 12; Gaps 2;

QY 1 EVKPGASVKVSKASGYTFSTYDINWRQATCGGLEWGNWNPNSGVTGYAQKFGQRTV 60
DB 29 EVKPGSSVKVSKASGSGTTFSSYAISSWRQAPGQLEWNGGIPIFGTANYAQKFGQRTV 88
QY 61 MTRNTSISTAYMELSSLRSEDTAVVYCAR-----BEWLVK-----YGMVDVWGQGTIV 108
DB 89 ITADESTSTAYMELSSLRSEDTAVVYCAKTKTGILGPYSSGWNPNDSYVYGMVDVWGQGTIV 148

Qy 109 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGF 168
Db 149 TVSSGSASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGF 208
Qy 169 PSVLGGKYAATSOVLLPSKQVMQGTDEHKV 199
Db 209 PSVLGGKYAATSOVLLPSKQVMQGTDEHV 239

RESULT 2
US-10-108-260A-4112
; Sequence 4112, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: H1-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4112
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4112

Query Match 71.1%; Score 749.5; DB 15; Length 595;
Best Local Similarity 71.6%; Pred. No. 2.6e-47;
Matches 141; Conservative 29; Mismatches 26; Indels 1; Gaps 1;

Qy 4 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMNPNNGTGYAQKFGQRTVTR 63
Db 33 QPGSRLRLSCAASGTFPSFMHWVRQAPGKGLVYSIISNGRQKYGESVKGRTVTR 92
Qy 64 NTSISTAYMELSLRSEDPAVYICAREEVLVRY-YGMVDMVGQTTVTSSGSASAPTLFP 122
Db 93 DSSKNTLFQMGSLREDDPAVYICARGHSIDNHYGVDMVGQTTVTSSGSASAPTLFP 152
Qy 123 LVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQ 182
Db 153 LVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQ 212
Qy 183 VLLPSKQVMQGTDEHKV 199
Db 213 VLLPSKQVMQGTDEHV 229

RESULT 3
US-10-104-047-3224
; Sequence 3224, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: H1-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3224
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3224

Query Match 67.1%; Score 707.5; DB 15; Length 533;
Best Local Similarity 70.3%; Pred. No. 2.9e-44;
Matches 142; Conservative 21; Mismatches 28; Indels 11; Gaps 4;

Qy 4 KPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMNPNNGTGYAQKFGQRTVTR 63

Db 32 QPGSRLRLSCAASGPDVSSNTYMSWRQSPGKPEWATMY-GGGNTYYAESVKGRTVTR 90
Qy 64 NTSISTAYMELSLRSEDPAVYICAREEVLVRYGMDV-----WGQGTVTVTSSGSASA 117
Db 91 DGSQNTLYLESSLRPDDPAVYICVRDH---RNVA-DTSPYGRKMGQGTTLVTSSGSASA 146
Qy 118 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKY 177
Db 147 PTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKY 206
Qy 178 AATSOVLLPSKQVMQGTDEHKV 199
Db 207 AATSOVLLPSKQVMQGTDEHV 228

RESULT 4
US-09-747-669-3
; Sequence 3, Application US/09747669
; Patent No. US20020122807A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5 THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS
; TITLE OF INVENTION: AND DETECTION OF CANCERS
; FILE REFERENCE: 316082001001
; CURRENT APPLICATION NUMBER: US/09/747,669
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 09/111,286
; PRIOR FILING DATE: 1998-07-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic construct
US-09-747-669-3

Query Match 61.0%; Score 643; DB 9; Length 476;
Best Local Similarity 62.7%; Pred. No. 1.5e-39;
Matches 128; Conservative 21; Mismatches 43; Indels 12; Gaps 5;

Qy 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMNPNNGTGYAQKFGQRTV 60
Db 29 EVKPGASVKVSKASGYTFTSFDLNWVRQAPGQGLEWGMNPNNGTGYAQKFGQRTV 88
Qy 61 MTRNTSISTAYMELSLRSEDPAVYICARE-----EWLVRYGMDVVGQGTVTVTSSGS 114
Db 89 MTRNTSISTAYMELSGLRSEDPAVYFCARNADNVEAMAIHYHYGMDVVGQGTVTVTSSAS 148
Qy 115 ASAPTFLFVLSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR- 173
Db 149 TKGPSVFFPLAPSCKSTSG-GTAAALCCLVKDYFPPEPTVTSW--NSGALTSGVHTFFAVLQS 205
Qy 174 GGYAATSOVLLPSKQVMQGTDEH 197
Db 206 SGLYSLSVTVTPSSSL--GTQTY 227

RESULT 5
US-10-290-703-3
; Sequence 3, Application US/10290703
; Publication No. US20030118593A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Saleh, Mansoor
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS, DESIGNATED
; TITLE OF INVENTION: 4B5, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
; TITLE OF INVENTION: ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS


```

; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match      56.9%; Score 600; DB 9; Length 470;
Best Local Similarity 58.9%; Pred. No. 2.2e-36;
Matches 123; Conservative 26; Mismatches 44; Indels 16; Gaps 7;

QY 1 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 60
DB 29 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 88
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEWL--VRY--GMDVWGQGTWTVTVSSGAS 116
DB 89 MTRDTSISTAYMELSLRSDDTAVYCARYYDSSGYHDAFDIWGQGTWTVTVSSASTK 148
QY 117 APTLPFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-GG 175
DB 149 GSVFPLAPCSRSTSE--STAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSG 205
QY 176 KYAATSQVLLPSKDVMOGTD-----EHK 198
DB 206 LYSLSVVTVPSNPF--GTQTYTCNVDHK 232

RESULT 9
US-10-625-105-28
; Sequence 28, Application US/10625105
; Publication No. US20040180052A1
; GENERAL INFORMATION:
; APPLICANT: Teuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE A11M AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/10/625,105
; CURRENT FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-625-105-28

Query Match      56.9%; Score 600; DB 16; Length 470;
Best Local Similarity 58.9%; Pred. No. 2.2e-36;
Matches 123; Conservative 26; Mismatches 44; Indels 16; Gaps 7;

QY 1 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 60
DB 29 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 88
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEWL--VRY--GMDVWGQGTWTVTVSSGAS 116
DB 89 MTRDTSISTAYMELSLRSDDTAVYCARYYDSSGYHDAFDIWGQGTWTVTVSSASTK 148
QY 117 APTLPFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-GG 175
DB 149 GSVFPLAPCSRSTSE--STAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSG 205
QY 176 KYAATSQVLLPSKDVMOGTD-----EHK 198
DB 206 LYSLSVVTVPSNPF--GTQTYTCNVDHK 232
```

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RESULT 10
US-10-128-520-174
; Sequence 174, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 174
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-174

Query Match      56.7%; Score 598; DB 16; Length 221;
Best Local Similarity 61.1%; Pred. No. 1.5e-36;
Matches 121; Conservative 23; Mismatches 44; Indels 10; Gaps 5;

QY 1 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 60
DB 10 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEWLRYRYGMDVWGQGTWTVTVSSGASAPT 120
DB 70 MTRDTSISTAYMELSLRSEDVAVYCAR----ITYIGDFWGQGTWTVTVSSASTKGP 125
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-GGKYAA 179
DB 126 PFLAPSSKSTSG-GTAAAGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQSSGLISL 182
QY 180 TSQVLLPSKDVMOGTDDEH 197
DB 183 SSVTVTPSSSL--GTQTY 198

RESULT 11
US-10-292-088-46
; Sequence 46, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-46

Query Match      56.4%; Score 594.5; DB 15; Length 471;
Best Local Similarity 57.5%; Pred. No. 5.6e-36;
Matches 122; Conservative 28; Mismatches 41; Indels 21; Gaps 7;

QY 1 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 60
DB 29 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 88
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QY 61 MTRNTSISTAYMELSLRSEDVAVYCCAREWLV-----VRYGMDVWGQTTVTVSSG 113
DB 89 MTRNTSISTAYMELNLRSDDTAVYCCARDQQLGYCTNGVCYF--DYWGQTLTVTSSA 146
QY 114 SASAPTLFPLVSCENSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSRGRFPVLR 173
DB 147 STKGSPVFLPACSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTFAVLQ 203
QY 174 -CGKVAATSQVLLPSKDVWQGT-----EHK 198
DB 204 SSGLYSLSSVVTVPSSNF--GTQYTCNVNDHK 233

RESULT 12

US-10-041-860-238
; Sequence 238, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 238
; LENGTH: 125
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-238

Query Match 53.1%; Score 559.5; DB 14; Length 125;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;
QY 1 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60
DB 9 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 68
QY 61 MTRNTSISTAYMELSLRSEDVAVYCCAREWLV-----YVGMDVWGQTTVTVSS 112
DB 69 MTRNTSISTAYMELSLRSEDVAVYCCAREGIAVAGTYYYYYGMVWGQTTVTVSS 125

RESULT 13

US-10-041-860-19
; Sequence 19, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19

; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-19

Query Match 53.1%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;
QY 1 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60
DB 10 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCCAREWLV-----YVGMDVWGQTTVTVSS 112
DB 70 MTRNTSISTAYMELSLRSEDVAVYCCAREGIAVAGTYYYYYGMVWGQTTVTVSS 126

RESULT 14

US-10-041-860-201
; Sequence 201, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-201

Query Match 53.1%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;
QY 1 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60
DB 10 EVKKEGASVKVCKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCCAREWLV-----YVGMDVWGQTTVTVSS 112
DB 70 MTRNTSISTAYMELSLRSEDVAVYCCAREGIAVAGTYYYYYGMVWGQTTVTVSS 126

RESULT 15

US-10-041-860-288
; Sequence 288, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; FILE REFERENCE: ABGENIX.051A

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; CURRENT APPLICATION NUMBER: US/10/041.860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 288
; LENGTH: 126
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-041-860-288

Query Match      53.1%; Score 559.5; DB 14; Length 126;
Best Local Similarity 92.3%; Pred. No. 5.9e-34;
Matches 108; Conservative 0; Mismatches 4; Indels 5; Gaps 1;

Qy      1 EVKKEGASVKVCKASGYFTSYDINWVRQATGQGLEWGMNPNNGNTGYAQKFGQGRVT 60
      |||
Db      10 EVKKEGASVKVCKASGYFTSYDINWVRQATGQGLEWGMNPNNGNTGYAQKFGQGRVT 69
      |||

Qy      61 MTRNTSISTAYMELSSLRSEDTAVYYCAREEWLYR-----YYGMDVMQGGTTVTVSS 112
      |||
Db      70 MTRNTSISTAYMELSSLRSEDTAVYYCAREGIAGTAVYYGYGMDVMQGGTTVTVSS 126
      |||
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Search completed: March 8, 2005, 07:05:52
Job time : 107.604 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 21.8813 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-29
Perfect score: 1054
Sequence: 1 EVKPGASVKVCKASGYTF.....TSQVLLPSKDVNQGTDEHKV 199

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep.*
6: /cgn2_6/prodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	600	56.9	470	US-09-859-053-28	Sequence 28, Appl
2	544.5	51.7	462	US-09-627-896B-24	Sequence 24, Appl
3	537.5	51.0	467	US-07-916-098A-45	Sequence 45, Appl
4	526.5	50.0	279	US-08-397-411-13	Sequence 13, Appl
5	511	48.5	468	US-09-485-737B-67	Sequence 67, Appl
6	511	48.5	468	US-10-071-485-67	Sequence 67, Appl
7	511	48.5	711	US-09-485-737B-90	Sequence 90, Appl
8	511	48.5	711	US-10-071-485-90	Sequence 90, Appl
9	510	48.4	472	US-09-301-593-43	Sequence 43, Appl
10	509	48.3	222	US-08-458-516-22	Sequence 22, Appl
11	509	48.3	235	US-08-458-516-23	Sequence 23, Appl
12	509	48.3	449	US-08-458-516-13	Sequence 13, Appl
13	501.5	47.6	235	US-08-444-644-28	Sequence 28, Appl
14	501.5	47.6	235	US-08-444-644-28	Sequence 28, Appl
15	496.5	47.1	235	US-08-444-644-42	Sequence 42, Appl
16	496.5	47.1	235	US-08-444-644-42	Sequence 42, Appl
17	487	46.2	476	US-08-332-246A-42	Sequence 42, Appl
18	485.5	46.1	120	US-08-378-939-10	Sequence 10, Appl
19	485.5	46.1	120	US-09-025-769B-36	Sequence 36, Appl
20	485.5	46.1	120	US-09-025-769B-59	Sequence 59, Appl
21	485.5	46.1	120	US-09-490-070A-36	Sequence 36, Appl
22	485.5	46.1	120	US-09-490-070A-59	Sequence 59, Appl
23	485.5	46.1	120	US-09-490-153-36	Sequence 36, Appl
24	485.5	46.1	120	US-09-490-324-36	Sequence 36, Appl
25	485.5	46.1	120	US-09-490-324-59	Sequence 59, Appl
26	484.5	46.0	235	US-08-444-644-19	Sequence 19, Appl
27	484.5	46.0	235	US-08-232-246A-19	Sequence 19, Appl

28	484.5	46.0	468	2	US-08-116-247-7	Sequence 7, Appl
29	484.5	46.0	468	4	US-09-348-224-7	Sequence 7, Appl
30	483.5	45.9	453	4	US-09-301-593-18	Sequence 18, Appl
31	481	45.6	117	3	US-09-025-769B-22	Sequence 22, Appl
32	481	45.6	117	4	US-09-490-070A-22	Sequence 22, Appl
33	481	45.6	117	4	US-09-490-153-22	Sequence 22, Appl
34	481	45.6	117	4	US-09-490-324-22	Sequence 22, Appl
35	479.5	45.5	233	3	US-08-444-644-33	Sequence 33, Appl
36	479.5	45.5	233	3	US-08-232-246A-33	Sequence 33, Appl
37	479.5	45.5	468	2	US-08-303-569B-7	Sequence 7, Appl
38	479.5	45.5	468	4	US-09-795-515-7	Sequence 7, Appl
39	478.5	45.4	445	1	US-08-353-400-33	Sequence 33, Appl
40	478.5	45.4	464	1	US-08-353-400-36	Sequence 36, Appl
41	477.5	45.3	253	3	US-09-027-449-52	Sequence 52, Appl
42	477.5	45.3	253	3	US-08-804-444A-52	Sequence 52, Appl
43	477.5	45.3	253	4	US-09-026-985-52	Sequence 52, Appl
44	477.5	45.3	253	4	US-09-121-952A-52	Sequence 52, Appl
45	477.5	45.3	253	4	US-09-234-340A-52	Sequence 52, Appl

ALIGNMENTS

RESULT 1
US-09-859-053-28
; Sequence 28, Application US/09859053
; Patent No. 6803039
; GENERAL INFORMATION:
; APPLICANT: Teuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; CURRENT FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-28

Query Match	56.9%	Score 600;	DB 4;	Length 470;
Best Local Similarity	58.9%;	Pred. No. 7.5e-46;		
Matches 123;	Conservative 26;	Mismatches 44;	Indels 16;	Gaps 7;
QY	1	EVKPGASVKVCKASGYTF	TSYDINWYRQATCGLEWGNWNPNSGNTGYAOKFGQRTV	60
DB	29	EVKPGASVKVCKASGYTF	TCGYWVRQAPGQGLEWGNWNPNSGNTGYAOKFGQRTV	88
QY	61	MYRNTSISTAYMELSLRSED	TAIVYICAREEVL--VRY--GMDVMGQGTITVTVSSGSAS	116
DB	89	MYRNTSISTAYMELSLRSED	TAIVYICARTYYDSSGYTHDAFDINGQGTWTVSSASTK	148
QY	117	APTLFPLVSCENSPDTS	SVAVGCLAQDPLPDSITFPMKYKNNSDTSSTRGPFVLR--GG	175
DB	149	GSFVFLAPCSRSTSE	--STAALGCLVKDYFPEPTVSM--NSGALTSGVHTFPAVLQSSG	205
QY	176	KYAATSQVLLPSKDVNQGT	D-----EHK	198
DB	206	LYSLSSVTVTPSSNF	--GTQTYTCNVDHK	232

RESULT 2
US-09-627-896B-24
; Sequence 24, Application US/09627896B

```
; Patent No. 6827934
; GENERAL INFORMATION:
; APPLICANT: CO, MAN SUNG
; APPLICANT: VASQUEZ, MAXIMILIANO
; APPLICANT: CARRENO, BEATRIZ CHERYL
; APPLICANT: CELNIKER, ABBIE CHERYL
; APPLICANT: COLLINS, MARY
; APPLICANT: GOLDMAN, SAMUEL
; APPLICANT: GRAY, GARY S.
; APPLICANT: KNIGHT, ANDREA
; APPLICANT: O'HARA, DENISE
; APPLICANT: RUP, BONITA
; APPLICANT: VELDMAN, GEERTRUIDA M.
; TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
; FILE REFERENCE: 08702.0081-01000
; CURRENT APPLICATION NUMBER: US/09/627,896B
; CURRENT FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 462
; TYPE: PRT
; ORGANISM: 3D1 heavy chain
; US-09-627-896B-24

Query Match          51.7%; Score 544.5; DB 4; Length 462;
Best Local Similarity 55.6%; Pred.No. 7.1e-41;
Matches 114; Conservative 24; Mismatches 50; Indels 17; Gaps 6;

QY 1 EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 60
Db 29 EVKPGSSVKVCKASGYTFTSYDINWVRQAPGQGLEWMGVININYNQKFKGKAT 88

QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEWLVRYGMDVWGQGTITTVSSGSASAPTL 120
Db 89 MTRVDSSTSTAYMELSLRSEDVAVYCARAAWY-----MDYWGQGTITLVTSASTKGPSV 143

QY 121 RFLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKKNDSISSTRGPPSVLR 179
Db 144 FLAPCSRSTSE-STAAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSL 200

QY 180 TSQVLLPSKDVNQGTGTD-----EHK 198
Db 201 SSVVTVFPSSNF--GTQTYTCNVNDHK 223

RESULT 3
US-07-916-098A-45
; Sequence 45, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.
; APPLICANT: CHISHOLM, PATRICIA L.
; APPLICANT: THOMAS, DAVID W.
; APPLICANT: ROSA, MARGARET D.
; APPLICANT: ROSA, JOSEPH J.
; TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
; TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ALLEGRETTI & WITCOFF, LTD.
; STREET: 10 SOUTH WACKER DRIVE
; CITY: CHICAGO
; STATE: ILLINOIS
; COUNTRY: U.S.A.
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
```

```
; APPLICATION NUMBER: US/07/916,098A
; FILING DATE: July 24, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/08843
; FILING DATE: No. 5871732ember 27, 1991
; CLASSIFICATION: 424
; APPLICATION NUMBER: 07/618,542
; FILING DATE: No. 5871732ember 27, 1990
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: JOHN J. MC DONNELL
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,310-G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 715-1000
; TELEFAX: (312) 715-1234
; TELEX: 910/221-5317
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-916-098A-45

Query Match          51.0%; Score 537.5; DB 2; Length 467;
Best Local Similarity 52.8%; Pred.No. 3.1e-40;
Matches 112; Conservative 30; Mismatches 45; Indels 25; Gaps 7;

QY 1 EVKPGASVKVCKASGYTFTSYDINWVRQATGQGLEWMGNPNNGNTGYAQKFGQGRVT 60
Db 29 EVKPGASVKVCKASGYTFTSYDINWVRQAPGQGLEWMGVININYNQKFKGKAT 88

QY 61 MTRNTSISTAYMELSLRSEDVAVYCARB-----WLVRYGMDVWGQGTITTVSSG 113
Db 89 VTLPSTNTAYMELSLRSEDVAVYCARDKDNATGAWFA-----YWGQGTITLVTSVA 142

QY 114 SASAPTLPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKKNDSISSTRGPPSVLR 173
Db 143 STKGPSVFLAPCSRSTSE-STAAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQ 199

QY 174 -GGKYAATSQVLLPSKDVNQGTGTD-----EHK 198
Db 200 SSGLYSLSSVTVFPSSSL--GTQTYTCNVNDHK 229

RESULT 4
US-08-397-411-13
; Sequence 13, Application US/08397411
; Patent No. 6129914
; GENERAL INFORMATION:
; APPLICANT: Weiner, George
; APPLICANT: Gingrich, Roger
; APPLICANT: Link, Brian
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Bispecific Antibody Effective to Treat
; TITLE OF INVENTION: B-Cell Lymphoma and Cell Line
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Crew
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,411
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; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/859,583
; FILING DATE: 27-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 011823-004901
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 279 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-397-411-13

Query Match 50.0%; Score 526.5; DB 3; Length 279;
Best Local Similarity 55.1%; Pred. No. 1.6e-39;
Matches 109; Conservative 26; Mismatches 56; Indels 7; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQGRVT 60
DB 10 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQGRVT 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTTVTVSSGSASAPTL 120
DB 70 L7ADKASATYMELSLRSEDVAVYCARSAI-YDYGFAWGQGTFTTVTVSSASTKGPVS 128
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFPSVLR-GGKYAA 179
DB 129 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTFPAVLQSSGLYSL 185
QY 180 TSQVLLPSKDVMOQTDEH 197
DB 186 SSVWTVPPSSSL--GTQTY 201

RESULT 5
US-09-485-737B-67
; Sequence 67, Application US/09485737B
; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/09/485,737B
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-09-485-737B-67

Query Match 48.5%; Score 511; DB 3; Length 468;
Best Local Similarity 49.5%; Pred. No. 7.4e-38;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQGRVT 60
DB 30 ELKKEGASVKISCKASGYTFTDYGNNWVKQAPGQGLKMWGINTYTGESTYYVDDFKGRFV 89
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTTVTVSSGSASAPTL 120
DB 90 FSLDTSVSNAYLQISLKAEDTATYFCARR----GFYANDYWGQGTFTTVTVSSASTKGPVS 145
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFPSVLR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTFPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOQTDEH 197
DB 203 SSVWTVPPSSSL--GTQTY 218

RESULT 6
US-10-071-485-67
; Sequence 67, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; TITLE OF INVENTION: SHOCK,
; FILE REFERENCE: INNS:015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 67
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
; US-10-071-485-67

Query Match 48.5%; Score 511; DB 4; Length 468;
Best Local Similarity 49.5%; Pred. No. 7.4e-38;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKKEGASVKVSKASGYTFTSYDINWVRQATGQGLEWGWNPNSGNTGYAQKFGQGRVT 60
DB 30 ELKKEGASVKISCKASGYTFTDYGNNWVKQAPGQGLKMWGINTYTGESTYYVDDFKGRFV 89
QY 61 MTRNTSISTAYMELSLRSEDVAVYCARAEELVRYGMDVWGQGTFTTVTVSSGSASAPTL 120
DB 90 FSLDTSVSNAYLQISLKAEDTATYFCARR----GFYANDYWGQGTFTTVTVSSASTKGPVS 145
QY 121 PFLVSCENSPDTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFPSVLR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTFPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOQTDEH 197
DB 203 SSVWTVPPSSSL--GTQTY 218

RESULT 7
US-09-485-737B-90
; Sequence 90, Application US/09485737B
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; Patent No. 6350860
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
; FILE REFERENCE: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; CURRENT APPLICATION NUMBER: US/09/485,737B
; CURRENT FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-09-485-737B-90
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Query Match 48.5%; Score 511; DB 3; Length 711;
Best Local Similarity 49.5%; Pred. No. 1.2e-37;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
DB 30 ELKPGASVKISCKASGYTFTDYGNNWVKQAPGQGLKWMGWINTYTGESTYVDDFKGRFV 89
QY 61 MTRNTSISTAYMELSSLRSEDTAVYICAREEHLVRYYGMDVWVGQGTITVTVSSGSASAPTL 120
DB 90 FSLDTSVSAALYQISSLKAEDTATVFCARR----GFYAMDYWGQGTITVTVSSASTKGPVS 145
QY 121 PPLVSCENSPDSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGFPVSILR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOGQGTDEH 197
DB 203 SSVTVTPSSSL--GIQTY 218
```

```
RESULT 8
US-10-071-485-90
; Sequence 90, Application US/10071485
; Patent No. 6830752
; GENERAL INFORMATION:
; APPLICANT: Buyse, Marie-Ange
; APPLICANT: Sablon, Erwin
; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
; FILE REFERENCE: SHOCK,
; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
; FILE REFERENCE: INNS-015
; CURRENT APPLICATION NUMBER: US/10/071,485
; CURRENT FILING DATE: 2002-02-07
; PRIOR APPLICATION NUMBER: 09/485,737
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
; PRIOR FILING DATE: 1998-08-14
; PRIOR APPLICATION NUMBER: EPO 98870139.7
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: EPO 97870122.5
; PRIOR FILING DATE: 1997-08-18
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 90
; LENGTH: 711
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: SYNTHETIC
US-10-071-485-90

Query Match 48.5%; Score 511; DB 4; Length 711;
Best Local Similarity 49.5%; Pred. No. 1.2e-37;
Matches 98; Conservative 36; Mismatches 54; Indels 10; Gaps 5;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
DB 30 ELKPGASVKISCKASGYTFTDYGNNWVKQAPGQGLKWMGWINTYTGESTYVDDFKGRFV 89
QY 61 MTRNTSISTAYMELSSLRSEDTAVYICAREEHLVRYYGMDVWVGQGTITVTVSSGSASAPTL 120
DB 90 FSLDTSVSAALYQISSLKAEDTATVFCARR----GFYAMDYWGQGTITVTVSSASTKGPVS 145
QY 121 PPLVSCENSPDSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGFPVSILR-GGKYAA 179
DB 146 PFLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOGQGTDEH 197
DB 203 SSVTVTPSSSL--GIQTY 218
```

```
RESULT 9
US-09-301-593-43
; Sequence 43, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-43
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```
Query Match 48.4%; Score 510; DB 4; Length 472;
Best Local Similarity 54.2%; Pred. No. 9.2e-38;
Matches 109; Conservative 24; Mismatches 58; Indels 10; Gaps 6;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGQGRVT 60
DB 29 EVKPGASVKVSKTSRYTFTYTHWVRQAPGQGLEWIGGINPNNGIPNINQKFKGRAT 88
QY 61 MTRNTSISTAYMELSSLRSEDTAVYICAREEHLVRY---YGMVDVWGQGTITVTVSSGSASA 117
DB 89 LTVGKSASTAYMELSSLRSEDTAVYICARRRAYGDEGHAMDYWGQGTITVTVSS-STKG 147
QY 118 PTLFPLVSCENSPDSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGFPVSILR-GGK 176
DB 148 PSVFPPLAPSSKSTSG-GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTTTPAVLQSSGL 204
QY 177 YAATSOVLLPSKDVMOGQGTDEH 197
DB 205 YLSLSSVTVTPSSSL--GIQTY 223
```


RESULT 10
US-08-458-516-22
; Sequence 22, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 222 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-22
; Query Match 48.3%; Score 509; DB 1; Length 222;
; Best Local Similarity 53.5%; Pred. No. 4.4e-38;
; Matches 106; Conservative 28; Mismatches 56; Indels 8; Gaps 5;
QY 1 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGRTV 60
Db 10 EVKPGSSVKVSKASGYFTSYDINWVRQAPGQGLEWIGVTPGSGGTNYNEKFKGRVT 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCAEEWLVRYGNDVWGQGTITVTVSSGSASAPTL 120
Db 70 LVVDESTNAYMELSLRSEDVAVYFCARRDG--NYGMFAYWGQGTITVTVSSASTKGPSV 127
QY 121 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGFPVLR--GKYYAA 179
Db 128 PFLAPSSKSTSG-GTAALGCLVKDYFPEPTVYSW--NSGALTSGVHTTTPAVLQSSGLYS 184
QY 180 TSQVLLPSKDVWGQGTDEH 197
Db 185 SSVWTVPSSSL--GTQTY 200
RESULT 11
US-08-458-516-23
; Sequence 23, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-23
; Query Match 48.3%; Score 509; DB 1; Length 235;
; Best Local Similarity 53.5%; Pred. No. 4.7e-38;
; Matches 106; Conservative 28; Mismatches 56; Indels 8; Gaps 5;

; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-458-516-23
; Query Match 48.3%; Score 509; DB 1; Length 235;
; Best Local Similarity 53.5%; Pred. No. 4.7e-38;
; Matches 106; Conservative 28; Mismatches 56; Indels 8; Gaps 5;
QY 1 EVKPGASVKVSKASGYFTSYDINWVRQATGQGLEWMGNPNPNSGNTGYAQKFGRTV 60
Db 10 EVKPGSSVKVSKASGYFTSYDINWVRQAPGQGLEWIGVTPGSGGTNYNEKFKGRVT 69
QY 61 MTRNTSISTAYMELSLRSEDVAVYCAEEWLVRYGNDVWGQGTITVTVSSGSASAPTL 120
Db 70 LVVDESTNAYMELSLRSEDVAVYFCARRDG--NYGMFAYWGQGTITVTVSSASTKGPSV 127
QY 121 PFLVSCNSPDSSTSSVAVGCLAQDFLPDSITPSWKYKNNSDISSTRGFPVLR--GKYYAA 179
Db 128 PFLAPSSKSTSG-GTAALGCLVKDYFPEPTVYSW--NSGALTSGVHTTTPAVLQSSGLYS 184
QY 180 TSQVLLPSKDVWGQGTDEH 197
Db 185 SSVWTVPSSSL--GTQTY 200
RESULT 12
US-08-458-516-13
; Sequence 13, Application US/08458516
; Patent No. 5777085
; GENERAL INFORMATION:
; APPLICANT: Co, Man Sung
; APPLICANT: Tso, J. Yun
; TITLE OF INVENTION: Humanized Antibodies Reactive with
; TITLE OF INVENTION: GPIIB/IIIA
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; CITY: San Francisco

STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 48.3%; Score 509; DB 1; Length 449;
Best Local Similarity 53.5%; Pred. No. 1.1e-37;
Matches 106; Conservative 28; Mismatches 56; Indels 8; Gaps 5;
QY 1 EVKPGASVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60
DB 10 EVKPGSSVSKASGYAFTNYLIEWRQAPGQGLEWIGVYPCSGGTNYNEKPKGRVT 69
QY 61 MTRNTSISTAYMELSSLRSEDVAVYCARAEWLVRVYGMVWGQTTTTVSSGSASAPTL 120
DB 70 LTVDSTNTAYMELSSLRSEDVAVFCARRDG--NYGWFAYWGQGTTLVTSSASTKGPSV 127
QY 121 PPLVSCNSPDTSSVAVGCLAQDLPDSITFSWKYKNSDISSTRGSPSVLR--CGKYAA 179
DB 128 PPLAPSSKTSGL--GTAALGCLVKDYFPPEPVTVSW--NSGALTSGVHTTFAVLQSSGLYSL 184
QY 180 TSQVLLPSKDVMOGTDEH 197
DB 185 SSVTVVPSSSL--GTQTY 200

RESULT 13
US-08-444-644-28
Sequence 28, Application US/08444644
Patent No. 6015555
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/444,644
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/232,246
FILING DATE: 07-JUL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/800,458
FILING DATE: 26-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US90/05077
FILING DATE: 07-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/404,089
FILING DATE: 07-SEP-1989
ATTORNEY/AGENT INFORMATION:
NAME: Wagner, Richard W.
REGISTRATION NUMBER: 34,480
REFERENCE/DOCKET NUMBER: ALK88-15AAAZ
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: N-terminal
US-08-444-644-28

Query Match 47.6%; Score 501.5; DB 3; Length 235;
Best Local Similarity 48.8%; Pred. No. 2.2e-37;
Matches 100; Conservative 39; Mismatches 51; Indels 15; Gaps 6;
QY 1 EVKPGASVSKASGYTFTSYDINWVRQATGQGLEWGMWNPNSGNTGYAQKFGQGRVT 60
DB 29 ELVKPGAMKLSCKASGYSTGYTMWVKQSHGENLEWIGRINPANGGTDYNAKEFKDAP 88
QY 61 MTRNTSISTAYMELSSLRSEDVAVYCARAEWLVRVYGMVWGQTTTTVSSGSASAPTL 120
DB 89 LTVDKSSNTAYMELSLTSEDSAVYVCARGYV--YSLDYWGQGTSTVSSASTKGPSV 145
QY 121 PPLVSCNSPDTSSVAVGCLAQDLPDSITFSWKYKNSDISSTRGSPSVLR--CGKYAA 179
DB 146 PPLAPCSRSTSE--STAALGCLVKDYFPPEPVTVSW--NSGALTSGVHTTFAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVMOGTD-----EHK 198
DB 203 SSVTVVPSSNF--GTQTYTCNVDPK 225

RESULT 14
US-08-232-246A-28
Sequence 28, Application US/08232246A
Patent No. 6329508
GENERAL INFORMATION:
APPLICANT: Friden, Phillip M.
TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
TITLE OF INVENTION: CONJUGATES
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STATE: MA
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

```

;
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,246A
; FILING DATE: 04-MAY-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 28:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; US-08-232-246A-28.

Query Match 47.6%; Score 501.5; DB 3; Length 235;
Best Local Similarity 48.8%; Pred. No. 2.2e-37;
Matches 100; Conservative 39; Mismatches 51; Indels 15; Gaps 6;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMNPNNGNTGYAQKFGQGRVT 60
DB 29 ELVKPGASVKISCKASGYSTGYTMWVKQSHGENLEWIGRINPHNGGTDYDYNQKFKDKAP 88
QY 61 MTRNTSISTAYMELSLRSEDATVYVCAREEWLVRYGMDVWGQGTITVTVSSGSASAPTL 120
DB 89 LTVDKSSNTAYMELSLTSEDSAVYVCARGY---YSLDYWGQGTISVTSSASTKGPSV 145
QY 121 PFLVSCNSPSTSSVAVGCLAQDFLPDSITPSWKYKNSDISSTRGPPSVLR-GGKYAA 179
DB 146 FPLAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVWGQTD-----EHK 198
DB 203 SSVTVTPSSNF--GTQTYTCNVDPK 225

RESULT 15
US-08-444-644-42
; Sequence 42, Application US/08444644
; Patent No. 6015555
; GENERAL INFORMATION:
; APPLICANT: Eriden, Phillip M.
; TITLE OF INVENTION: TRANSFERRIN RECEPTOR SPECIFIC
; TITLE OF INVENTION: ANTIBODY-NEUROPHARMACEUTICAL OR DIAGNOSTIC AGENT
; TITLE OF INVENTION: CONJUGATES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
; STREET: Two Militia Drive
; CITY: Lexington
; STATE: MA
; COUNTRY: USA
; ZIP: 02173
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/444,644
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/232,246
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/800,458
; FILING DATE: 26-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US90/05077
; FILING DATE: 07-SEP-1990
; APPLICATION NUMBER: US 07/404,089
; FILING DATE: 07-SEP-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Wagner, Richard W.
; REGISTRATION NUMBER: 34,480
; REFERENCE/DOCKET NUMBER: ALK88-15AAA
; TELEPHONE: (617) 861-6240
; TELEFAX: (617) 861-9540
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
; US-08-444-644-42

Query Match 47.1%; Score 496.5; DB 3; Length 235;
Best Local Similarity 48.3%; Pred. No. 6.2e-37;
Matches 99; Conservative 39; Mismatches 52; Indels 15; Gaps 6;

QY 1 EVKPGASVKVSKASGYTFTSYDINWVRQATGQGLEWGMNPNNGNTGYAQKFGQGRVT 60
DB 29 ELVKPGASVKISCKASGYSTGYTMWVKQSHGENLEWIGRINPHNGGTDYDYNQKFKDKAP 88
QY 61 MTRNTSISTAYMELSLRSEDATVYVCAREEWLVRYGMDVWGQGTITVTVSSGSASAPTL 120
DB 89 LTVDKSSNTAYMELSLTSEDSAVYVCARGY---YSLDYWGQGTISVTSSASTKGPSV 145
QY 121 PFLVSCNSPSTSSVAVGCLAQDFLPDSITPSWKYKNSDISSTRGPPSVLR-GGKYAA 179
DB 146 FPLAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSL 202
QY 180 TSQVLLPSKDVWGQTD-----EHK 198
DB 203 SSVTVTPSSSL--GTQTYTCNVDPK 225

Search completed: March 8, 2005, 05:54:07
Job time : 22.8813 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.4472 Seconds
(without alignment)
1353.842 Million cell updates/sec

Title: US-09-784-950-30
Perfect score: 769
Sequence: 1 GQSPSSLSASVGDRTVTTCR.....VVCLNNFYPREXKEHOKSP 147

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	567.5	73.8	215	2 JE0242	Ig kappa chain NIG
2	562.5	73.1	215	2 JE0244	Ig kappa chain NIG
3	529.5	68.9	215	2 JE0243	Ig kappa chain NIG
4	513.5	66.8	215	2 A23746	Ig kappa chain V-I
5	500	65.0	141	2 A49134	Ig kappa chain V-I
6	500	65.0	234	2 S14237	Ig kappa chain pre
7	494	64.2	230	2 S33161	Ig kappa chain - s
8	487	63.3	234	2 S01320	Ig kappa chain pre
9	487	63.3	240	2 S06084	Ig kappa chain pre
10	482	62.7	108	1 K1HUWE	Ig kappa chain V-I
11	481	62.5	125	2 S40353	Ig kappa chain V-J
12	481	62.5	216	2 JE0241	Ig kappa chain Am3
13	475	61.8	210	2 A56169	Ig kappa chain V r
14	470	61.1	214	2 S68212	Ig kappa chain (Ma
15	468	60.9	108	1 K1HUGL	Ig kappa chain V-I
16	465	60.5	127	2 S40367	Ig kappa chain V-J
17	463	60.2	123	2 S40313	Ig kappa chain V-J
18	462	60.1	125	2 S40333	Ig kappa chain V-J
19	461	59.9	139	2 S40365	Ig kappa chain - h
20	460	59.8	126	2 S40335	Ig kappa chain V-J
21	457	59.4	144	2 P01005	Ig kappa chain pre
22	457	59.4	218	2 JC5810	monoclonal antibody
23	456.5	59.4	124	2 S40336	Ig kappa chain V-J
24	456	59.3	130	2 S40368	Ig kappa chain - h
25	456	59.3	132	2 S40334	Ig kappa chain - h
26	455.5	59.2	225	2 S37484	Ig kappa chain - m
27	455	59.2	129	2 S40369	Ig kappa chain - h
28	454.5	59.1	235	2 S25058	Ig kappa chain - m
29	454	59.0	218	2 S68241	Ig kappa chain V r

ALIGNMENTS

RESULT 1

JE0242

Ig kappa chain NIG26 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0242

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mult

A:Reference number: JE0241

A:Accession: JE0242

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 73.8%; Score 567.5; DB 2; Length 215;

Best Local Similarity 74.5%; Pred. No. 1.6e-39;

Matches 108; Conservative 13; Mismatches 23; Indels 1; Gaps 1;

Qy 2 QSPSSLSASVGDRTVTTCRASQDIRDN-LGWYQKPGKAPKELIYAASNLQSGVPSRSG 60

Db 6 QSPGTLTSLSPGERATLSCRASQSVSNLYAWYQKPGQAPSLIYDASSRATGPDPSDEQ 65

Qy 61 SCSGTFTLTISLQPEDFATYVCLQYKTYPTWTFQGQTKVEIKRTVAAPSVPFPPSDEQ 120

Db 66 SCSGTDFILTISGLEPEDFATYVCCQYDRPPTWTFQGQTKVEIKRTVAAPSVPFPPSDEQ 125

Qy 121 LKSGTASVVCLLNNFYPREXKEHOK 145

Db 126 LKSGTASVVCLLNNFYPREAKVQWK 150

RESULT 2

JE0244

Ig kappa chain NIG2 precursor - human

C:Species: Homo sapiens (man)

C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JE0244

R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T

submitted to JIPID, November 1998

A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy

A:Reference number: JE0243

A:Accession: JE0244

A:Molecule type: protein

A:Residues: 1-215 <ALI>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 562.5; DB 2; Length 215;

Best Local Similarity 74.5%; Pred. No. 4.2e-39;

Matches 108; Conservative 14; Mismatches 22; Indels 1; Gaps 1;

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Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLOSQVPSRFSGS 61
Db 6 QSPATLSVSPGERATLSQASQSVHNSLAWYQKPGQAPRLIIYRASTRATGIPARFSGS 65
Qy 62 GSGTEFTLTSSLOPEDFATYCYQKTY-PWTGQGTKEIKRTVAAPSFIIPPDSDEQ 120
Db 66 GSGTDFLTITSSLOSDFALYCCQYNTWPLTTEGGGTKEIKRTVAAPSFIIPPDSDEQ 125
Qy 121 LKSGTASVVCLLNNFYPREXKEHQK 145
Db 126 LKSGTASVVCLLNNFYPREAKVQWK 150
RESULT 3
A9134
Ig kappa chain V-I region (ISE) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: J02043
R:Alim, M.A.; Hara, Y.; Hoseain, M.S.; Takeda, K.; Yamagata, P.; Yamaki, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A:Reference number: J02043
A:Accession: J02043
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>
Query Match 68.9%; Score 529.5; DB 2; Length 215;
Best Local Similarity 72.4%; Pred. No. 2.1e-36;
Matches 105; Conservative 13; Mismatches 26; Indels 1; Gaps 1;
Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLOSQVPSRFSGS 61
Db 6 QSPATLSVSPGERATLSQASQSVATNVVMQKLGQAPRLIIYDASTRATGVPARFSGS 65
Qy 62 GSGTEFTLTSSLOPEDFATYCYQKTY-PWTGQGTKEIK-RTVAAPSFIIPPDSDEQ 120
Db 66 GSGTEFTLTSSLOSDFALYCYQHNNAWPTFGGTKEIKRTVAAPSFIIPPDSDEQ 125
Qy 121 LKSGTASVVCLLNNFYPREXKEHQK 145
Db 126 LKSGTASVVCLLNNFYPREAKVQWK 150
RESULT 4
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>
Query Match 66.8%; Score 513.5; DB 2; Length 215;
Best Local Similarity 71.0%; Pred. No. 4.3e-35;
Matches 103; Conservative 15; Mismatches 26; Indels 1; Gaps 1;
Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLOSQVPSRFSG 60
Db 6 QSPATLSVSPGERATLSGASQSVSNLAWYQKPGQAPRLIIYDASTRATGIPDRFSG 65
```

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Qy 61 GSGTEFTLTSSLOPEDFATYCYQKTY-PWTGQGTKEIKRTVAAPSFIIPPDSDEQ 120
Db 66 GSGTDFLTITSLRLEPEDFATYCYQKTY-PWTGQGTKEIKRTVAAPSFIIPPDSDEQ 125
Qy 121 LKSGTASVVCLLNNFYPREXKEHQK 145
Db 126 LKSGTASVVCLLNNFYPREAKVQWK 150
RESULT 5
A49134
Ig kappa chain V-I region (ISE) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49134; S25115
R:Rocca, A.; Khamlichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.L.
Clin. Exp. Immunol. 91, 506-509, 1993
A:Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light
A:Reference number: A49134; MUID:93185310; PMID:7680298
A:Accession: A49134
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-141 <ROC>
A:Cross-references: EMBL:X67322; NID:g33268; PIDN:CAA47736.1; PID:g33269
A:Note: sequence extracted from NCBI backbone (NCBIp:127088)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>
Query Match 65.0%; Score 500; DB 2; Length 141;
Best Local Similarity 85.1%; Pred. No. 3.6e-34;
Matches 97; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLOSQVPSRFSGS 61
Db 28 QSPSTLSASVGDRTVITCRASLGINIWLAWYQKPGKAPNLLIYKATNLOSQVPSRFSAS 87
Qy 62 GSGTEFTLTSSLOPEDFATYCYQKTY-PWTGQGTKEIKRTVAAPSFIIPP 115
Db 88 GSGTEFTLTISGLQDDFATYCYQYDSY-PWTGQGTKEIKRTVAAPSFIIPP 141
RESULT 6
S14237
Ig kappa chain precursor (15C5) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S14237
R:Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A:Title: Construction and characterization of a recombinant murine monoclonal antibody di
A:Reference number: S14236; MUID:91006173; PMID:2209622
A:Accession: S14237
A:Molecule type: mRNA
A:Residues: 1-234 <VAN>
A:Cross-references: EMBL:X56394; NID:g51622; PIDN:CAA39805.1; PID:g51623
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>
Query Match 65.0%; Score 500; DB 2; Length 234;
Best Local Similarity 66.9%; Pred. No. 6e-34;
Matches 93; Conservative 20; Mismatches 26; Indels 0; Gaps 0;
Qy 2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLOSQVPSRFSGS 61
Db 26 QSPSSMVASLGERVTVTKASQDINSYLSWTQKPGKSPKTLIYRGNLAVGVSFRFSGS 85
Qy 62 GSGTEFTLTSSLOPEDFATYCYQKTY-PWTGQGTKEIKRTVAAPSFIIPPDSDEQ 121
Db 86 GSGGDSLTITSSLSYEDVGVIYCLRYDEFPPTFGSGTKLEIKRADAAPTVSFIIPPSEQL 145
Qy 122 KSGTASVVCLLNNFYPREX 140
```



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Db 6 QSPSSLASVGDVRTITCRASQGRNDLTWYQQPGTAPKRLIYCATSLQSGVPSRFSGS 65
Qy 62 GSGTEFTLTISLQPEDPATYICLYQKTYPTWTFQGGTKVEIKR 104
Db 66 GSGTEFTLTISLQPEDPATYICLYQSSFPWTFQGGTKVEIKR 108

RESULT 11
S40353
Ig kappa chain V-J-C region - human
C:Species: Homo sapiens (man)
C:Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40353
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40353
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-125 <KLE>
A:Cross-references: EMBL:X72463
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-104/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 481; DB 2; Length 125;
Best Local Similarity 87.7%; Pred. No. 1.2e-32;
Matches 93; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDVRTITCRASQDIRDNLGWYQQKPGKAPKRLIYAASNLQSGVPSRFSGS 61
Db 20 QSPSSLASVGDVRTITCRASQIGNDLGWYQQKPGKAPKRLIYAASFSQSGVPSRFSGS 79

Qy 62 GSGTEFTLTISLQPEDPATYICLYQKTYPTWTFQGGTKVEIKRTVA 107
Db 80 GSGTEFTLTISLQPEDPATYICLHNSYPLTFGGTRVEIKRTVA 125

RESULT 12
JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 62.5%; Score 481; DB 2; Length 216;
Best Local Similarity 66.2%; Pred. No. 2e-32;
Matches 98; Conservative 18; Mismatches 26; Indels 6; Gaps 3;

Qy 2 QSPSSLASVGDVRTITCRASQDIRDNLGWYQQKPGKAPKRLIYAASNLQSGVPSR 57
Db 6 QSPDFLAVSLGERATINCKSSQSVLYNSKNFLAWYQQKPGQ- PKLLIW-ANVRESGVDR 63

Qy 58 FSGSGSGTEFTLTISLQPEDPATYICLYQKTYPTWTFQGGTKVEIKRTVAAPSFIIPPS 117
Db 64 FRSGVGVDFTLTISNLQAEVLAVYICQYYSTPTYSFGQGRLEIKRTVAAPSFIIPPS 123

Qy 118 DEQLKSGTASVVCLLNNFYPREXKEHOK 145
Db 124 DEQLKSGTASVVCLLNNFYPREAKVQWK 151
```

```
RESULT 13
A56169
Ig kappa chain V region (clone 23.2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C:Accession: A56169
R:Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godillie,
J. Biol. Chem. 270, 6628-6638, 1995
A:Title: Recombinant antibodies in bioactive peptide design.
A:Reference number: A56169; MUID:95204454; PMID:7896802
A:Accession: A56169
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-210 <MON>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 61.8%; Score 475; DB 2; Length 210;
Best Local Similarity 62.9%; Pred. No. 6e-32;
Matches 90; Conservative 20; Mismatches 29; Indels 4; Gaps 1;

Qy 2 QSPSSLASVGDVRTITCRASQDIRDNLGWYQQKPGKAPKRLIYAASNLQSGVPSR 57
Db 6 QSPASLTVSLGQRATISCRASKSVSSSGSYMMHYQQKPGQPPKVLILYASNLQSGVPPR 65

Qy 58 FSGSGSGTEFTLTISLQPEDPATYICLYQKTYPTWTFQGGTKVEIKRTVAAPSFIIPPS 117
Db 66 FSGSGSGCTDFTLNHPVEEDAATYYCQHSRELPTWTFGGTRLEIKRADAAPTYSIIPPS 125

Qy 118 DEQLKSGTASVVCLLNNFYPREX 140
Db 126 SEQLTSGGASVVCFLNNFYPKDI 148

RESULT 14
S68212
Ig kappa chain (Wab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 61.1%; Score 470; DB 2; Length 214;
Best Local Similarity 61.4%; Pred. No. 1.6e-31;
Matches 89; Conservative 25; Mismatches 25; Indels 6; Gaps 1;

Qy 2 QSPSSLASVGDVRTITCRASQDI-----RDNLGWYQQKPGKAPKRLIYAASNLQSGVP 55
Db 6 QSPSSLAWSVGQKVTMSCKSSQSLNSRNQKNYLAWYQQKPGQSPKLLVYFASFTRESGVP 65

Qy 56 SRPSGSGSGTEFTLTISLQPEDPATYICLYQKTYPTWTFQGGTKVEIKRTVAAPSFIIP 115
Db 66 DRFTGSGSGDFTLTISTVQAEDLADYFCQCHYSTPTFTFGGTTKLEIKRADAAPTYSIIF 125

Qy 116 PSDQLKSGTASVVCFLNNFYPREX 140
Db 126 PSEQLTSGGASVVCFLNNFYPKDI 150

RESULT 15
K1HUGL
Ig kappa chain V-I region (Gal) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
```


C:Accession: A01867
R:laure, C.J.; Watanabe, S.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 354, 1503-1504, 1973
A:Title: The primary structure of a monoclonal IGM-immunoglobulin (macroglobulin Gal), I
A:Reference number: A01867; MUID:75059122; PMID:4215718
A:Accession: A01867
A:Molecule type: protein
A:Residues: 1-108 <LAU>
A:Cross-references: UNIPROT:P01599
A:Note: the C region of this chain has the Inv (3) marker
C:Comment: This chain was isolated from a Waldenstrom's macroglobulin.
C:Genetics:
A:Gene: GDB:IGKV1
A:Cross-references: GDB:136264
A:Map position: 2p12-2p12
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:16-90/Domain: immunoglobulin homology <IMM>
F:23-88/Disulfide bonds: #status predicted

Query Match	60.9%;	Score	468;	DB	1;	Length	108;
Best Local Similarity	88.3%;	Pred	No. 1.2e-31;				
Matches	91;	Conservative	5;	Mismatches	7;	Indels	0;
						Gaps	0;
Qy	2	QSPSLSASVGDRTTTCRASQDIRDNLGWYQKFGKAPKRLIYAASNLSQGVPSRPSGS	61				
Db	6	QSPSLSASVGDRTTTCRASQDIRDNLGWYQKFGKAPKRLIYAASNLSQGVPSRPSGS	65				
Qy	62	GSQTEFTLTISLQPEDFATYCYQKTYPTWTFGQGTKEIKR	104				
Db	66	GAGTEFTLTISLQPEDFATYCYQKTYPTWTFGQGTKEIKR	108				

Search completed: March 8, 2005, 06:39:25
Job time : 11.4972 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 54.8971 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-30

Perfect score: 769

Sequence: 1 GQSPSSLSASVGDRTVTCR.....VCLLNFPYEXXEHQKSP 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	670	87.1	236	2	Q6GMW1	Q6gmw1 homo sapien
2	639	83.1	236	2	Q7Z3Y4	Q7z3y4 homo sapien
3	633	82.3	234	2	Q7Z473	Q7z473 homo sapien
4	629	81.8	236	2	Q6GMX8	Q6gmxx8 homo sapien
5	622	80.9	236	2	Q6GMX9	Q6gmxx9 homo sapien
6	619	80.5	236	2	Q6PIH7	Q6pih7 homo sapien
7	618	80.4	236	2	Q6PIT5	Q6pit5 homo sapien
8	607	78.9	236	2	Q6GMX0	Q6gmxx0 homo sapien
9	598	77.8	236	2	Q6PIH4	Q6pih4 homo sapien
10	554.5	72.1	235	2	Q6GMW0	Q6gmw0 homo sapien
11	538	70.0	236	2	Q6PIL8	Q6pil8 homo sapien
12	535.5	69.6	235	2	Q6GMV9	Q6gmvv9 homo sapien
13	531	69.1	236	2	Q6P5S8	Q6p5s8 homo sapien
14	527.5	68.6	235	2	Q6PJF2	Q6pjf2 homo sapien
15	506	65.8	236	2	Q7TS98	Q7ts98 mus musculus
16	496	64.5	240	2	Q6PIH6	Q6pih6 homo sapien
17	492.5	64.0	239	2	Q8NEK0	Q8nek0 homo sapien
18	492.5	64.0	239	2	Q8TCD0	Q8tcd0 homo sapien
19	482	62.7	108	1	KV1R_HUMAN	P01610 homo sapien
20	470.5	61.2	239	2	Q6P491	Q6p491 homo sapien
21	468	60.9	108	1	KV1G_HUMAN	P01599 homo sapien
22	464	60.3	238	2	Q6GJS7	Q6gjs7 mus musculus
23	451	58.6	108	1	KV1B_HUMAN	P01594 homo sapien
24	444	57.7	108	2	Q9UL77	Q9ul77 homo sapien
25	440	57.2	108	1	KV1V_HUMAN	P04430 homo sapien
26	434.5	56.5	219	2	Q65ZC0	Q65zc0 mus musculus
27	434	56.4	116	2	Q9GPF6	Q9gpf6 homo sapien
28	433	56.3	108	2	Q9UL70	Q9ul70 homo sapien
29	429.5	55.9	107	2	Q9GSA9	Q9gsa9 homo sapien
30	429	55.8	108	1	KV1O_HUMAN	P01607 homo sapien
31	427	55.5	108	1	KV1H_HUMAN	P01600 homo sapien

32	425	55.3	108	1	KV1C_HUMAN	P01595 homo sapien
33	425	55.3	244	2	Q65ZC8	Q65zc8 homo sapien
34	424.5	55.2	243	2	Q6NTU5	Q6ntu5 xenopus lae
35	422	54.9	108	1	KV1L_HUMAN	P01604 homo sapien
36	421	54.7	108	2	Q9UL79	Q9ul79 homo sapien
37	420	54.6	108	1	KV1Y_HUMAN	P80362 homo sapien
38	418	54.4	237	2	Q7S236	Q7sz36 xenopus lae
39	417	54.2	108	1	KV1A_HUMAN	P01593 homo sapien
40	417	54.2	240	2	Q65ZC9	Q65zc9 homo sapien
41	415	54.0	108	1	KV1E_HUMAN	P01597 homo sapien
42	415	54.0	108	1	KV1M_HUMAN	P01605 homo sapien
43	415	54.0	108	1	KV1S_HUMAN	P01611 homo sapien
44	414.5	53.9	107	1	KV1D_HUMAN	P01596 homo sapien
45	414	53.8	108	1	KV1F_HUMAN	P01598 homo sapien

ALIGNMENTS

RESULT 1

ID	Q6GMW1	PRELIMINARY;	PRT;	236 AA.
AC	Q6GMW1;			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Splicein;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J.J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marz M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RL	and mouse cDNA sequences."			
Proc. Natl. Acad. Sci. U.S.A.	99:16899-16903(2002).			
[2]				
SEQUENCE FROM N.A.				
TISSUE=Splicein;				
RC	Strausberg R.;			
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC073791; AAH73791.1; -			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG MHC.			
DR	InterPro; IPR003596; IG v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	Pfam; PF00047; IG; 2.			
DR	SMART; SM00409; IGC1; 1.			
DR	SMART; SM00407; IGC1; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			

	Best Local Similarity	85.4%	Pred. No. 2.4e-55;	Mismatches	4;	Mismatches	17;	Indels	0;	Gaps	0
Qy	2	QSPSLGASVGRVTITCRASQDINDNLGWYQQKPGKAPKGLIIYAASNLSQGVPSPRFGS	61								
Dd	26	QSPSSFASASTGRVTITCRASQSIGSYLAWYQQKPGKAPQLLIYAASLTQSGVPSRFGS	85								
Qy	62	GSGETFTLTISSLOPEDPATYTCIQKYTPMTFGOGTKVEIKRTVAASPVIFFPDSBQL	121								
Dd	86	ASGTDFTLSTISLCLOSEDPATYYCQYYTYPMTFGQTKVEIKRTVAASPVIFFPDSBQL	145								
Qy	122	KSGTASVVCLLNFPYPREXKHQK	145								
Dd	146	KSGTASVVCLLNFPYPREAKQWK	169								

RESULT 4

Q6GMX8 PRELIMINARY; PRT; 236 AA.

AC Q6GMX8;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI_TaxID=9606;

OC [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Primary B-Cells;

RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Datschenko L., Marubina K., Farmer A.A., Rubin G.W., Hong L.,

RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan K.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RT [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Primary B-Cells;

RC Strausberg R.

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

RL EMBL; BC073764; AAH73764.1; -

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG cl.

DR InterPro; IPR003006; IG MHC.

DR InterPro; IPR003596; IG v.

DR Pfam; PF07654; Cl-set; 1.

DR Pfam; PF00047; Ig; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGcl; 1.

DR SMART; SM00406; Igv; 1.

DR PROSITE; PS50835; IG LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein.

SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match	81.8%;	Score 629;	DB 2;	Length 236;
Best Local Similarity	85.4%;	Pred. No. 6.2e-55;		
Matches 123;	Conservative 8;	Mismatches 13;	Indels 0;	Gaps 0
Qy	2	QSPSSLSASVGDRTVITCRASQDTRDNLGNWQOKPGKAPKELIIYAASNLQSGVPSRFFSGS	61	
Db	28	QSPSSVSASVGDRTVITCRASQGISSWLAWYQQKPGKAPKLLIIYAASLSQSGVPSRFFSGS	87	
Qy	62	GSGETFTLTISSLPQDFATYCYLQYKTYPMWTFQGTKEIKRTVAASPFIFFPSDEQL	121	
Db	88	GSGETFTLTISSLPQDFATYCYCOAHSFPFTFGPGTKVDIKRTVAASPFIFFPSDEQL	147	
Qy	122	KSGTASVVCLLNNFYPREXKEHQK	145	
Db	148	KSGTASVVCLLNNFYPREAKVQWK	171	

RESULT 5

Q6GMX9 PRELIMINARY; PRT; 236 AA.

Q6GMX9

AC 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

DE Hypothetical protein.

DE Homo sapiens (Human).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_Taxid=9606;

[1]

RN SEQUENCE FROM N.A.

RP

RP TISSUE=Primary B-Cells;

RC MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Haile S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Wahing J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywicki M.I., Skalak U., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

[2]

RN SEQUENCE FROM N.A.

RP

RP TISSUE=Primary B-Cells;

RX Strausberg R.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBSJ databases.

DR EMBL; BC073763; AAH73763.1; -;

DR InterPro; IPR003599; IG.

DR InterPro; IPR007110; IG-like.

DR InterPro; IPR003597; IG cl.

DR InterPro; IPR003006; IG_WHC.

DR InterPro; IPR003596; IG_v.

DR Pfam; PF07654; Cl-set; 1.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00407; IGC1; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG-LIKE; 2.

DR PROSITE; PS00290; IG_WHC; UNKNOWN_1.

DR Hypothetical protein.

KW

SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFE7 CRC64;

KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FE8E351 CRC64;
Query Match 80.4%; Score 618; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 8e-54;
Matches 120; Conservative 8; Mismatches 16; Indels 0; Gaps 0;
QY 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPKAPKRLIYAASNLQSGVPSRFGS 61
DB 28 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPKAPKRLIYAASNLQSGVPSRFGS 87
QY 62 GSGTEFTLTISLQPEDFATYVCLOQKTYPTVFGGTVKVEIKRTVAAPSVFIFPPSDQL 121
DB 88 GSGTEFTLTISLQPEDFATYVCLOQKTYPTVFGGTVKVEIKRTVAAPSVFIFPPSDQL 147
QY 122 KSGTASVCLLNPNFYPREKHEQK 145
DB 148 KSGTASVCLLNPNFYPREKQVQWK 171
RESULT 8
Q6GMXO
ID Q6GMXO PRELIMINARY; PRT; 236 AA.
AC Q6GMXO
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;
Query Match 78.9%; Score 607; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 1e-52;
Matches 120; Conservative 7; Mismatches 17; Indels 0; Gaps 0;
QY 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPKAPKRLIYAASNLQSGVPSRFGS 61
DB 28 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPKAPKRLIYAASNLQSGVPSRFGS 87
QY 62 GSGTEFTLTISLQPEDFATYVCLOQKTYPTVFGGTVKVEIKRTVAAPSVFIFPPSDQL 121
DB 88 GSGTEFTLTISLQPEDFATYVCLOQKTYPTVFGGTVKVEIKRTVAAPSVFIFPPSDQL 147
QY 122 KSGTASVCLLNPNFYPREKHEQK 145
DB 148 KSGTASVCLLNPNFYPREKQVQWK 171
RESULT 9
Q6PIH4
ID Q6PIH4 PRELIMINARY; PRT; 236 AA.
AC Q6PIH4
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
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RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034146; AAH34146.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igcl; 1.
DR SMART; SM00406; IGV; 1.

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DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 236 AA; 25871 MW; B801A28CD06BEE26 CRC64;

Query Match 77.8%; Score 598; DB 2; Length 236;
Best Local Similarity 82.6%; Pred. No. 8.1e-52;
Matches 119; Conservative 6; Mismatches 19; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPGKAPKELIYAAASNLQSGVPSRSGS 61
Db 28 QSPSTLSASVGDRTVITCRASQISDWLAWYQKPGKAPKLLIYDASRLKESGVPSRSGS 87
Qy 62 GSGTEFTLTISLQPEDPATYCYCQYKTYPTWFGQGTQKVEIKRTVAAPSVEIFFPSDEQL 121
Db 88 GSGTEFTLTISGLQDDPATYCYCQYNSNSPFGQGTQKVEIKRTVAAPSVEIFFPSDEQL 147
Qy 122 KSGTASVCLNNFYPREXKEHOK 145
Db 148 KSGTASVCLNNFYPREXKEHOK 171

RESULT 10
Q6GMW0 PRELIMINARY; PRT; 235 AA.
ID Q6GMW0
AC Q6GMW0
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003596; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein_
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 72.1%; Score 554.5; DB 2; Length 235;
Best Local Similarity 73.1%; Pred. No. 1.9e-47;
Matches 106; Conservative 18; Mismatches 20; Indels 1; Gaps 1;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQKPGKAPKELIYAAASNLQSGVPSRSGS 61
Db 26 QSPSTLSASVGDRTVITCRASQISDWLAWYQKPGKAPKLLIYDASRLKESGVPSRSGS 85
Qy 62 GSGTEFTLTISLQPEDPATYCYCQYKTYPTWFGQGTQKVEIKRTVAAPSVEIFFPSDEQ 120
Db 86 GSGTEFTLTISLQSEDPAVYFCQYNDWLLTYFGQGTQKLEIKRTVAAPSVEIFFPSDEQ 145
Qy 121 LKSGTASVCLNNFYPREXKEHOK 145
Db 146 LKSGTASVCLNNFYPREXKEHOK 170

RESULT 11
Q6PIL8 PRELIMINARY; PRT; 236 AA.
ID Q6PIL8
AC Q6PIL8
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032451; AAH32451.1; -.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
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DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match          70.0%; Score 538; DB 2; Length 236;
Best Local Similarity 71.2%; Pred. No. 8.7e-46;
Matches 104; Conservative 17; Mismatches 23; Indels 2; Gaps 2;

QY 2 QSPSLSASVGDRTTICRASQDIRDN-LGWYQQKPGKAPKRLIYAASNLSQGVPSRFSG 60
DB 26 QSPGLTSLSPGRATLSCRASQSLSSYLAWTQQPGQAPRLIYGVSSRATGIPDRFSG 85
QY 61 SGSSTFTLTSSLOPEDFATYICLQYKT-YPWTFQGTQKVEIKRTVAAPSFIIPPSPDE 119
DB 86 SGSSTFTLTSLRLEPEDFATYICQYGTSPRITFGQGTRLDKETVAAPSFIIPPSPDE 145
QY 120 QKSGTASVVCLLNNFYPREKHEQK 145
DB 146 QKSGTASVVCLLNNFYPREKQVWK 171

RESULT 12
Q6GMV9 PRELIMINARY; PRT; 235 AA.
AC Q6GMV9;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH3793.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003596; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
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DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match          69.6%; Score 535.5; DB 2; Length 235;
Best Local Similarity 71.7%; Pred. No. 1.5e-45;
Matches 104; Conservative 14; Mismatches 26; Indels 1; Gaps 1;

QY 2 QSPSLSASVGDRTTICRASQDIRDN-LGWYQQKPGKAPKRLIYAASNLSQGVPSRFSG 60
DB 26 QSPGLTSLSPGRATLSCRASQSLSSYLAWTQQPGQAPRLIYGVSSRATGIPDRFSG 85
QY 61 SGSSTFTLTSSLOPEDFATYICLQYKTYPWTFTQGTQKVEIKRTVAAPSFIIPPSPDEQ 120
DB 86 SGSSTFTLTSLRLESEDFALYFCQYGTSPITFGGQTKVEIKRTVAAPSFIIPPSPDEQ 145
QY 121 LKSGTASVVCLLNNFYPREKHEQK 145
DB 146 LKSGTASVVCLLNNFYPREKQVWK 170

RESULT 13
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8;
DT 05-JUL-2004 (TReMBLrel. 27, Created)
DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
```

DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;

Query Match 69.1%; Score 531; DB 2; Length 236;
Best Local Similarity 70.5%; Pred. No. 4.4e-45;
Matches 103; Conservative 18; Mismatches 23; Indels 2; Gaps 2;

Qy 2 QSPSSLASVGDRTVITCRASQDI-RNLLGWYQKPGKAPKRLIYAASNLSQGVPSRFSG 60
Db 26 QSPGTLSPGGERATLSGASQTVFSSHLAWYQKPGQAPRLLIYGASSRATGIPDRFSG 85

Qy 61 SGSGTEFTLTISLQPEDFATYICLYQKTYT-WTFGQTKVEIKRTVAAPSVFIPPPSDE 119
Db 86 SGSGTDFTLITLLEPEDFAVYFCQYGTSPSLTFGGGTRVEIKRTVAAPSVFIPPPSDE 145

Qy 120 QLKSGTASVCLNNFYPREKHEQK 145
Db 146 QLKSGTASVCLNNFYPREAKVQWK 171

RESULT 14

ID Q6PJF2 PRELIMINARY; PRT; 235 AA.
AC Q6PJF2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinstead J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
DR Submitted (OCT-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC016380; AAH16380.1; --
DR HSSP; P01837; 1KCU.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.

DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 68.6%; Score 527.5; DB 2; Length 235;
Best Local Similarity 69.7%; Pred. No. 9.9e-45;
Matches 101; Conservative 19; Mismatches 24; Indels 1; Gaps 1;

Qy 2 QSPSSLASVGDRTVITCRASQDI-RNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSG 60
Db 26 QSPATLSLSPGERATLSGASQIVSSAYLAWYQKPGQAPRLLMFGSSSRATGIPDRFSG 85

Qy 61 SGSGTEFTLTISLQPEDFATYICLYQKTYT-WTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
Db 86 SGSGTDFTLITLLEPEDFAVYFCQYGTSPSGTGTGKVDIKRTVAAPSVFIPPPSDEQ 145

Qy 121 LKSGTASVCLNNFYPREKHEQK 145
Db 146 LKSGTASVCLNNFYPREAKVQWK 170

RESULT 15

ID Q7TS98 PRELIMINARY; PRT; 236 AA.
AC Q7TS98;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Anti-colorectal carcinoma light chain.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=93383497; PubMed=8372513;
RX Tonge D.W., Hennam J.F., Greene A.R., Lee I.D., Edge M.D.;
RT "Cloning and characterization of 1116N919.9 heavy and light chain
cDNAs and expression of antibody fragments in *Escherichia coli*.";
RL Year Immunol. 7:56-62(1993).
DR EMBL; S65921; AAB28160.1; --
DR HSSP; P01837; 1KBS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA10F4C CRC64;

Query Match 65.8%; Score 506; DB 2; Length 236;
Best Local Similarity 69.1%; Pred. No. 1.4e-42;
Matches 96; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTVITCRASQDI-RNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGS 61
Db 28 QSPSSMTASGERVTITCRASQDINSYLSYFQQKPGKSPKTLIYRANLVDGVSFRFSGS 87

Qy 62 SGSGTEFTLTISLQPEDFATYICLYQKTYT-WTFGQTKVEIKRTVAAPSVFIPPPSDEQ 121
Db 88 GSGQDYSLTISLSEYEDMGVIYCYQYDFPRFTGGTKLEIKRADAAPTVSIFPPSSQ 147

Qy 122 KSGTASVCLNNFYPREX 140
Db 148 TSGGASVVCFLNNFYPKDI 166

Search completed: March 8, 2005, 06:35:50
Job time : 54.8971 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 68.1532 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-30

Perfect score: 769

Sequence: 1 GQSPSSLSASVGRVTTCR.....VCLLNFFPREXKHQKSP 147

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	769	100.0	147	2	AAY34312 Igm antib
2	706	91.8	147	2	AAY34310 Igm antib
3	694	90.2	236	5	ABG77164 Germline
4	694	90.2	236	8	ADR28586 Human ant
5	688	89.5	236	8	ADP07905 Human imm
6	684	88.9	234	8	ADS84458 Human ant
7	684	88.9	234	8	ADR68600 Human ant
8	683	88.8	184	8	ADR68581 Human ant
9	683	88.8	184	8	ADR68581 Human ant
10	682	88.7	236	5	ABG77160 Germline
11	682	88.7	236	8	ADR28582 Human ant
12	680	88.4	215	8	ADH10328 Anti-HIV-
13	675	87.8	152	8	ADK52390 Human ant
14	675	87.8	152	8	ADK52354 Human ant
15	674	87.6	234	8	ADS84470 Human ant
16	674	87.6	234	8	ADR68612 Human ant
17	671	87.3	234	8	ADS84452 Human ant
18	671	87.3	234	8	ADR68594 Human ant
19	670	87.1	234	8	ADS84464 Human ant
20	670	87.1	234	8	ADR68606 Human ant
21	668	86.9	234	8	ADS84476 Human ant
22	668	86.9	234	8	ADR68618 Human ant
23	666	86.6	236	5	ABG77163 Amino aci
24	666	86.6	236	8	ADR28585 Human ant
25	663	86.2	164	7	ADD28242 Human het

26	657	85.4	236	5	ABG77159	Abg77159 Amino aci
27	657	85.4	236	8	ADR28581	Adr28581 Human ant
28	655	85.2	212	6	AAO31100	Aao31100 Human A2-
29	650	84.5	224	4	RAA75043	Raa75043 TRO005 Hu
30	649	84.4	214	7	ADC26154	Adc26154 Parent an
31	649	84.4	237	5	ABB81107	Abb81107 Anti-VEGF
32	649	84.4	237	5	ABP51952	Abp51952 Plasmid p
33	649	84.4	237	8	ADO14128	Ado14128 Plasmid p
34	649	84.4	237	8	ADO14131	Ado14131 Plasmid p
35	649	84.4	237	8	ADQ90703	Adq90703 Anti-VEGF
36	649	84.4	237	8	ADQ90701	Adq90701 Anti-VEGF
37	649	84.4	237	8	ADQ90705	Adq90705 Anti-VEGF
38	649	84.4	237	8	ADQ90709	Adq90709 Anti-VEGF
39	649	84.4	237	8	ADQ90723	Adq90723 Anti-VEGF
40	649	84.4	237	8	ADQ90721	Adq90721 Anti-VEGF
41	649	84.4	237	8	ADQ90707	Adq90707 Anti-VEGF
42	647	84.1	237	2	AAW70703	Aaw70703 Protein e
43	647	84.1	650	5	ABP61241	Abp61241 Phage-dis
44	645.5	83.9	241	4	RAA82912	Raa82912 Human imm
45	644	83.7	236	5	AAU74297	Aau74297 Anti-huma

ALIGNMENTS

RESULT 1
AAY34312
ID AAY34312 standard; protein; 147 AA.
XX
AC AAY34312;
XX
DT 19-NOV-1999 (first entry)
XX
DE Igm antibody CEM 10.12 G5 kappa chain sequence.
XX
KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 140
FT /label= unknown
FT /note= "encoded by GMC"
XX
XX WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
XX
N-PSDB; AAZ20413.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 61; Fig 27; 245pp; English.
XX
CC This sequence represents the kappa chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAb) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the Igm MAb ABX-CBL, providing that the antibody is not CBL1. The MAb

CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 147 AA;

Query Match 100.0%; Score 769; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 9.1e-50;
Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GQSPSSLSASVGDRTVITCRASQDIRNLGWYQQKPGKAPKRLIYAASNLSQGVPSRFSG 60
Db 1 GQSPSSLSASVGDRTVITCRASQDIRNLGWYQQKPGKAPKRLIYAASNLSQGVPSRFSG 60

Qy 61 SGSCTEFTLTSSLOPEDFATYYCLOYKTPWTFGQGTKEIKRTVAAPSVFIFFPSDEQ 120
Db 61 SGSCTEFTLTSSLOPEDFATYYCLOYKTPWTFGQGTKEIKRTVAAPSVFIFFPSDEQ 120

Qy 121 LKSGTASVVCLLNNFYPREXKEHQSP 147
Db 121 LKSGTASVVCLLNNFYPREXKEHQSP 147

RESULT 2
AAY34310
ID AAY34310 standard; protein; 147 AA.
XX
AC AAY34310;
XX
DT 19-NOV-1999 (first entry)
XX
DE IgM antibody CEM 10.1 G10 kappa chain sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
FN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
DR N-PSDB; AAZ20411.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 61; Fig 25; 245pp; English.
XX
CC This sequence represents the kappa chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft

CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 147 AA;

Query Match 91.8%; Score 706; DB 2; Length 147;
Best Local Similarity 93.2%; Pred. No. 4.4e-45;
Matches 136; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRNLGWYQQKPGKAPKRLIYAASNLSQGVPSRFSG 61
Db 2 QSPSSLSASVGERVITTCRASQGIREDLWYQQKPGKAPKRLIYVASSLSQGVPSRFSG 61

Qy 62 GSGTEFTLTSSLOPEDFATYYCLOYKTPWTFGQGTKEIKRTVAAPSVFIFFPSDEQL 121
Db 62 GSGTEFTLTSSLOPEDFATYYCLOYKTPWTFGQGTKEIKRTVAAPSVFIFFPSDEQL 121

Qy 122 KSGTASVVCLLNNFYPREXKEHQSP 147
Db 122 KSGTASVVCLLNNFYPREXKEHQSP 147

RESULT 3
ABG77164
ID ABG77164 standard; protein; 236 AA.
XX
AC ABG77164;
XX
DT 24-OCT-2002 (first entry)
XX
DE Germline protein sequence of anti-IGF-IR antibody AJ30/Jk1.
XX
KW Insulin-like growth factor I receptor; antibody; human; cytostatic;
KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour;
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
KW acromegaly; gigantism; psoriasis; atherosclerosis.
XX
OS Homo sapiens.
XX
FN WO200253596-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-US051113.
XX
PR 05-JAN-2001; 2001US-0259927P.
XX
PA (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
DR WPI; 2002-575410/61.
XX
PT Novel humanized, chimeric monoclonal antibody that specifically binds to
PT insulin-like growth factor I (IGF-1) receptor useful for inhibiting
PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
XX
PS Disclosure; Fig 19E; 172pp; English.
XX
CC This invention relates to a novel humanised, chimeric or human monoclonal
CC antibody or its antigen binding portion that specifically binds to
CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the
CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
CC phosphorylation. The antibodies of the invention are useful for
CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
CC subject. The antibody or its antigen-binding portion is also useful for
CC treating cancer in a human. The method for this further involves an anti
CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
CC antibodies may also be useful for increasing IGF-IR activity and thus

CC restoring IGF-IR activity in a condition characterised by low IGF-IR
CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
CC also useful for inducing apoptosis of specific cells in a patient, and to
CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,
CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
CC minimise the immunogenic and allergic responses intrinsic to mouse or
CC mouse-derived monoclonal antibodies and thus increase the efficacy
CC and safety of the administered antibodies. The present sequence
CC represents an anti-insulin-like growth factor I receptor antibody of the
XX invention
XX
SQ Sequence 236 AA;

Query Match 90.2%; Score 694; DB 5; Length 236;
Best Local Similarity 92.4%; Pred. No. 5.5e-44;
Matches 133; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRNDLIGWYQKPGKAPKRLIYAASNLQSGVPSRFGSGS 61
Db 28 QSPSSLSASVGDRTVITCRASQDIRNDLIGWYQKPGKAPKRLIYAASNLQSGVPSRFGSGS 87

Qy 62 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 121
Db 88 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 147

Qy 122 KSGTASVVCLLNFPYREXKEHQK 145
Db 148 KSGTASVVCLLNFPYREXKEHQK 171

RESULT 4
ADR28586
ID ADR28586 standard; protein; 236 AA.
XX
AC ADR28586;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human anti-IGF-IR antibody heavy chain A30/Jk1 protein SEQ ID NO:52.
XX
KW aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;
KW T-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;
KW neurodegenerative disorder; human;
KW anti-insulin-like growth factor I receptor antibody;
KW anti-IGF-IR antibody; cytostatic; immunosuppressive; endocrine;
KW vasotropic; neuroprotective; nootropic; antithyroid; vaccine;
KW gene therapy.
XX
OS Homo sapiens.
XX
FN WO2004071529-A2.
XX
PD 26-AUG-2004.
XX
PF 03-FEB-2004; 2004WO-IB000366.
XX
PR 13-FEB-2003; 2003US-047353P.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;
PI Cuemano JD, Guyot DJ, Page KL;
XX
DR WPI; 2004-625776/60.
XX
PT Treating or preventing aging or a disorder (e.g. multiple myeloma,
PT autoimmune disease or neurodegenerative disorder) in humans comprises
PT administering an amount of a human anti-insulin-like growth factor I
PT receptor antibody.
XX
PS Disclosure; SEQ ID NO 52; 105pp; English.
XX
CC The present invention describes a method for treating or preventing aging

CC or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
CC ischaemia or neurodegenerative disorder) in a mammal. The method
CC comprises administering to the mammal an amount of a human anti-insulin-
CC like growth factor I receptor (IGF-IR) antibody. Also described is a
CC pharmaceutical composition for treating or preventing the above-mentioned
CC disorder in a mammal, comprising an amount of the human anti-IGF-IR
CC antibody and a pharmaceutical carrier. The composition has cytostatic,
CC immunosuppressive, endocrine, vasotropic, neuroprotective, nootropic and
CC antithyroid activities, and can be used in vaccines and in gene therapy.
CC The method and composition are useful for preventing or treating aging or
CC a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
CC ischaemia or neurodegenerative disorder) in mammals, such as humans. The
CC human IGF-IR antibody is used in preparing a composition for the
CC treatment or prevention of the above-mentioned disorders. The present
CC sequence represents a human anti-IGF-IR antibody light chain amino acid
XX sequence, which is used in the exemplification of the present invention.
XX
SQ Sequence 236 AA;

Query Match 90.2%; Score 694; DB 8; Length 236;
Best Local Similarity 92.4%; Pred. No. 5.5e-44;
Matches 133; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRNDLIGWYQKPGKAPKRLIYAASNLQSGVPSRFGSGS 61
Db 28 QSPSSLSASVGDRTVITCRASQDIRNDLIGWYQKPGKAPKRLIYAASNLQSGVPSRFGSGS 87

Qy 62 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 121
Db 88 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 147

Qy 122 KSGTASVVCLLNFPYREXKEHQK 145
Db 148 KSGTASVVCLLNFPYREXKEHQK 171

RESULT 5
ADP07905
ID ADP07905 standard; protein; 236 AA.
XX
AC ADP07905;
XX
DT 29-JUL-2004 (first entry)
XX
DE Human immunoglobulin light chain variable region.
XX
KW monoclonal antibody; tumour growth factor-beta type II receptor;
KW TGF-beta type II receptor; kidney disease; nephrosclerosis;
KW pulmonary fibrosis; liver cirrhosis; blood-vessel restenosis;
KW arteriosclerosis; psoriasis; scleroderma; atopy; keloid; arthritis;
KW human; light chain variable region.
XX
OS Homo sapiens.
XX
FN JP2004121001-A.
XX
PD 22-APR-2004.
XX
PF 07-AUG-2002; 2002JP-00230851.
XX
PR 07-AUG-2002; 2002JP-00230600.
XX
PA (NISB) JAPAN TOBACCO INC.
XX
XX WPI; 2004-322721/30.
DR N-PSDB; ADP07904.
XX
PT Novel monoclonal antibody coupled with human transforming growth factor
PT (TGF)-beta type II receptor, useful for treating or preventing
PT arteriosclerosis, psoriasis, scleroderma, atopy, keloid, arthritis.
XX

PS Claim 31; SEQ ID NO 9; 78pp; Japanese.

XX The invention comprises a monoclonal antibody coupled with human tumour

CC growth factor-beta (TGF-beta) type II receptor. The monoclonal antibody

CC coupled with human TGF-beta type II receptor of the invention is useful

CC for treating or preventing: kidney disease, nephrosclerosis, pulmonary

CC fibrosis, liver cirrhosis, blood-vessel restenosis, arteriosclerosis,

CC psoriasis, scleroderma, atopy, keloid and arthritis. The present amino

CC acid sequence represents a human immunoglobulin light chain variable

CC region.

XX

SQ Sequence 236 AA;

Query Match 89.5%; Score 688; DB 8; Length 236;

Best Local Similarity 91.7%; Pred. No. 1.5e-43;

Matches 132; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITTCRASQDIRNDLNGWYQKPGKAPKRLIYAASNLSQGVSRFSGS 61

Db 28 QSPSSLSASVGDRTVITTCRASQDIRNDLNGWYQKPGKAPKRLIYAASNLSQGVSRFSGS 87

Qy 62 GSGTEFTLTISLQPEDFATYCYLQYKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121

Db 88 GSGTEFTLTISLQPEDFATYCYLQYKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 147

Qy 122 KSGTASVVCLLNFFPREKXEHQK 145

Db 148 KSGTASVVCLLNFFPREKXQWK 171

RESULT 6

ADS84458

ID ADS84458 standard; protein; 234 AA.

AC ADS84458;

XX

DT 18-NOV-2004 (first entry)

XX

DE Human anti-EPO-R antibody Ab412 light chain SEQ ID NO:97.

XX

KW human; erythropoietin receptor; EPO receptor;

KW erythropoietin receptor binding antibody; EPO receptor binding antibody;

KW antianaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;

KW wound healing; neural cell damage protection;

KW neural tissue damage protection; brain injury; spinal cord injury;

KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.

XX

OS Homo sapiens.

XX

PN WO2004035603-A2.

XX

PD 29-APR-2004.

XX

PF 14-OCT-2003; 2003WO-US032243.

XX

PR 14-OCT-2002; 2002US-00269711.

XX

PR 10-OCT-2003; 2003US-00684109.

XX

PA (ABBO) ABBOTT LAB.

XX

PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;

XX

DR WPI; 2004-348433/32.

DR N-PSDB; ADS84456, ADS84457.

XX

XX New antibodies that bind to or activate an endogenous human

PT erythropoietin receptor, useful for diagnosing, preventing or treating

PT disorders associated with dysfunctional erythropoietin receptor, e.g.

PT anaemia.

XX

PS Disclosure; SEQ ID NO 97; 192pp; English.

XX

CC The present invention describes an antibody or its fragment that binds to

or activates an endogenous activity of a human erythropoietin (EPO) receptor in a mammal, but does not interact with a peptide having a sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1) methods of modulating or activating an endogenous activity of a human EPO receptor in a mammal, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (2) a method of treating a mammal suffering from aplasia, comprising administering to the mammal a therapeutic amount of the above antibody or its fragment to modulate or activate the receptor; (3) a pharmaceutical composition comprising a therapeutic amount of the above antibody or antibody fragment, and a pharmaceutical excipient; (4) an isolated and purified polynucleotide sequence, and their fragments, complements and degenerate codon equivalents; and (5) an isolated and purified amino acid sequence, and their fragments. The EPO receptor binding antibody has antianaemic, neuroprotective and vulnary activities, and can be used in gene therapy. The compositions and methods from the present invention can be used for modulating an endogenous activity of a human EPO receptor or for treating mammals suffering from aplasia or anaemia. They may also be used for identifying mammals having a dysfunctional EPO receptor. The composition may also be used in promoting wound healing or in protecting against neural cell and/or tissue damage resulting from brain/spinal cord injury, stroke and the like. The present sequence represents a human anti-EPO-R antibody light chain, which is given in the exemplification of the present invention.

XX

SQ Sequence 234 AA;

Query Match 88.9%; Score 684; DB 8; Length 234;

Best Local Similarity 92.4%; Pred. No. 3e-43;

Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITTCRASQDIRNDLNGWYQKPGKAPKRLIYAASNLSQGVSRFSGS 61

Db 26 QSPSSLSASVGDRTVITTCRASQDIRNDLNGWYQKPGKAPKRLIYAASNLSQGVSRFSGS 85

Qy 62 GSGTEFTLTISLQPEDFATYCYLQYKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121

Db 86 GSGTEFTLTISLQPEDFATYCYLQYKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 145

Qy 122 KSGTASVVCLLNFFPREKXEHQK 145

Db 146 KSGTASVVCLLNFFPREKXQWK 169

RESULT 7

ADR68600

ID ADR68600 standard; protein; 234 AA.

XX

AC ADR68600;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human antibody Ab412 light chain polypeptide seqid 97.

XX

KW antianaemic; respiratory; vulnary; gene therapy; vaccine;

KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;

KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;

KW wound healing; neural cell damage; tissue damage; brain injury;

KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain; AB412.

XX

OS Homo sapiens.

XX

PN US2004175379-A1.

XX

PD 09-SEP-2004.

XX

PF 10-OCT-2003; 2003US-00684109.

XX

PR 14-OCT-2002; 2002US-0418031P.

XX

PA (DEVRI/) DEVRIES P J.

FA (OSTR/) OSTROW D H.

PA (REIL/) REILLY E B.
 PA (GREE/) GREEN L L.
 PA (WIEL/) WIELER J.
 XX
 PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
 DR WPI: 2004-661369/64.
 DR N-PSDB; ADR68598.
 XX
 XX New antibody or its antibody fragment that activates an endogenous
 PT activity or is capable of binding to a human erythropoietin receptor in a
 PT mammal, useful for treating a mammal suffering aplasia or anemia.
 XX
 PS Disclosure; SEQ ID NO 97; 156pp; English.
 XX
 CC The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin
 CC receptor in a mammal, or that comprises at least one heavy or light chain
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOs between SEQ ID NO: 2-56) given in
 CC the specification, and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOs between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This sequence represents a human Ab412 antibody
 CC light chain polypeptide.
 XX
 SQ Sequence 234 AA;
 Query Match 88.9%; Score 684; DB 8; Length 234;
 Best Local Similarity 92.4%; Pred. No. 3e-43;
 Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 61
 Db 26 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 85
 QY 62 GSGTEFTLTISLQPEDFATYICLYQKTYPTWTFQGTKEIKRTVAAPSVFIFFPSDQL 121
 Db 86 GSGTEFTLTISLQPEDFATYICLYQKTYPTWTFQGTKEIKRTVAAPSVFIFFPSDQL 145
 QY 122 KSGTASVVCLNNFYPREXKEHQK 145
 Db 146 KSGTASVVCLNNFYPREXKEHQK 169
 RESULT 8
 ADS84439
 ID ADS84439 standard; protein; 184 AA.
 XX
 AC ADS84439;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human anti-EPO-R antibody Ab12 light chain SEQ ID NO:78.
 XX

KW human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianaemic; neuroprotective; vulnary; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO2004035603-A2.
 PD 29-APR-2004.
 XX
 PF 14-OCT-2003; 2003WO-US032243.
 XX
 PR 14-OCT-2003; 2002US-00269711.
 PR 10-OCT-2003; 2003US-00684109.
 XX
 PA (ABBO) ABBOTT LAB.
 PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 DR WPI: 2004-348433/32.
 DR N-PSDB; ADS84437; ADS84438.
 XX
 PT New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.
 XX
 PS Claim 41; SEQ ID NO 78; 192pp; English.
 XX
 CC The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,
 CC complements and degenerate codon equivalents; and (5) an isolated and
 CC purified amino acid sequence, and their fragments. The EPO receptor
 CC binding antibody has antianaemic, neuroprotective and vulnary
 CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from
 CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence represents a human anti-EPO-R antibody light
 CC chain, which is given in the exemplification of the present invention.
 XX
 SQ Sequence 184 AA;
 Query Match 88.8%; Score 683; DB 8; Length 184;
 Best Local Similarity 92.4%; Pred. No. 2.8e-43;
 Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 QY 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 61
 Db 28 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 87
 QY 62 GSGTEFTLTISLQPEDFATYICLYQKTYPTWTFQGTKEIKRTVAAPSVFIFFPSDQL 121
 Db 88 GSGTEFTLTISLQPEDFATYICLYQKTYPTWTFQGTKEIKRTVAAPSVFIFFPSDQL 147
 QY 122 KSGTASVVCLNNFYPREXKEHQK 145

CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
 CC also useful for inducing apoptosis of specific cells in a patient, and to
 CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,
 CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
 CC minimise the immunogenic and allergic responses intrinsic to mouse or
 CC mouse-derived monoclonal antibodies and thus increase the efficacy
 CC and safety of the administered antibodies. The present sequence
 CC represents an anti-insulin-like growth factor I receptor antibody of the
 CC invention
 XX
 SQ Sequence 236 AA;

Query Match 88.7%; Score 682; DB 5; Length 236;
 Best Local Similarity 91.0%; Pred. No. 4.3e-43;
 Matches 131; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTTITCRASQDIRNDLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 61
 DB 28 QSPSSLSASVGDRTTITCRASQDIRNDLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 87

QY 62 GSGTEFTLTISLQPEDPATYCYLYKTPWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121
 DB 88 GSGTEFTLTISLQPEDPATYCYLYKTPWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 147

QY 122 KSGTASVVCLNNFYPREXKEHQK 145
 DB 148 KSGTASVVCLNNFYPREXKEHQK 171

RESULT 11
 ADR28582
 ID ADR28582 standard; protein; 236 AA.
 AC
 XX
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human anti-IGF-IR antibody light chain A30/Jk2 protein SEQ ID NO:48.
 XX
 KW aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;
 KW T-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;
 KW neurodegenerative disorder; human;
 KW anti-insulin-like growth factor I receptor antibody;
 KW anti-IGF-IR antibody; cytostatic; immunosuppressive; endocrine;
 KW vasotropic; neuroprotective; nontropic; antithyroid; vaccine;
 KW gene therapy.
 XX
 OS Homo sapiens.
 XX
 XX WO2004071529-A2.
 XX
 XX 26-AUG-2004.
 XX
 XX 03-FEB-2004; 2004WO-IB000366.
 XX
 XX 13-FEB-2003; 2003US-0447353P.
 XX
 XX (PFIZ) PFIZER PROD INC.
 XX
 XX Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;
 PI Cusmano JD, Guyot DU, Page KU;
 XX
 XX WPI; 2004-625776/60.
 XX
 XX Treating or preventing aging or a disorder (e.g. multiple myeloma,
 PT autoimmune disease or neurodegenerative disorder) in humans comprises
 PT administering an amount of a human anti-insulin-like growth factor I
 PT receptor antibody.
 XX
 XX Disclosure; SEQ ID NO 48; 105pp; English.
 PS
 CC The present invention describes a method for treating or preventing aging
 CC or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus

CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
 CC ischaemia or neurodegenerative disorder) in a mammal. The method
 CC comprises administering to the mammal an amount of a human anti-insulin-
 CC like growth factor I receptor (IGF-IR) antibody. Also described is a
 CC pharmaceutical composition for treating or preventing the above-mentioned
 CC disorder in a mammal, comprising an amount of the human anti-IGF-IR
 CC antibody and a pharmaceutical carrier. The composition has cytostatic,
 CC immunosuppressive, endocrine, vasotropic, neuroprotective, nontropic and
 CC antithyroid activities, and can be used in vaccines and in gene therapy.
 CC The method and composition are useful for preventing or treating aging or
 CC a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
 CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
 CC ischaemia or neurodegenerative disorder) in mammals, such as humans. The
 CC human IGF-IR antibody is used in preparing a composition for the
 CC treatment or prevention of the above-mentioned disorders. The present
 CC sequence represents a human anti-IGF-IR antibody light chain amino acid
 CC sequence, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 236 AA;

Query Match 88.7%; Score 682; DB 8; Length 236;
 Best Local Similarity 91.0%; Pred. No. 4.3e-43;
 Matches 131; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTTITCRASQDIRNDLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 61
 DB 28 QSPSSLSASVGDRTTITCRASQDIRNDLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 87

QY 62 GSGTEFTLTISLQPEDPATYCYLYKTPWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 121
 DB 88 GSGTEFTLTISLQPEDPATYCYLYKTPWTFGGTKVEIKRTVAAPSVFIFFPSDEQL 147

QY 122 KSGTASVVCLNNFYPREXKEHQK 145
 DB 148 KSGTASVVCLNNFYPREXKEHQK 171

RESULT 12
 ADH10328
 ID ADH10328 standard; protein; 215 AA.
 AC ADH10328;
 XX
 DT 11-MAR-2004 (first entry)
 XX
 DE Anti-HIV-gp120-antibody light chain sequence.
 XX
 KW Glycoprotein; gp120; anti-HIV; vaccine; antibody S8; human; antibody S19;
 KW antibody S20.
 XX
 OS Homo sapiens.
 XX
 XX EP1371660-A1.
 XX
 XX 17-DEC-2003.
 XX
 XX 14-JUN-2002; 2002EP-00380126.
 XX
 XX 14-JUN-2002; 2002EP-00380126.
 XX
 XX (CNSJ) CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
 PA (PHAA) PHARMACIA SPAIN.
 XX
 XX Toran JL, Martinez Alonso C;
 PI
 XX
 XX WPI; 2004-055251/06.
 DR N-FSDB; ADH10327.
 XX
 XX Novel antibody or its fragment comprising a light chain and/or heavy
 PT chain which is capable of binding to glycoprotein gp120 of human
 PT immunodeficiency virus (HIV) useful for treating HIV infection.
 XX
 XX Claim 1; SEQ ID NO 2; 56pp; English.

XX The invention relates to an antibody (I) or its fragment comprising heavy
CC chain and/or light chain, capable of binding to glycoprotein gp120
CC protein of HIV, anti-HIV vaccine (I) or a chemical compound identified by
CC (I) is useful for preventing and treating HIV infections. They are also
CC useful for inhibiting binding of HIV to a viral co-receptor. The present
CC sequence represents the light chain sequence of anti-HIV-gp120 antibody
CC S8, S19 and S20.
XX
SQ Sequence 215 AA;

Query Match 88.4%; Score 680; DB 8; Length 215;
Best Local Similarity 91.7%; Pred. No. 5.5e-43;
Matches 132; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRSGS 61
Db 4 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRSGG 63
Qy 62 GSGTEFTLTISLQPEDPATYCYKQYKTPWTFQGTKEIKRTVAAPSVPFPPSDEQL 121
Db 64 GSGTEFTLTISLQPEDPATYCYKQYKTPWTFQGTKEIKRTVAAPSVPFPPSDEQL 123
Qy 122 KSGTASVVCLLNPNFYPREXKEHQK 145
Db 124 KSGTASVVCLLNPNFYPREAKVQWK 147

RESULT 13
ADK52390
ID ADK52390 standard; protein; 152 AA.
XX
AC ADK52390;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #24.
XX
KW monocytic chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
FN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52389.
XX

XX New human monoclonal antibody that binds to monocytic chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 96; 154pp; English.

XX The present invention relates to a human monoclonal antibody that binds
CC to monocytic chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast

CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX
SQ Sequence 152 AA;

Query Match 87.8%; Score 675; DB 8; Length 152;
Best Local Similarity 90.3%; Pred. No. 9.3e-43;
Matches 130; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRSGS 61
Db 6 QSPSSLSASVGDRTVITTCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRSGS 65
Qy 62 GSGTEFTLTISLQPEDPATYCYKQYKTPWTFQGTKEIKRTVAAPSVPFPPSDEQL 121
Db 66 GSGTEFTLTISLQPEDPATYCYKQYKTPWTFQGTKEIKRTVAAPSVPFPPSDEQL 125
Qy 122 KSGTASVVCLLNPNFYPREXKEHQK 145
Db 126 KSGTASVVCLLNPNFYPREAKVQWK 149

RESULT 14
ADK52354
ID ADK52354 standard; protein; 152 AA.
XX
AC ADK52354;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #15.
XX
KW monocytic chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
FN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52353.
XX

XX New human monoclonal antibody that binds to monocytic chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 60; 154pp; English.

XX The present invention relates to a human monoclonal antibody that binds
CC to monocytic chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or

CC inflammatory conditions. The neoplastic disease is selected from breast
 CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
 CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
 CC pancreatic cancer or prostate cancer. The inflammatory condition is
 CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
 CC psoriasis, reestenosis, autoimmune disease or multiple sclerosis. The
 CC antibodies are also useful for diagnosing the above diseases. It is also
 CC useful for the determining the level of MCP-1 and MCP-1 family members in
 CC patient samples. The present sequence represents a human anti-MCP-1
 CC variable region light chain sequence.

XX Sequence 152 AA;

Query Match 87.8%; Score 675; DB 8; Length 152;
 Best Local Similarity 90.3%; Pred. No. 9.3e-43;
 Matches 130; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDTRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 61
 DB 6 QSPSSLSASVGDRTVITCRASQDTRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 65
 QY 62 GSGTEFTLTISLQPEDFATYCYKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 121
 DB 66 GSGTEFTLTISLQPEDFATYCYKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 125

QY 122 KSGTASVVCLLNFPYREXKEHQK 145
 DB 126 KSGTASVVCLLNFPYREXKEHQK 149

RESULT 15

ADS84470
 ID ADS84470 standard; protein; 234 AA.

AC ADS84470;

DT 18-NOV-2004 (first entry)

DE Human anti-EPO-R antibody Ab467 light chain SEQ ID NO:109.

KW human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianemic; neuroprotective; vulnerary; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.

XX Homo sapiens.

XX WO2004035603-A2.

XX 29-APR-2004.

PF 14-OCT-2003; 2003WO-US032243.

PR 14-OCT-2002; 2002US-00269711.

XX 10-OCT-2003; 2003US-00684109.

PA (ABBO) ABBOTT LAB.

PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;

XX WPI; 2004-348433/32.

DR N-PSDB; ADS84468, ADS84469.

XX New antibodies that bind to or activate an endogenous human

PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.

XX Disclosure; SEQ ID NO 109; 192pp; English.

XX The present invention describes an antibody or its fragment that binds to

CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,
 CC complements and degenerate codon equivalents; and (5) an isolated and
 CC purified amino acid sequence, and their fragments. The EPO receptor
 CC binding antibody has antianemic, neuroprotective and vulnerary
 CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from
 CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence represents a human anti-EPO-R antibody light
 CC chain, which is given in the exemplification of the present invention.

XX Sequence 234 AA;

Query Match 87.6%; Score 674; DB 8; Length 234;
 Best Local Similarity 90.3%; Pred. No. 1.7e-42;
 Matches 130; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDTRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 61

DB 26 QSPSSLSASVGDRTVITCRASQDTRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFSGS 85

QY 62 GSGTEFTLTISLQPEDFATYCYKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 121

DB 86 GSGTEFTLTISLQPEDFATYCYKTYPTWTFGGTKVEIKRTVAAPSVFIFFPSDQL 145

QY 122 KSGTASVVCLLNFPYREXKEHQK 145

DB 146 KSGTASVVCLLNFPYREXKEHQK 169

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	694	90.2	236	15	US-10-038-591-52
2	684	88.9	234	16	US-10-684-109-97
3	683	88.8	184	16	US-10-684-109-78
4	682	88.7	236	15	US-10-038-591-48
5	680	88.4	215	16	US-10-462-040A-2
6	674	87.6	153	15	US-10-309-762-245
7	674	87.6	234	16	US-10-684-109-109
8	671	87.3	234	16	US-10-684-109-91
9	670	87.1	234	16	US-10-684-109-103
10	668	86.9	234	16	US-10-684-109-115
11	666	86.6	236	15	US-10-038-591-51
12	657	85.4	236	15	US-10-038-591-47
13	655	85.2	212	14	US-10-320-231A-77
					Sequence 52, Appl
					Sequence 97, Appl
					Sequence 78, Appl
					Sequence 48, Appl
					Sequence 2, Appli
					Sequence 245, App
					Sequence 109, App
					Sequence 91, Appl
					Sequence 103, App
					Sequence 115, App
					Sequence 51, Appl
					Sequence 47, Appl

14	649	84.4	213	16	US-10-379-392-135	Sequence 135, App
15	649	84.4	214	15	US-10-364-953-1	Sequence 1, Appli
16	649	84.4	237	14	US-10-020-786-10	Sequence 10, Appl
17	647.5	84.2	163	15	US-10-364-743-20	Sequence 20, Appl
18	647	84.1	237	9	US-09-056-160B-100	Sequence 100, App
19	647	84.1	237	14	US-10-234-671-100	Sequence 100, App
20	647	84.1	491	13	US-10-011-125-2	Sequence 2, Appli
21	646	84.0	213	16	US-10-379-392-137	Sequence 137, App
22	645.5	83.9	241	14	US-10-221-945-1	Sequence 1, Appli
23	645	83.9	213	16	US-10-379-392-155	Sequence 155, App
24	644	83.7	236	9	US-09-859-053-30	Sequence 30, Appl
25	644	83.7	236	16	US-10-625-105-30	Sequence 30, Appl
26	642	83.5	214	15	US-10-408-901-44	Sequence 44, Appl
27	641	83.4	214	14	US-10-153-382-19	Sequence 19, Appl
28	640	83.2	213	16	US-10-379-392-153	Sequence 153, App
29	639	83.1	367	15	US-10-291-265-899	Sequence 899, App
30	638	83.0	214	15	US-10-364-953-3	Sequence 3, Appli
31	638	83.0	214	15	US-10-364-953-11	Sequence 11, Appl
32	638	83.0	214	16	US-10-379-392-170	Sequence 170, App
33	638	83.0	237	14	US-10-020-786-8	Sequence 8, Appli
34	638	83.0	237	14	US-10-227-694-4	Sequence 4, Appli
35	638	83.0	237	17	US-10-754-212-5	Sequence 5, Appli
36	635	82.6	208	15	US-10-634-581-1	Sequence 1, Appli
37	635	82.6	214	9	US-09-949-559-128	Sequence 128, App
38	635	82.6	214	10	US-09-875-221A-128	Sequence 128, App
39	635	82.6	214	14	US-10-310-454-4	Sequence 4, Appli
40	635	82.6	214	15	US-10-364-953-4	Sequence 4, Appli
41	635	82.6	214	17	US-10-728-420B-113	Sequence 113, App
42	634	82.4	214	15	US-10-423-299-3	Sequence 3, Appli
43	633	82.3	136	15	US-10-038-591-2	Sequence 2, Appli
44	632	82.2	213	16	US-10-379-392-157	Sequence 157, App
45	631	82.1	139	14	US-10-153-382-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-038-591-52
; Sequence 52, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-52

Query Match 90.2%; Score 694; DB 15; Length 236;
Best Local Similarity 92.4%; Pred. No. 6.1e-44;
Matches 133; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

Qy	2	QSPSSLASVGDRTVITCRASQDTRDNLGWTQKPGKAPKRLIYAASNLQSGVPSRFGS	61
Db	28	QSPSSLASVGDRTVITCRASQDTRDNLGWTQKPGKAPKRLIYAASNLQSGVPSRFGS	87
Qy	62	GSGETFTLTSSLOPEDPATVYCYQKTYPTWFGGTVKVKRTVAAPSVIFPPPSDQL	121
Db	88	GSGETFTLTSSLPEDPATVYCYQKTYPTWFGGTVKVKRTVAAPSVIFPPPSDQL	147

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Qy 122 KSGTASVCLNNFYPREXKEHQK 145
    |||||
Db 148 KSGTASVCLNNFYPREAKVQWK 171

RESULT 2
US-10-684-109-97
; Sequence 97, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wiele, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-97

Query Match 88.7%; Score 684; DB 16; Length 234;
Best Local Similarity 92.4%; Pred. No. 3.3e-43;
Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTTTCRASQDIRNLGWYQKPGKAPKRLIYAASNLOSGVPSRFSGS 61
    |||||
Db 26 QSPSSLASVGDRTTTCRASQDIRNLGWYQKPGKAPKRLIYAASNLOSGVPSRFSGS 85

Qy 62 GSGTEFTLTISLQPEDFATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVPFPPSDEQL 121
    |||||
Db 86 GSGTEFTLTISLQPEDFATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVPFPPSDEQL 145

Qy 122 KSGTASVCLNNFYPREXKEHQK 145
    |||||
Db 146 KSGTASVCLNNFYPREAKVQWK 169

RESULT 3
US-10-684-109-78
; Sequence 78, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wiele, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; PRIOR FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-78
```

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Query Match 88.8%; Score 683; DB 16; Length 184;
Best Local Similarity 92.4%; Pred. No. 3.1e-43;
Matches 133; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTTTCRASQDIRNLGWYQKPGKAPKRLIYAASNLOSGVPSRFSGS 61
    |||||
Db 28 QSPSSLASVGDRTTTCRASQDIRNLGWYQKPGKAPKRLIYAASNLOSGVPSRFSGS 87

Qy 62 GSGTEFTLTISLQPEDFATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVPFPPSDEQL 121
    |||||
Db 88 GSGTEFTLTISLQPEDFATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVPFPPSDEQL 147

Qy 122 KSGTASVCLNNFYPREXKEHQK 145
    |||||
Db 148 KSGTASVCLNNFYPREAKVQWK 171

RESULT 4
US-10-038-591-48
; Sequence 48, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 48
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-48

Query Match 88.7%; Score 682; DB 15; Length 236;
Best Local Similarity 91.0%; Pred. No. 4.7e-43;
Matches 131; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTTTCRASQDIRNLGWYQKPGKAPKRLIYAASNLOSGVPSRFSGS 61
    |||||
Db 28 QSPSSLASVGDRTTTCRASQDIRNLGWYQKPGKAPKRLIYAASNLOSGVPSRFSGS 87

Qy 62 GSGTEFTLTISLQPEDFATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVPFPPSDEQL 121
    |||||
Db 88 GSGTEFTLTISLQPEDFATYCYLQYKTYPWTFGQGTKEIKRTVAAPSVPFPPSDEQL 147

Qy 122 KSGTASVCLNNFYPREXKEHQK 145
    |||||
Db 148 KSGTASVCLNNFYPREAKVQWK 171

RESULT 5
US-10-462-040A-2
; Sequence 2, Application US/10462040A
; Publication No. US20040106105A1
; GENERAL INFORMATION:
; APPLICANT: TORAN GARCIA, JOSE LUIS
; APPLICANT: MARTINEZ ALONSO, CARLOS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 621032-8/JP/B-5129
; CURRENT APPLICATION NUMBER: US/10/462,040A
; CURRENT FILING DATE: 2003-06-12
; PRIOR APPLICATION NUMBER: EP 02380126.9
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 69
```



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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Light chain
US-10-462-040A-2

Query Match      88.4%; Score 680; DB 16; Length 215;
Best Local Similarity 91.7%; Pred. No. 6.1e-43;
Matches 132; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy  2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 61
Db  4 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 63

Qy  62 GSGTEFTLTISLQPEDFATYCYCQYKTPWTFGGKVEIKRTVAAPSVFIFFPSDEQL 121
Db  64 GSGTEFTLTISLQPEDFATYCYCQYKTPWTFGGKVEIKRTVAAPSVFIFFPSDEQL 123

Qy  122 KSGTASVVCLLNFPYREXKEHQK 145
Db  124 KSGTASVVCLLNFPYREXKEHQK 147

RESULT 6
US-10-309-762-245
; Sequence 245, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudae, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 245
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-245

Query Match      87.6%; Score 674; DB 15; Length 153;
Best Local Similarity 91.0%; Pred. No. 1.2e-42;
Matches 131; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy  2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 61
Db  6 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 65

Qy  62 GSGTEFTLTISLQPEDFATYCYCQYKTPWTFGGKVEIKRTVAAPSVFIFFPSDEQL 121
Db  66 GSGTEFTLTISLQPEDFATYCYCQYKTPWTFGGKVEIKRTVAAPSVFIFFPSDEQL 125

Qy  122 KSGTASVVCLLNFPYREXKEHQK 145
Db  126 KSGTASVVCLLNFPYREXKEHQK 149

RESULT 7
US-10-684-109-109
; Sequence 109, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-109

Query Match      87.3%; Score 671; DB 16; Length 234;
Best Local Similarity 89.6%; Pred. No. 3e-42;
Matches 129; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

Qy  2 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 61
Db  26 QSPSSLASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGS 85

Qy  62 GSGTEFTLTISLQPEDFATYCYCQYKTPWTFGGKVEIKRTVAAPSVFIFFPSDEQL 121
Db  86 GSGTEFTLTISLQPEDFATYCYCQYKTPWTFGGKVEIKRTVAAPSVFIFFPSDEQL 145
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Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
    |||||:|||||:|||||:|||||:
Db 146 KSGTASVVCLLNNFYPREAKVQWK 169

RESULT 9
US-10-684-109-103
; Sequence 103, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 103
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-103

Query Match 87.1%; Score 670; DB 16; Length 234;
Best Local Similarity 90.3%; Pred. No. 3.6e-42;
Matches 130; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 61
Db 26 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 85

Qy 62 GSGTEFTLTISLQPEDPATYCYLQYKTYPMWTFQGTKEIKRTVAAPSVEIFFPSDEQL 121
Db 86 GSGTEFTLTISLQPEDPATYCYLQHNSYPTFGGTKEIKRTVAAPSVEIFFPSDEQL 145

Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
    |||||:|||||:|||||:|||||:
Db 146 KSGTASVVCLLNNFYPREAKVQWK 169

RESULT 10
US-10-684-109-115
; Sequence 115, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-115

Query Match 86.9%; Score 668; DB 16; Length 234;
```

```
Best Local Similarity 90.3%; Pred. No. 5.1e-42;
Matches 130; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 61
Db 26 QSPSSLASVGDVRTITCRSQRINDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 85

Qy 62 GSGTEFTLTISLQPEDPATYCYLQYKTYPMWTFQGTKEIKRTVAAPSVEIFFPSDEQL 121
Db 86 GSGTEFTLTISLQPEDPATYCYLQHNSYPTFGGTKEIKRTVAAPSVEIFFPSDEQL 145

Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
    |||||:|||||:|||||:|||||:
Db 146 KSGTASVVCLLNNFYPREAKVQWK 169

RESULT 11
US-10-038-591-51
; Sequence 51, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-51

Query Match 86.6%; Score 666; DB 15; Length 236;
Best Local Similarity 90.3%; Pred. No. 7.2e-42;
Matches 130; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 61
Db 28 QSPSSLASVGDVRTITCRASQDIRDLGNLWYQOKPGKAPKRLIYAASNLQSGVPSRFSGS 87

Qy 62 GSGTEFTLTISLQPEDPATYCYLQYKTYPMWTFQGTKEIKRTVAAPSVEIFFPSDEQL 121
Db 88 GSGTEFTLTISLQPEDPATYCYLQHNNYPTFGGTKEIKRTVAAPSVEIFFPSDEQL 147

Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
    |||||:|||||:|||||:|||||:
Db 148 KSGTASVVCLLNNFYPREAKVQWK 171

RESULT 12
US-10-038-591-47
; Sequence 47, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
```

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; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 47
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-47

Query Match      85.4%; Score 657; DB 15; Length 236;
Best Local Similarity 88.2%; Pred. No. 3.3e-41;
Matches 127; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGSG 61
DB 28 QPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASRLHRGVPSPRFGSG 87

QY 62 GSGTEFTLTISLQPEDFATYCYQKTPWTFGGTKVEIKRTVAAPSVFIFFPPSDQL 121
DB 88 GSGTEFTLTISLQPEDFATYCYQKTPWTFGGTKVEIKRTVAAPSVFIFFPPSDQL 147

QY 122 KSGTASVVCLNNFYPREKKEHQK 145
DB 148 KSGTASVVCLNNFYPREKQVWK 171

RESULT 13
US-10-320-231A-77
; Sequence 77, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 77
; LENGTH: 212
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-77

Query Match      85.2%; Score 655; DB 14; Length 212;
Best Local Similarity 88.9%; Pred. No. 4.3e-41;
Matches 128; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGSG 61
DB 4 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYASNLQSGVPSRFGSG 63

QY 62 GSGTEFTLTISLQPEDFATYCYQKTPWTFGGTKVEIKRTVAAPSVFIFFPPSDQL 121
DB 64 GSGTEFTLTISLQPEDFATYCYQKTPWTFGGTKVEIKRTVAAPSVFIFFPPSDQL 123

QY 122 KSGTASVVCLNNFYPREKKEHQK 145
DB 124 KSGTASVVCLNNFYPREKQVWK 147

RESULT 14
US-10-379-392-135
; Sequence 135, Application US/10379392
; Publication No. US20040110226A1

; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 135
; LENGTH: 213
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Humanized
US-10-379-392-135

Query Match      84.4%; Score 649; DB 16; Length 213;
Best Local Similarity 87.5%; Pred. No. 1.2e-40;
Matches 126; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGSG 61
DB 6 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYFTSSLHSGVPSRFGSG 65

QY 62 GSGTEFTLTISLQPEDFATYCYQKTPWTFGGTKVEIKRTVAAPSVFIFFPPSDQL 121
DB 66 GSGTEFTLTISLQPEDFATYCYQKTPWTFGGTKVEIKRTVAAPSVFIFFPPSDQL 125

QY 122 KSGTASVVCLNNFYPREKKEHQK 145
DB 126 KSGTASVVCLNNFYPREKQVWK 149

RESULT 15
US-10-364-953-1
; Sequence 1, Application US/10364953
; Publication No. US2003024397A1
; GENERAL INFORMATION:
; APPLICANT: LOWMAN, HENRY B.
; APPLICANT: MARVIN, JONATHAN S.
; TITLE OF INVENTION: ANTIBODY VARIANTS WITH PASTER ANTIGEN ASSOCIATION RATES
; FILE REFERENCE: P1951R1
; CURRENT APPLICATION NUMBER: US/10/364,953
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/355,895
; PRIOR FILING DATE: 2002-02-11
; PRIOR APPLICATION NUMBER: US 60/409,685
; PRIOR FILING DATE: 2002-09-10
; NUMBER OF SEQ ID NOS: 14
; SEQ ID NO 1
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: Full
; OTHER INFORMATION: Y0101-VL
US-10-364-953-1

Query Match      84.4%; Score 649; DB 15; Length 214;
Best Local Similarity 87.5%; Pred. No. 1.2e-40;
Matches 126; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

QY 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLQSGVPSRFGSG 61
DB 6 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKRLIYFTSSLHSGVPSRFGSG 65
```

Qy	62	GSCTEFTLTSSQLQDPEDFATYYCQKTYPWTFTGQTKVEIKRTVAAPSVEIFPPSDEQL	121
		:	
Db	66	GSQTDFTLTSSQLQDPEDFATYYCQKTYSTVPWFTFGQTKVEIKRTVAAPSVEIFPPSDEQL	125

Db 66 GSGDFTLTISLQPEDFATYYCQOYSTVPWTFGQGTKEIKRTVAAPSVFIFPPSDEQL 125

QY 122 KSGTASVCLNMFYPREXKEHQK 145

Db 126 KSGTASVVCLNNFYPREAKVQWK 149

Search completed: March 8, 2005, 07:05:52
Job time : 78.009 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.1636 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-30

Perfect score: 769

Sequence: 1 QSPSSLSASVGDRTVTTCR.....VCLLNFFPREXKEHQSP 147

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A.COMB.pap:*

2: /cgn2_6/ptodata/1/iaa/5B.COMB.pap:*

3: /cgn2_6/ptodata/1/iaa/6A.COMB.pap:*

4: /cgn2_6/ptodata/1/iaa/6B.COMB.pap:*

5: /cgn2_6/ptodata/1/iaa/PTCUS.COMB.pap:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	647	84.1	491	4	US-10-011-125A-2
2	644	83.7	236	4	US-09-859-053-30
3	641	83.4	214	4	US-09-472-087-71
4	637	82.8	233	4	US-08-030-175-43
5	631	82.1	139	4	US-09-472-087-22
6	631	82.1	139	4	US-09-472-087-96
7	630	81.9	214	2	US-07-934-373C-39
8	630	81.9	214	3	US-08-437-642B-39
9	630	81.9	214	5	PCT-US93-07832-39
10	629	81.8	218	5	PCT-US96-13152-2
11	628	81.7	214	2	US-07-934-373C-40
12	628	81.7	214	2	US-08-788-800-11
13	628	81.7	214	3	US-08-437-642B-40
14	628	81.7	214	3	US-09-097-309-2
15	628	81.7	214	3	US-09-097-171A-2
16	628	81.7	214	3	US-09-460-587-2
17	628	81.7	214	4	US-09-940-166A-2
18	628	81.7	214	5	PCT-US93-07832-40
19	628	81.7	233	2	US-07-934-373C-25
20	628	81.7	233	3	US-08-437-642B-25
21	628	81.7	233	4	US-08-146-206C-25
22	628	81.7	233	4	US-09-705-686-25
23	628	81.7	233	4	US-09-705-392A-25
24	628	81.7	233	4	US-09-705-398-25
25	628	81.7	233	5	PCT-US93-07832-25
26	628	81.7	237	3	US-09-097-309-6
27	628	81.7	237	3	US-09-097-171A-10

28	628	81.7	237	3	US-09-422-712B-2	Sequence 2, Appli
29	628	81.7	237	3	US-09-607-756-2	Sequence 2, Appli
30	628	81.7	237	3	US-09-460-587-6	Sequence 6, Appli
31	628	81.7	237	4	US-09-940-166A-6	Sequence 6, Appli
32	627.5	81.6	232	1	US-08-704-744-80	Sequence 80, Appli
33	625	81.3	214	1	US-08-458-516-12	Sequence 12, Appli
34	624	81.1	236	1	US-08-157-101A-5	Sequence 5, Appli
35	622	80.9	214	3	US-09-679-397-1	Sequence 1, Appli
36	622	80.9	214	4	US-09-680-148-1	Sequence 1, Appli
37	622	80.9	214	4	US-09-304-465A-1	Sequence 25, Appli
38	622	80.9	237	2	US-08-463-587A-25	Sequence 3, Appli
39	622	80.9	237	2	US-08-463-667A-3	Sequence 25, Appli
40	622	80.9	237	3	US-08-923-854-25	Sequence 26, Appli
41	622	80.9	237	5	PCT-US91-09133-26	Sequence 13, Appli
42	615	80.0	218	2	US-08-887-352B-13	Sequence 9, Appli
43	615	80.0	218	3	US-08-466-151-9	Sequence 13, Appli
44	615	80.0	218	3	US-09-109-207C-13	Sequence 13, Appli
45	615	80.0	218	3	US-09-296-005-13	Sequence 13, Appli

ALIGNMENTS

RESULT 1

US-10-011-125A-2

; Sequence 2, Application US/10011125A

; Patent No. 6828121

; GENERAL INFORMATION:

; APPLICANT: Chen, Christina Yu-Ching

; TITLE OF INVENTION: BACTERIAL HOST STRAINS

; FILE REFERENCE: P1804R1

; CURRENT APPLICATION NUMBER: US/10/011.125A

; CURRENT FILING DATE: 2001-12-07

; PRIOR APPLICATION NUMBER: US 60/256,162

; PRIOR FILING DATE: 2000-12-14

; NUMBER OF SEQ ID NOS: 12

; SEQ ID NO 2

; LENGTH: 491

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Sequence is synthesized.

; Patent No. 6828121

US-10-011-125A-2

Query Match 84.1%; Score 647; DB 4; Length 491;

Best Local Similarity 86.8%; Pred. No. 1.6e-51;

Matches 125; Conservative 5; Mismatches 14; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVTTCRASQDTRDNLGWYQQKPGKAPKRLIYAASNLQSGVPSRPSGS 61

Db 29 QSPSSLSASVGDRTVTTCRASQDTRDNLGWYQQKPGKAPKRLIYTSSLHSGVPSRPSGS 88

Qy 62 GSGTEFTLTSSLQPEDPATYCYQYTPMTFGGTVKVEIKRTVAAPSVFIFFPSDQL 121

Db 89 GSGTYTLTSSLQPEDPATYCYQYTPMTFGGTVKVEIKRTVAAPSVFIFFPSDQL 148

Qy 122 KSGTASVVCLLNFFPREXKEHQK 145

Db 149 KSGTASVVCLLNFFPREXKEHQK 172

RESULT 2

US-09-859-053-30

; Sequence 30, Application US/09859053

; Patent No. 6803039

; GENERAL INFORMATION:

; APPLICANT: Tsuji, Takashi

; APPLICANT: Tezuka, Katsunari

; APPLICANT: Hori, No. 6803039uaki

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A

; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND

; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF

; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-22

Query Match 82.1%; Score 631; DB 4; Length 139;
Best Local Similarity 89.1%; Pred. No. 1.1e-50;
Matches 123; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 4 PSSLSASVGDRTTITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGSGS 63
Db 1 PSSLSASVGDRTTITCRASQINSYLDWYQKPGKAPKLLIYAASSLSQGVPSRFSGSGS 60
Qy 64 GTEFTLTSSLOPEDFATYICLYQKTYPTWTFQGTGKVEIKRTVAAPSVEIFPPSDQLKS 123
Db 61 GTDFLTLTSSLOPEDFATYICQYQYVSTFTFGPGTKVEIKRTVAAPSVEIFPPSDQLKS 120
Qy 124 GTASVVCLLNNFYPREXK 141
Db 121 GTASVVCLLNNFYPREAK 138

RESULT 6

US-09-472-087-96
; Sequence 96, Application US/09472087
; Patent No. 6862736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 96
; LENGTH: 139
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-96

Query Match 82.1%; Score 631; DB 4; Length 139;
Best Local Similarity 89.1%; Pred. No. 1.1e-50;
Matches 123; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

Qy 4 PSSLSASVGDRTTITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGSGS 63
Db 1 PSSLSASVGDRTTITCRASQINSYLDWYQKPGKAPKLLIYAASSLSQGVPSRFSGSGS 60
Qy 64 GTEFTLTSSLOPEDFATYICLYQKTYPTWTFQGTGKVEIKRTVAAPSVEIFPPSDQLKS 123
Db 61 GTDFLTLTSSLOPEDFATYICQYQYVSTFTFGPGTKVEIKRTVAAPSVEIFPPSDQLKS 120
Qy 124 GTASVVCLLNNFYPREXK 141

Db 121 GTASVVCLLNNFYPREAK 138
RESULT 7
US-07-934-373C-39
; Sequence 39, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-39

Query Match 81.9%; Score 630; DB 2; Length 214;
Best Local Similarity 86.1%; Pred. No. 2.2e-50;
Matches 124; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTTITCRASQDIRDNLGWYQKPGKAPKRLIYAASNLSQGVPSRFSGSGS 61
Db 6 QSPSSLSASVGDRTTITCRASQDIRDNLGWYQKPGKAPKRLIYTTSTLESQGVPSRFSGSGS 65
Qy 62 GSGTFTLTSSLOPEDFATYICLYQKTYPTWTFQGTGKVEIKRTVAAPSVEIFPPSDQL 121
Db 66 GSGTDTLTSSLOPEDFATYICQYQYVSTFTFGPGTKVEIKRTVAAPSVEIFPPSDQL 125
Qy 122 KSGTASVVCLLNNFYPREXKEHOK 145
Db 126 KSGTASVVCLLNNFYPREAKVQWK 149

RESULT 8

US-08-437-642B-39
; Sequence 39, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta

;/ TITLE OF INVENTION: Immunoglobulin Variants
;/ NUMBER OF SEQUENCES: 47
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Genentech, Inc.
;/ STREET: 1 DNA Way
;/ CITY: South San Francisco
;/ STATE: California
;/ COUNTRY: USA
;/ ZIP: 94080
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: WinPatIn (Genentech)
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/437,642B
;/ FILING DATE: 09-May-1995
;/ CLASSIFICATION: 530
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 07/934373
;/ FILING DATE: 17-NOV-1993
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US92/05126
;/ FILING DATE: 15-JUN-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 07/715272
;/ FILING DATE: 14-JUN-1991
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Lee, Wendy M.
;/ REGISTRATION NUMBER: 40,378
;/ REFERENCE/DOCKET NUMBER: P0709P2C1
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: 650/225-1994
;/ TELEFAX: 650/952-9881
;/ INFORMATION FOR SEQ ID NO: 39:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 214 amino acids
;/ TYPE: Amino Acid
;/ TOPOLOGY: Linear
;/ US-08-437-642B-39

Query Match 81.9%; Score 630; DB 3; Length 214;
Best Local Similarity 86.1%; Pred. No. 2.2e-50;
Matches 124; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKELIYAASNLSQGVPSRFSGS 61
Db 6 QSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLSGVSFRFSGS 65

Qy 62 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFQGGTKVEIKRTVAAPSVFIFPPSDEQL 121
Db 66 GSGTDYTLTISLQPEDPATYCYQCGNTLPTFTFGGKVEIKRTVAAPSVFIFPPSDEQL 125

Qy 122 KSGTASVVCLLNNFYPREXKEHOK 145
Db 126 KSGTASVVCLLNNFYPREAKVQWK 149

RESULT 9
PCT-US93-07832-39
;/ Sequence 39, Application PC/TUS9307832
;/ GENERAL INFORMATION:
;/ APPLICANT: Genentech, Inc.
;/ TITLE OF INVENTION: Immunoglobulin Variants
;/ NUMBER OF SEQUENCES: 40
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Genentech, Inc.
;/ STREET: 460 Point San Bruno Blvd
;/ CITY: South San Francisco
;/ STATE: California

;/ COUNTRY: USA
;/ ZIP: 94080
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: patin (Genentech)
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US93/07832
;/ FILING DATE: 19930820
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 07/715272
;/ FILING DATE: 14-JUN-1991
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: PCT/US92/05126
;/ FILING DATE: 15-JUN-1992
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: 07/934373
;/ FILING DATE: 21-AUG-1992
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME:
;/ REGISTRATION NUMBER:
;/ REFERENCE/DOCKET NUMBER: 709P2PCT
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE:
;/ TELEFAX: 415/952-9881
;/ TELEX: 910/371-7168
;/ INFORMATION FOR SEQ ID NO: 39:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 214 amino acids
;/ TYPE: amino acid
;/ TOPOLOGY: linear
;/ PCT-US93-07832-39

Query Match 81.9%; Score 630; DB 5; Length 214;
Best Local Similarity 86.1%; Pred. No. 2.2e-50;
Matches 124; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKELIYAASNLSQGVPSRFSGS 61
Db 6 QSPSSLSASVGDRTVITCRASQDINNLYNWYQKPGKAPKLLIYYTSTLSGVSFRFSGS 65

Qy 62 GSGTEFTLTISLQPEDPATYCYQKTYPTWTFQGGTKVEIKRTVAAPSVFIFPPSDEQL 121
Db 66 GSGTDYTLTISLQPEDPATYCYQCGNTLPTFTFGGKVEIKRTVAAPSVFIFPPSDEQL 125

Qy 122 KSGTASVVCLLNNFYPREXKEHOK 145
Db 126 KSGTASVVCLLNNFYPREAKVQWK 149

RESULT 10
PCT-US96-13152-2
;/ Sequence 2, Application PC/TUS9613152
;/ GENERAL INFORMATION:
;/ APPLICANT: Martin, Ulrich, et al.
;/ TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
;/ NUMBER OF SEQUENCES: 4
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Felfe & Lynch
;/ ADDRESSEE: Attn: Norman D. Hanson
;/ STREET: 805 Third Avenue
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: U.S.A.
;/ ZIP: 10022
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: 3.5" Computer Disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: ASCII
;/ CURRENT APPLICATION DATA:


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; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-2

Query Match 81.8%; Score 629; DB 5; Length 218;
Best Local Similarity 83.1%; Pred. No. 2.8e-50;
Matches 123; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

Qy 2 QSPSSLSASVGDRTVITCRASQDI----RDNLGWYQKPGKAPKELIYAASNLSQGVPSR 57
Db 6 QSPSSLSASVGDRTVITCRASQDYNMYQKPGKAPKELIYAASNLSGIPSR 65
Qy 58 FSGSGSGTEFTLTITSSLOPEFATYCYQKTYPTWTFQGTGKVEIKRTVAAPSVFIFPPS 117
Db 66 FSGSGSGTDFLTITSSLOPEFATYCYQKTYPTWTFQGTGKVEIKRTVAAPSVFIFPPS 125
Qy 118 DEQLKSGTASVVCLLNNFYPREXKEHQK 145
Db 126 DEQLKSGTASVVCLLNNFYPREAKVQWK 153

RESULT 11
US-07-934-373C-40
; Sequence 40, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: 07/715272
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; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-07-934-373C-40

Query Match 81.7%; Score 628; DB 2; Length 214;
Best Local Similarity 86.1%; Pred. No. 3.4e-50;
Matches 124; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 2 QSPSSLSASVGDRTVITCRASQDIRDNLGWYQKPGKAPKELIYAASNLSQGVPSRPSGS 61
Db 6 QSPSSLSASVGDRTVITCRASQDINNMYQKPGKAPKELIYTTSTLHSGVPSRPSGS 65
Qy 62 GSGTEFTLTITSSLOPEFATYCYQKTYPTWTFQGTGKVEIKRTVAAPSVFIFPPSDEQL 121
Db 66 GSGTDYTLTITSSLOPEFATYCYQKTYPTWTFQGTGKVEIKRTVAAPSVFIFPPSDEQL 125
Qy 122 KSGTASVVCLLNNFYPREXKEHQK 145
Db 126 KSGTASVVCLLNNFYPREAKVQWK 149

RESULT 12
US-08-788-800-11
; Sequence 11, Application US/08788800
; Patent No. 5914112
; GENERAL INFORMATION:
; APPLICANT: Bednar, Martin M.
; APPLICANT: Thomas, G. Roger
; APPLICANT: Grohs, Cordell E.
; TITLE OF INVENTION: ANTI-CD18 ANTIBODIES IN STROKE
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,800
; FILING DATE: 22-Jan-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0987r1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-788-800-11
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Query Match 81.7%; Score 628; DB 2; Length 214;
Best Local Similarity 86.1%; Pred. No. 3.4e-50;
Matches 124; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTVITCRASQDINLNGWYQKPGKAPKRLIYAASNLOSGVPSRFSGS 61
Db 6 QSPSSLASVGDRTVITCRASQDINLNNYQKPGKAPKLLIYTTSTLHSGVPSRFSGS 65

Qy 62 GSGTEFTLTISLLOPEDPATYCYQKTYPWTFCGGTKVEIKRTVAAPSVPFIFFPSDEQL 121
Db 66 GSGTDYTLTISLLOPEDPATYCYQCGNTLPTPTFCGGTKVEIKRTVAAPSVPFIFFPSDEQL 125

Qy 122 KSGTASVVCLNNFYPREXKEHQK 145
Db 126 KSGTASVVCLNNFYPREAKVQWK 149

RESULT 13
US-08-437-642B-40
; Sequence 40, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 40:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-437-642B-40

Query Match 81.7%; Score 628; DB 3; Length 214;
Best Local Similarity 86.1%; Pred. No. 3.4e-50;
Matches 124; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTVITCRASQDINLNGWYQKPGKAPKRLIYAASNLOSGVPSRFSGS 61

Db 6 QSPSSLASVGDRTVITCRASQDINLNNYQKPGKAPKLLIYTTSTLHSGVPSRFSGS 65

Qy 62 GSGTEFTLTISLLOPEDPATYCYQKTYPWTFCGGTKVEIKRTVAAPSVPFIFFPSDEQL 121
Db 66 GSGTDYTLTISLLOPEDPATYCYQCGNTLPTPTFCGGTKVEIKRTVAAPSVPFIFFPSDEQL 125

Qy 122 KSGTASVVCLNNFYPREXKEHQK 145
Db 126 KSGTASVVCLNNFYPREAKVQWK 149

RESULT 14
US-09-097-309-2
; Sequence 2, Application US/09097309
; Patent No. 6121428
; GENERAL INFORMATION:
; APPLICANT: Blank, Gregory S.
; APPLICANT: Narindray, Daljit S.
; APPLICANT: Zapata, Gerardo A.
; TITLE OF INVENTION: Protein Recovery
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/097,309
; FILING DATE: 12-Jun-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050951
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Schwartz, Timothy R.
; REGISTRATION NUMBER: 32171
; REFERENCE/DOCKET NUMBER: P1105R1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-7467
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 214 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-097-309-2

Query Match 81.7%; Score 628; DB 3; Length 214;
Best Local Similarity 86.1%; Pred. No. 3.4e-50;
Matches 124; Conservative 4; Mismatches 16; Indels 0; Gaps 0;

Qy 2 QSPSSLASVGDRTVITCRASQDINLNGWYQKPGKAPKRLIYAASNLOSGVPSRFSGS 61
Db 6 QSPSSLASVGDRTVITCRASQDINLNNYQKPGKAPKLLIYTTSTLHSGVPSRFSGS 65

Qy 62 GSGTEFTLTISLLOPEDPATYCYQKTYPWTFCGGTKVEIKRTVAAPSVPFIFFPSDEQL 121
Db 66 GSGTDYTLTISLLOPEDPATYCYQCGNTLPTPTFCGGTKVEIKRTVAAPSVPFIFFPSDEQL 125

Qy 122 KSGTASVVCLNNFYPREXKEHQK 145
Db 126 KSGTASVVCLNNFYPREAKVQWK 149

RESULT 15

Search completed: March 8, 2005, 05:54:08
Job time : 17.1636 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 14.356 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-31

Perfect score: 1064

Sequence: 1 KLPETLSLTCAVYGGSPSGY.....LP SKDVMQGTDEHVVTGSK 202

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	911	85.6	231	2 B23746	Ig Fab region IV-J
2	734.5	69.0	627	2 S14683	Ig mu chain precu
3	574.5	54.0	143	2 B49028	Ig heavy chain v-1
4	536.5	50.4	592	2 S25705	Ig mu chain, shee
5	498	46.8	146	1 GHU02	Ig mu chain, shee
6	494	46.4	140	2 S78052	Ig heavy chain pre
7	491.5	46.2	220	2 A49444	Ig gamma-1 heavy c
8	486	45.7	126	2 S47010	Ig heavy chain v4.
9	485.5	45.6	140	2 A49045	Ig heavy chain v r
10	475.5	44.7	288	2 S29690	Ig heavy chain vDJ
11	471.5	44.3	116	2 S37456	Ig mu chain - huma
12	465.5	43.8	155	2 S31512	Ig heavy chain - h
13	465.5	43.8	155	2 S31511	Ig heavy chain - h
14	456	42.9	137	2 S31676	Ig heavy chain v r
15	450.5	42.3	114	2 I72667	cold agglutinin FS
16	450	42.3	106	2 S37454	Ig mu chain - huma
17	449.5	42.2	130	2 S31690	Ig heavy chain v r
18	447.5	42.1	140	2 I37782	Ig variable region
19	447	42.0	452	1 MHU	Ig mu chain C regi
20	447	42.0	453	2 S37768	Ig mu chain C regi
21	447	42.0	473	1 MHUM	Ig mu chain C regi
22	447	42.0	474	2 S15590	Ig heavy chain - h
23	446	41.9	122	2 JL0047	Ig heavy chain v r
24	440	41.4	97	2 S26898	Ig heavy chain v r
25	437	41.1	97	2 S26805	Ig heavy chain v r
26	431	40.5	97	2 S14474	Ig heavy chain v r
27	430	40.4	97	2 S26806	Ig heavy chain v r
28	430	40.4	97	2 G34964	Ig heavy chain v-I
29	429.5	40.4	146	2 S09711	Ig heavy chain v r

30	429	40.3	130	2 S30534	Ig heavy chain v r
31	429	40.3	139	2 S31586	Ig heavy chain v r
32	429	40.3	568	2 A34891	Ig heavy chain pre
33	425.5	40.0	135	2 S78051	Ig heavy chain pre
34	422	39.7	145	2 S78055	Ig heavy chain pre
35	421	39.6	470	2 S22080	Ig heavy chain pre
36	420	39.5	231	2 PC4155	Ig gamma-2b chain
37	415	39.0	129	2 S44114	Ig heavy chain v r
38	414.5	39.0	147	2 S13519	Ig heavy chain v r
39	411.5	38.7	146	2 S09710	Ig heavy chain v r
40	408.5	38.4	134	2 S54906	Ig heavy chain v r
41	407.5	38.3	127	2 S19668	Ig heavy chain v r
42	407	38.3	118	2 S24443	Ig heavy chain v r
43	405.5	38.1	123	2 S30529	Ig heavy chain v r
44	405	38.1	97	2 JH0428	Ig gamma chain v r
45	404.5	38.0	121	2 S44113	Ig heavy chain v r

ALIGNMENTS

RESULT 1

B23746

Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000

C:Accession: B23746

R;Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.

J. Biol. Chem. 266, 2836-2842, 1991

A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin

A:Reference number: A23746; MUID:91131575; PMID:1993660

A:Accession: B23746

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-231 <LEO>

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F140-209/Domain: immunoglobulin homology <IMM>

Query Match 85.6%; Score 911; DB 2; Length 231;
Best Local Similarity 86.5%; Pred. No. 5.3e-65;
Matches 180; Conservative 7; Mismatches 13; Indels 8; Gaps 2;

Qy	1	KLPETLSLTCAVYGGSPGYWIRPPGKGLWIGEHNSGNTNPNPSLKSRTISVD	60
Db	12	KPSETLSLTCAVYGGSPDYWIRPPGKGLWIGEHNSGNTNPNPSLKSRTISVD	71
Qy	61	TSKNQPSLKSSVTAADTAIVYCGAAYYYYGYMDVWGQGTVTYSSGSASAPTLPP	120
Db	72	TSKNQPSLKSSVTAADTAIVYCGAAYYYYGYMDVWGQGTVTYSSGSASAPTLPP	129
Qy	121	LVSCNSPSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPSVLRGGKYAATSQ	180
Db	130	LVSCNSPSTSSVAVGCLAQDFLPDSITTFMKYKNNSDISSTRGFPSVLRGGKYAATSQ	189
Qy	181	VLLPSKDVMOQTDEHV-----TGSKE	202
Db	190	VLLPSKDVMOQTDEHVVKVQHPNGNKE	217

RESULT 2

S14683

Ig mu chain precursor, membrane-bound (clone 201) - human

C:Species: Homo sapiens (man)

C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999

C:Accession: S14683; S08047

R;Friedlander, R.M.; Nussenzeig, M.C.; Leder, P.

Nucleic Acids Res. 18, 4278, 1990

A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.

A:Reference number: S14683; MUID:90332450; PMID:2115996

A:Accession: S14683

A:Molecule type: mRNA

A:Residues: 1-627 <FRI>

A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451

Db 93 TSKNLSLKLSSVTAADTAVVYCARGLLRGCGNDVDVYYGMDVWGQGTVTIVSS 146

RESULT 6
S78052
Ig heavy chain precursor V-D-J region (clone mAB 63VH) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78052; S23717
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78052
A:Molecule type: mRNA
A:Residues: 1-140 <HAR>
A:Cross-references: EMBL:X54441; NID:G37815; PIDN:CAA38308.1; PID:G930118
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23717
A:Molecule type: mRNA
A:Residues: 15-111 <HAW>
A:Cross-references: EMBL:X54441
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-14/Domain: signal sequence (fragment) #status predicted <SIG>
F:15-140/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:29-111/Domain: immunoglobulin homology <IMM>

Query Match 46.4%; Score 494; DB 2; Length 140;
Best Local Similarity 84.2%; Pred. No. 3e-32;
Matches 96; Conservative 2; Mismatches 12; Indels 4; Gaps 1;

Qy 1 KLPETLSLTCVAVGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 60
Db 27 KPSETLSLTCVAVGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 86

Qy 61 TSKNQFSLKLSVTAADTAVVYCARGAAY----YYYGMDVWGQGTVTIVSS 110
Db 87 TSKNQFSLKLSVTAADTAVVYCARGGSLRFLWLLYPADFVWGQGLTVIVSS 140

RESULT 7
A49444
Ig gamma-1 heavy chain (New) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999
C:Accession: A49444
R:Saul, F.A.; Poljak, R.J.
Proteins 14, 363-371, 1992
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res
A:Reference number: A49444; MUID:93066153; PMID:1438175
A:Accession: A49444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-220 <SAU>
A:Note: this sequence modified after extraction from NCBI backbone
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 46.2%; Score 491.5; DB 2; Length 220;
Best Local Similarity 50.5%; Pred. No. 8e-32;
Matches 98; Conservative 35; Mismatches 50; Indels 11; Gaps 5;

Qy 4 ETLSLTCVAVGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVDTSK 63
Db 16 QTLSTCTVCTGSDDDYTWVWRQPPGKGLWIGVYFTGTLDDPSLRGRVTLVNTSK 75

Qy 64 NQFSLKLSVTAADTAVVYCARGAAEYIIYYGMDVWGQGTVTIVSSGSASAPTLFPLVS 123

Db 76 NQFSLRSLSSVTAADTAVVYCARNLIA-----GGIDVWGQGLSVTVSSASTKPSVFFLAP 130

Qy 124 CENSPSDTSSVAVGCLAQDFLPDXITFXWKYKNNDSISSTRGPFPSVLK-CGKYAATSQVL 182
Db 131 SSRKSTSG-GTAAALGCLVKDYFPEPTVTSW--NSGALTSGVHTFPAVLQSSGLYSLSSVVT 187

Qy 183 LPSKDVVMQGTDEHV 196
Db 188 VPSSSL--GTQTYI 199

RESULT 8
S47010
Ig heavy chain V4.21-UniqueD-J5 region - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S47010
R:Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A:Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A:Reference number: S47009
A:Accession: S47010
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-126 <MAH>
A:Cross-references: EMBL:Z35492; NID:G517254; PIDN:CAA84625.1; PID:G517255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 45.7%; Score 486; DB 2; Length 126;
Best Local Similarity 83.6%; Pred. No. 1.2e-31;
Matches 97; Conservative 3; Mismatches 8; Indels 8; Gaps 2;

Qy 1 KLPETLSLTCVAVGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 60
Db 13 KPSETLSLTCVAVGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 72

Qy 61 TSKNQFSLKLSVTAADTAVVYCARG-----AAEYIIYYGMDVWGQGTVTIVSS 110
Db 73 TSKNQFSLKLSVTAADTAVVYCARGGQCPKCKKCYTKNWF--DPWGGGLTVIVSS 126

RESULT 9
A49045
Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C:Accession: A49045
R:Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rassenti, L.Z.; Labaume, S.; Silvermar
Eur. J. Immunol. 22, 1781-1788, 1992
A:Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i blc
A:Reference number: A49045; MUID:92324290; PMID:1623923
A:Accession: A49045
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-140 <GRI>
A:Cross-references: GB:S39381; NID:G250899; PIDN:AAB22441.1; PID:G250900
A:Note: sequence extracted from NCBI backbone (NCBIN:108088, NCBI:P:108089)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-116/Domain: immunoglobulin homology <IMM>

Query Match 45.6%; Score 485.5; DB 2; Length 140;
Best Local Similarity 86.6%; Pred. No. 1.4e-31;
Matches 97; Conservative 1; Mismatches 9; Indels 5; Gaps 2;

Qy 1 KLPETLSLTCVAVGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 60
Db 32 KPSETLSLTCVAVGSGFSGYWMIROPPGKGLWIGINHSNSTYNPSLKSRTVTSVD 91

Qy 61 TSKNQFSLKLSVTAADTAVVYCARG--AAEYIIYYGMDVWGQGTVTIVSS 110

Db 92 TSKNQFSLKLSVTAADTAVYVCARGGFAATIVESF---DYWGQGLTVTVSS 140
|||||

RESULT 10

S29690
Ig heavy chain VDJ region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C;Accession: S29690
R;Dammers, P.M.; Bos, N.A.; Kroese, F.G.M.
submitted to the EMBL Data Library, October 1992
A;Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.
A;Reference number: S29690
A;Accession: S29690
A;Molecule type: mRNA
A;Residues: 1-288 <DM>
A;Cross-references: EMBL:X68782; NID:g56442; PID:g1334294
A;Experimental source: strain D2B
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 44.7%; Score 475.5; DB 2; Length 288;
Best Local Similarity 46.2%; Pred. No. 2e-30;
Matches 92; Conservative 41; Mismatches 51; Indels 15; Gaps 4;

Qy 5 TSLTCAVYGGSPGYWSWIROPKGLWIGIN-HSGSTYNPSLKSRTVISVDTSK 63
Db 14 SVKTSKASGYTFDYVYHWHVKRQPEGLVWGRINPANGNTEYAEKFRATLTADKSS 73

Qy 64 NQFSLKLSVTAADTAVYVCARGAAEYVYVYG----MDVWGQGTTVTVSSGASAPTLF 119
Db 74 NTAYMQLSSLTSEDATYFCT-----IWGVVPFDYWGQGVMTVSESSPTVL 124

Qy 120 PLVSCENSPDTSVAVGCLAQDPLPXITPKWYKKNSDI-SSTRGPPSVLRGKYAAT 178
Db 125 PLVSCESPLSDENLVAMGLARDELPLSPISPMYQNNTEVMQGVRTFPTLTGDKYAT 184

Qy 179 SOVLLPSKDVWQGTDEHV 197
Db 185 SQVLLSAKNVLEGSDELIV 203

RESULT 11

S37456
Ig mu chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37456
R;McIntosh, R.S.; Tandon, N.; Weetman, A.P.
submitted to the EMBL Data Library, September 1993
A;Description: Cloning and analysis of human IgM anti-Thyroglobulin autoantibodies from
A;Reference number: S37453
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-116 <MC1>
A;Cross-references: EMBL:X75024; NID:g404313; PIDN:CAA52932.1; PID:g758095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: immunoglobulin
F;6-90/Domain: immunoglobulin homology <IMM>

Query Match 44.3%; Score 471.5; DB 2; Length 116;
Best Local Similarity 83.2%; Pred. No. 1.5e-30;
Matches 94; Conservative 3; Mismatches 13; Indels 3; Gaps 2;

Qy 1 KLPTLSLTCAVYGGSPF--GYWWSWIROPKGLWIGIENHSGSTYNPSLKSRTVIS 58
Db 4 KPSQTLSTLCTVSGGSISSGGYWSWIROPKGLWIGIYIYSGSYNPSLKSRTVIS 63

Qy 59 VDTSKNQFSLKLSVTAADTAVYVCARGAAEY-YYYYYGMVWGQGTTVTVSS 110
|||||

Db 64 VDTSKNQFSLKLSVTAADTAVYVCARGGYSGYYYYYYMDVWGKGTTVTVSS 116

RESULT 12

S31512
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31512
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31512
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69860; NID:g33082; PIDN:CAA49494.1; PID:g33083
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 465.5; DB 2; Length 155;
Best Local Similarity 80.2%; Pred. No. 6.1e-30;
Matches 89; Conservative 5; Mismatches 16; Indels 1; Gaps 1;

Qy 1 KLPTLSLTCAVYGGSPGYWSWIROPKGLWIGIENHSGSTYNPSLKSRTVISVD 60
Db 45 KPSETLSLTCTVSGGSISSYWSWIROPKGLWIGIYIYTSATYNPPLKSRVTISVD 104

Qy 61 TSKNQFSLKLSVTAADTAVYVCARGAA-EYIYIYVGMVWGQGTTVTVSS 110
Db 105 TSKNQFSLKLSVTAADTAVYVCARGGSISSYVYGMVWGQGTTVTVSS 155

RESULT 13

S31511
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31511
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-155 <CHA>
A;Cross-references: EMBL:X69866; NID:g33094; PIDN:CAA49500.1; PID:g33095
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;47-129/Domain: immunoglobulin homology <IMM>

Query Match 43.8%; Score 465.5; DB 2; Length 155;
Best Local Similarity 81.1%; Pred. No. 6.1e-30;
Matches 90; Conservative 4; Mismatches 16; Indels 1; Gaps 1;

Qy 1 KLPTLSLTCAVYGGSPGYWSWIROPKGLWIGIENHSGSTYNPSLKSRTVISVD 60
Db 45 KPSETLSLTCTVSGGSISSYWSWIROPKGLWIGIYIYTSATYNPPLKSRVTISVD 104

Qy 61 TSKNQFSLKLSVTAADTAVYVCARGAA-EYIYIYVGMVWGQGTTVTVSS 110
Db 105 TSKNQFSLKLSVTAADTAVYVCARGGSISSYWDYGMVWGQGTTVTVSS 155

RESULT 14

S31676
Ig heavy chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31676

Search completed: March 8, 2005, 06:39:26
Job time : 15.406 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 75.4368 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-31

Perfect score: 1064

Sequence: 1 KLPTLSLTCAVYGGSPSGY.....LPKDVVMQGTDEHVVTGSKE 202

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	930.5	87.5	595	2	Q8WUX4	Q8wux4 homo sapien
2	930.5	87.5	597	2	Q6GMX5	Q6gmx5 homo sapien
3	930.5	87.5	597	2	Q9BU10	Q9bu10 homo sapien
4	930.5	87.5	625	2	Q96AA6	Q96aa6 homo sapien
5	924.5	86.9	597	2	Q9BQB8	Q9bqb8 homo sapien
6	861	80.9	620	2	Q96EY0	Q96ey0 homo sapien
7	800	75.2	606	2	Q6GMX2	Q6gmx2 homo sapien
8	714	67.1	613	2	Q8WUK1	Q8wuk1 homo sapien
9	712.5	67.0	597	2	Q96BB9	Q96bb9 homo sapien
10	566	53.2	465	2	Q6GMX6	Q6gmx6 homo sapien
11	559.5	52.6	576	2	Q6P4I8	Q6p4i8 homo sapien
12	539.5	50.7	613	2	Q8VCX7	Q8vcx7 mus musculus
13	526.5	49.5	476	2	Q6GMX1	Q6gmx1 homo sapien
14	517.5	48.6	477	2	Q6GMX7	Q6gmx7 homo sapien
15	498	46.8	146	1	HV21_HUMAN	P06331 homo sapien
16	498	46.8	614	2	Q7TMT6	Q7tmt6 mus musculus
17	480.5	45.2	496	2	Q96KX8	Q96kx8 homo sapien
18	478	44.9	116	2	Q7Z3Y6	Q7z3y6 homo sapien
19	473	44.5	478	2	Q6N1H3	Q6n1h3 homo sapien
20	472.5	44.4	478	2	Q7Z379	Q7z379 homo sapien
21	472	44.4	492	2	Q7Z374	Q7z374 homo sapien
22	467	43.9	473	2	Q8TC63	Q8tc63 homo sapien
23	464.5	43.7	476	2	Q6MZX7	Q6mzx7 homo sapien
24	447.5	42.1	479	2	Q99M22	Q99m22 mus musculus
25	447	42.0	454	1	MUC_HUMAN	P01871 homo sapien
26	440	41.4	150	2	Q95973	Q95973 homo sapien
27	431.5	40.6	472	2	Q6N089	Q6n089 homo sapien
28	428.5	40.3	478	2	Q6P181	Q6p181 homo sapien
29	422.5	39.7	573	2	Q8WU38	Q8wu38 homo sapien
30	416.5	39.1	119	2	Q9UL73	Q9ul73 homo sapien
31	415.5	39.1	605	2	Q6GN83	Q6gn83 xenopus lae

Query Match 87.5%; Score 930.5; DB 2; Length 595;

32	414	38.9	482	2	Q91X92	Q91x92 mus musculus
33	406	38.2	593	2	Q6INM5	Q6inm5 xenopus lae
34	405.5	38.1	470	2	Q6PJA4	Q6pja4 homo sapien
35	402.5	37.8	482	2	Q7Z351	Q7z351 homo sapien
36	400	37.6	572	2	Q661Q7	Q661q7 xenopus lae
37	398	37.4	470	2	Q7TMK1	Q7tmk1 mus musculus
38	397	37.3	225	2	Q6PAF5	Q6paf5 xenopus lae
39	394.5	37.1	464	2	Q6MZU6	Q6mzu6 homo sapien
40	394	37.0	139	2	Q86SX2	Q86sx2 homo sapien
41	390.5	36.7	129	1	HV2F_HUMAN	P01824 homo sapien
42	390	36.7	465	2	Q6P6C4	Q6p6c4 homo sapien
43	383.5	36.0	614	2	Q6DDO7	Q6ddo7 xenopus lae
44	383	36.0	472	2	Q6PJA7	Q6pja7 mus musculus
45	383	36.0	475	2	Q6MZQ6	Q6mzq6 homo sapien

ALIGNMENTS

RESULT 1
Q8WUX4 ID Q8WUX4 PRELIMINARY; PRT; 595 AA.
AC Q8WUX4;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RT Jones S.J., Marz M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002)."
RT and mouse cDNA sequences."
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Straube R.;
RL Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019235; AAH19235.2; -.
DR PIR; G34964; G34964.
DR HSSP; P01861; 1ADQ.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 4.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;

Best Local Similarity 87.2%; Pred. No. 1.8e-74;
Matches 184; Conservative 4; Mismatches 14; Indels 9; Gaps 2;

QY 1 KLPTLSLTCAVYGGSPGYWWSWIROPKGLGEIWHSGSTNPNPSLKSRVTISVD 60
Db 39 KPSETLSLTGCVYGGSPGYWWSWIROPKGLGEIWHSGSTNPNPSLKSRVTISVD 98
QY 61 TSKNQPSLKLSVTAADTAVYYCAR---GAAEYYYYYYGMVDMVGQGTIVTVSSGSASAPT 117
Db 99 TSKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVDMVGQGTIVTVSSGSASAPT 158
QY 118 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPFSLRGKYYAA 177
Db 159 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFSLRGKYYAA 218
QY 178 TSQVLLPSKDVMOGTDEHV-----TGSKE 202
Db 219 TSQVLLPSKDVMOGTDEHVCKVQHPNGNKE 249

RESULT 2

Q6GMXS PRELIMINARY; PRT; 597 AA.

AC Q6GMXS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL: BC073767; AAH73767.1; -.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00407; Igi; 4.
DR SMART; SM00409; Igi; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; Igi; 1.
DR PROSITE; PS0835; IG_LIKE; 5.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 87.5%; Score 930.5; DB 2; Length 597;
Best Local Similarity 87.2%; Pred. No. 1.8e-74;
Matches 184; Conservative 4; Mismatches 14; Indels 9; Gaps 2;

QY 1 KLPTLSLTCAVYGGSPGYWWSWIROPKGLGEIWHSGSTNPNPSLKSRVTISVD 60
Db 32 KPSETLSLTGCVYGGSPGYWWSWIROPKGLGEIWHSGSTNPNPSLKSRVTISVD 91
QY 61 TSKNQPSLKLSVTAADTAVYYCAR---GAAEYYYYYYGMVDMVGQGTIVTVSSGSASAPT 117
Db 92 TSKQLSLKLSVNAADTAVYYCARVITRASPGTDGRYGMVDMVGQGTIVTVSSGSASAPT 151
QY 118 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPFSLRGKYYAA 177
Db 152 LFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPFSLRGKYYAA 211
QY 178 TSQVLLPSKDVMOGTDEHV-----TGSKE 202
Db 212 TSQVLLPSKDVMOGTDEHVCKVQHPNGNKE 242

RESULT 3

Q9BU10 PRELIMINARY; PRT; 597 AA.

AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RA EMBL: BC002963; AAH02963.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 4.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65274 MW; 2DAPAF8FB7E055851 CRC64;

Query Match      87.5%; Score 930.5; DB 2; Length 597;
Best Local Similarity 87.2%; Pred No. 1.8e-74;
Matches 184; Conservative 4; Mismatches 14; Indels 9; Gaps 2;

QY 1 KLPETLSITCAVYGGSFSGYWSWIRQPPGKLEWIGEINHSNSTYNPSLKSRTVISVD 60
Db 32 KPSETLSITCGVYGGSFSGYWSWIRQPPGKLEWIGEINHSNSTYNPSLKSRTVISVD 91
QY 61 TSKNQFSLKLSVTAADTAIVYCAR---GAAYEYIIYGYMDVWGQGTITVTVSSGSASAPT 117
Db 92 TSKKQLSLKLSVNAADTAIVYCARVITRASPGTDGRYGMVWGQGTITVTVSSGSASAPT 151
QY 118 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNSDISSTRGPSPVLRGKVA 177
Db 152 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPSPVLRGKVA 211
QY 178 TSQVLLPSKDVMOGTDEHV-----TGSKE 202
Db 212 TSQVLLPSKDVMOGTDEHVCKVQHPNGNKE 242

RESULT 4
Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzyski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.2; -
DR PIR; S15590; S15590.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.
```

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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; CI-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; FG2FAB3ADE7ECBFE CRC64;

Query Match      87.5%; Score 930.5; DB 2; Length 625;
Best Local Similarity 87.2%; Pred No. 1.9e-74;
Matches 184; Conservative 4; Mismatches 14; Indels 9; Gaps 2;

QY 1 KLPETLSITCAVYGGSFSGYWSWIRQPPGKLEWIGEINHSNSTYNPSLKSRTVISVD 60
Db 39 KPSETLSITCGVYGGSFSGYWSWIRQPPGKLEWIGEINHSNSTYNPSLKSRTVISVD 98
QY 61 TSKNQFSLKLSVTAADTAIVYCAR---GAAYEYIIYGYMDVWGQGTITVTVSSGSASAPT 117
Db 99 TSKKQLSLKLSVNAADTAIVYCARVITRASPGTDGRYGMVWGQGTITVTVSSGSASAPT 158
QY 118 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNSDISSTRGPSPVLRGKVA 177
Db 159 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPSPVLRGKVA 218
QY 178 TSQVLLPSKDVMOGTDEHV-----TGSKE 202
Db 219 TSQVLLPSKDVMOGTDEHVCKVQHPNGNKE 249

RESULT 5
Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
Blakesley R.W., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Kryzyski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -
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Db 92 TSKNQFSLRLNSVTAADTAVYCAHSS-----WDFADYWGQGLVTVSSASPTSPKVPF 147
Qy 121 LVSCNSPSTSSVAVGCLAQDFLP-DXITFXWKYKNNSDISSTRGFP--SVLRGGKYAA 177
Db 148 L-SLDSTPDQ-GNVVAVCLVQGFPPQBELSVTWSESGN--VTARNFFPSPQDASGDLVTT 203
Qy 178 TSQVLLPSKDVMOG 191
Db 204 SSQTLTPATQCPDG 217
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RESULT 15

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HV2I_HUMAN
ID HV2I_HUMAN STANDARD; PRT; 146 AA.
AC P06331;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V-II region ARH-77 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85205332; PubMed=3922855; DOI=10.1016/0378-1119(85)90092-7;
RA Kudo A., Ishihara T., Nishimura Y., Watanabe T.;
RT "A cloned human immunoglobulin heavy chain gene with a novel direct-
RT repeat sequence in 5' flanking region.";
RL Gene 33:181-189(1985).
DR PIR; A02101; GI|H042.
DR HSSP; P01825; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 146 Ig heavy chain V-II region ARH-77.
FT DOMAIN 20 117 V segment.
FT DOMAIN 118 127 D segment.
FT DOMAIN 128 146 J segment.
FT DISULFID 42 115 By similarity.
FT NON TER 146 146
SQ SEQUENCE 146 AA; 16228 MW; 8D7FD52BB218171F CRC64;
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Query Match 46.8%; Score 498; DB 1; Length 146;
Best Local Similarity 84.2%; Pred. No. 1.4e-36;
Matches 96; Conservative 4; Mismatches 10; Indels 4; Gaps 1;

Qy 1 KLPETLSLTCAVYGSFSGYWSWIRQPPGKLEWIGEINHSSTNNPNSLKSRVTISVD 60
Db 33 KPSETLSLTCAVFGSGFYWSWIRQPPGKLEWIGEINHSSTNYKTSLSKSRVTISLD 92
Qy 61 TSKNQFSLKLSVTAADTAVYCAHAEYYY-----YYYGNDVWGQFTTVTVSS 110
Db 93 TSKNLFSLKLSVTAADTAVYCAHLLRGGMNDVDVYYGMDVWGQFTTVTVSS 146
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Search completed: March 8, 2005, 06:35:51
Job time : 76.4368 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 93.6527 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-31

Perfect score: 1064

Sequence: 1 KLPTLSLTCAVYGGSPSGY.....LPKDVMOGTDEHVVTGSKE 202

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A_Geneseq_16Dec04:*
- 2: geneseqp1980s:*
- 3: geneseqp1990s:*
- 4: geneseqp2000s:*
- 5: geneseqp2001s:*
- 6: geneseqp2002s:*
- 7: geneseqp2003as:*
- 8: geneseqp2003bs:*
- 9: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1064	100.0	202	2 AAY34303	Aay34303 Igm antib
2	1041	97.8	205	2 AAY34299	Aay34299 Igm antib
3	920	86.5	190	2 AAY34304	Aay34304 Igm antib
4	876.5	82.4	197	2 AAY34300	Aay34300 Igm antib
5	734.5	69.0	627	7 ADE97370	Ad97370 Human imm
6	729.5	68.6	203	2 AAY34301	Aay34301 Igm antib
7	727	68.3	595	7 ADM05427	Adm05427 Human pro
8	718	67.5	223	2 AAY08598	Aay08598 Anti-huma
9	714.5	67.2	266	8 ADF69305	Adf69305 Human lun
10	713	67.0	588	2 AAU71880	Aau71880 Anti-huma
11	713	67.0	588	3 AAB12917	Aab12917 Anti-huma
12	713	67.0	596	4 AAM23924	Aam23924 Human EST
13	712	66.9	223	8 ADL70773	Adl70773 Anti-TNPa
14	706.5	66.4	228	8 ADL70776	Adl70776 Anti-TNPa
15	704.5	66.2	199	2 AAY34302	Aay34302 Igm antib
16	699	65.7	588	2 AAU71881	Aau71881 Anti-huma
17	699	65.7	588	3 AAB12918	Aab12918 Anti-huma
18	685	64.4	533	7 ADB65070	Adb65070 Human pro
19	684.5	64.3	570	8 ADR19329	Adr19329 Chimeric
20	683	64.2	569	8 ADR19330	Adr19330 Chimeric
21	675	63.4	571	8 ADP84970	Adp84970 Chimeric
22	646.5	60.8	450	6 ABP96294	Abp96294 4A5-3.1.1
23	633.5	59.5	453	6 ABP96295	Abp96295 4A5-3.1.1
24	624.5	58.7	472	2 AAR93166	Aar93166 Anti-rhes
25	617	58.0	229	7 ADJ32128	Adj32128 Human int

26	615	57.8	223	7 ADJ32112	Adj32112 Human int
27	607.5	57.1	230	7 ADJ32118	Adj32118 Human int
28	606	57.0	537	3 AAY96290	Aay96290 Human IGF
29	597.5	56.2	462	3 AAB26884	Aab26884 Human imm
30	584.5	54.9	464	7 ADE28411	Ad928411 Human ant
31	570.5	53.6	466	7 ADE28479	Ad928479 Human ant
32	568	53.4	473	4 AAB36206	Aab36206 Human imm
33	567.5	53.3	466	7 ADE28471	Ad928471 Human ant
34	563.5	53.0	580	6 AAO30915	Aao30915 di-NHS76
35	562	52.8	251	5 AEG80712	Age80712 Amyloid p
36	562	52.8	254	5 AEG80713	Age80713 Amyloid p
37	562	52.8	263	5 AEG80714	Age80714 Human IGF
38	559	52.5	580	6 AAO30913	Aao30913 di-NHS76
39	555.5	52.2	466	7 ADE28419	Ad928419 Human ant
40	554	52.1	152	6 ABO04857	Ab004857 Human epi
41	552	51.9	221	7 ADJ32126	Adj32126 Human int
42	545	51.2	229	3 AAB30593	Aab30593 Variable
43	544.5	51.2	172	3 AAY93713	Aay93713 The heavy
44	544.5	51.2	172	6 AAE35892	Aae35892 Human 2.1
45	544	51.1	241	8 ADS84467	Ads84467 Human ant

ALIGNMENTS

RESULT 1

AAY34303

ID AAY34303 standard; protein; 202 AA.

XX AAY34303;

DT 19-NOV-1999 (first entry)

XX

DE Igm antibody CEM 13.12 heavy chain sequence.

XX

KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 147 /label= unknown

FT /note= "encoded by TYC"

FT Misc-difference 151 /label= unknown

FT /note= "encoded by TYC"

FT

XX WO9945031-A2.

XX

XX 10-SEP-1999.

XX

XX 03-MAR-1999; 99WO-US004583.

XX

XX 03-MAR-1998; 98US-00034607.

XX

XX 03-FEB-1999; 99US-00244253.

XX

XX (ABGE-) ABGENIX INC.

XX

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX

XX WPI; 1999-540816/45.

XX

XX N-PSDB; AAZ20404.

XX

XX New monoclonal antibody. used for treating e.g. graft versus host

XX disease, cancers, autoimmune diseases and inflammatory diseases.

XX

PS Claim 60; Fig 28; 245pp; English.

XX

This sequence represents the heavy chain of an antibody of the invention.

XX New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.
 XX
 PS Claim 60; Fig 29; 245pp; English.
 XX
 CC This sequence represents the heavy chain of an antibody of the invention.
 CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
 CC complement and a variable region that binds to the epitope on CD147 bound
 CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
 CC can selectively kill activated T-cells, activated B-cells or resting or
 CC activated monocytes. The products and methods can be used for treating
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
 CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
 XX
 SQ Sequence 190 AA;

Query Match 86.5%; Score 920; DB 2; Length 190;
 Best Local Similarity 92.1%; Pred. No. 5.3e-57;
 Matches 176; Conservative 5; Mismatches 8; Indels 2; Gaps 1;
 Qy 4 ETLSLTCAVYGGSGFYWMIROPPGKLEWIGEHNSGNTNPNPSLKSRVTISVDTSK 63
 Db 2 ETLSLTCAVYGGSGFYWMIROPPGKLEWIGEHNSGNTNPNPSLKSRVTISVDTSK 61
 Qy 64 NQFSLKLSVTAADTAVYICARGAAEYVYVYVGMVQGTITVTVSSGSASAPTLFPLVS 123
 Db 62 NQFSLKLSVTAADTAVYICARGGTTVTDFAF--DINGQGTMTVTVSSGSASAPTLFPLVS 119
 Qy 124 CENSPSDTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 183
 Db 120 CENSPSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 179
 Qy 184 PSKDVMOGTDE 194
 Db 180 PSKDVMOGTDE 190

RESULT 4
 AAY34300
 ID AAY34300 standard; protein; 197 AA.
 AC AAY34300;
 XX
 DT 19-NOV-1999 (first entry)
 XX
 DE IgM antibody CEM 10.1 G10 heavy chain sequence.
 XX
 KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.
 XX
 OS Homo sapiens.
 XX
 PN WO9945031-A2.
 XX
 PD 10-SEP-1999.
 XX
 PF 03-MAR-1999; 99WO-US004583.
 XX
 PR 03-MAR-1998; 98US-00034607.
 PR 03-FEB-1999; 99US-00244253.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
 XX
 DR WPI; 1999-540816/45.

DR N-PSDB; AAZ20401.
 XX
 PT New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.
 XX
 PS Claim 60; Fig 25; 245pp; English.
 XX
 CC This sequence represents the heavy chain of an antibody of the invention.
 CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
 CC complement and a variable region that binds to the epitope on CD147 bound
 CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
 CC can selectively kill activated T-cells, activated B-cells or resting or
 CC activated monocytes. The products and methods can be used for treating
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
 CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
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 SQ Sequence 197 AA;

Query Match 82.4%; Score 876.5; DB 2; Length 197;
 Best Local Similarity 86.1%; Pred. No. 6.2e-54;
 Matches 173; Conservative 4; Mismatches 13; Indels 11; Gaps 2;
 Qy 1 KLPTLSLTCAVYGGSGFYWMIROPPGKLEWIGEHNSGNTNPNPSLKSRVTISVD 60
 Db 3 KPSETLSLTCTVSGSISYYWMIROPPGKLEWIGYIYVSGSTNPNPSLKSRVTISVD 62
 Qy 61 TSKNQPSLKLSVTAADTAVYICAR---GAAEYVYVYVGMVQGTITVTVSSGSASAP 116
 Db 63 TSKNQPSLKLSVTAADTAVYICARDRGVAT-----GFDYWGQGTITVTVSSGSASAP 115
 Qy 117 TLFLVSCNSPSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLRGGKYA 176
 Db 116 TLFLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYA 175
 Qy 177 ATSOVLLPSKDVMOGTDEHV 197
 Db 176 ATSOVLLPSKDVMOGTDEHKV 196

RESULT 5
 ADE97370
 ID ADE97370 standard; protein; 627 AA.
 AC ADE97370;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human immunoadhesin-related protein - SEQ ID 47.
 XX
 KW immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;
 KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;
 KW intercellular adhesion molecule; ICAM-1; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003064992-A2.
 XX
 PD 07-AUG-2003.
 XX
 PF 25-OCT-2002; 2002WO-US034197.
 XX
 PR 26-OCT-2001; 2001US-00047542.
 XX
 PA (PLAN-) PLANET BIOTECHNOLOGY INC.
 PA (LARR/) LARRICK J W.
 PA (WYCO/) WYCOFF K L.
 XX
 PI Larrick JW, Wycoff KL;
 XX
 DR WPI; 2003-636816/60.

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 107.196 Seconds

(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-31

Perfect score: 1064

Sequence: 1 KLPTLSLTCAVYGGSPSGY.....LPKDVQMGTDHVVTSKSE 202

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1391452.seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution..

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	734.5	69.0	627	13	US-10-047-542-47
2	727	68.3	595	15	US-10-108-260A-4112
3	685	64.4	533	15	US-10-104-047-3224
4	617	58.0	229	10	US-09-972-656-82
5	615	57.8	223	10	US-09-972-656-66
6	610.5	57.4	179	15	US-10-309-762-171
7	607.5	57.1	230	10	US-09-972-656-72
8	584.5	54.9	464	15	US-10-292-088-22
9	570.5	53.6	466	15	US-10-292-088-86
10	567.5	53.3	466	15	US-10-292-088-70
11	563.5	53.0	580	14	US-10-310-719-37
12	559	52.5	580	14	US-10-310-719-35
13	555.5	52.2	466	15	US-10-292-088-30

14	554	52.1	152	9	US-09-187-693-68	Sequence 68, Appl
15	552	51.9	221	10	US-09-972-656-80	Sequence 80, Appl
16	545	51.2	229	9	US-09-974-449-37	Sequence 37, Appl
17	544.5	51.2	172	14	US-10-153-382-21	Sequence 21, Appl
18	544	51.1	241	16	US-10-684-109-106	Sequence 106, Appl
19	541	50.8	241	16	US-10-684-109-71	Sequence 71, Appl
20	534	50.2	239	16	US-10-684-109-100	Sequence 100, Appl
21	533	50.1	241	16	US-10-684-109-88	Sequence 88, Appl
22	525	49.3	118	15	US-10-371-942-90	Sequence 90, Appl
23	521.5	49.0	193	15	US-10-264-049-4331	Sequence 4331, Ap
24	518	48.7	253	10	US-09-880-748-954	Sequence 954, App
25	518	48.7	253	15	US-10-293-418-954	Sequence 954, App
26	516	48.5	429	14	US-10-194-801C-6	Sequence 6, Appli
27	515	48.4	250	14	US-10-194-975-110	Sequence 110, App
28	515	48.4	255	10	US-09-880-748-1642	Sequence 1642, Ap
29	515	48.4	255	15	US-10-293-418-1642	Sequence 1642, Ap
30	512.5	48.2	250	10	US-09-880-748-993	Sequence 993, App
31	512.5	48.2	250	15	US-10-293-418-993	Sequence 993, App
32	512.5	48.2	254	10	US-09-880-748-1659	Sequence 1659, Ap
33	512.5	48.2	254	15	US-10-293-418-1659	Sequence 1659, Ap
34	510.5	48.0	252	10	US-09-880-748-1326	Sequence 1326, Ap
35	510.5	48.0	252	15	US-10-293-418-1326	Sequence 1326, Ap
36	510	47.9	235	16	US-10-684-109-112	Sequence 112, App
37	508	47.7	173	15	US-10-309-762-173	Sequence 173, App
38	508	47.7	447	14	US-10-194-801C-2	Sequence 2, Appli
39	507	47.7	249	10	US-09-880-748-957	Sequence 957, App
40	507	47.7	249	15	US-10-293-418-957	Sequence 957, App
41	505.5	47.5	250	10	US-09-880-748-1413	Sequence 1413, Ap
42	505.5	47.5	250	15	US-10-293-418-1413	Sequence 1413, Ap
43	504.5	47.4	125	15	US-10-371-942-110	Sequence 110, App
44	504.5	47.4	467	14	US-10-211-357-8	Sequence 8, Appli
45	504.5	47.4	467	14	US-10-211-357-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-10-047-542-47
; Sequence 47, Application US/10047542
; Publication No. US20020168367A1
; GENERAL INFORMATION:
; APPLICANT: LARRICK, JAMES W.
; APPLICANT: WYCOFF, KEITH L.
; TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL
; TITLE OF INVENTION: AND BACTERIAL DISEASES
; FILE REFERENCE: 030905.0004.CIP1
; CURRENT APPLICATION NUMBER: US/10/047,542
; CURRENT FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: PCT/US01/13932
; PRIOR FILING DATE: 2001-04-28
; PRIOR APPLICATION NUMBER: 60/200,298
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 101
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 627
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-047-542-47

Query Match 69.0%; Score 734.5; DB 13; Length 627;
Best Local Similarity 67.9%; Pred. No. 5.1e-46;
Matches 146; Conservative 23; Mismatches 29; Indels 17; Gaps 4;

Qy	5	TLSTCAVYGGSPSGYWSWIRPPGKLEWIGE-INHSSTNYPNPSLSRVTTISVDTSK	63
Db	36	SVKVSCKASGGTFSSYAIWSVRQPGQGLEWGGIIPFGTANYAQKFGQRTTADSET	95
Qy	64	NQFSLKLSSTVAADTAVVYCARG-----AAEY-----YYYGMDVMGQGTVTTVSSGSA	113
Db	96	STATNELLSLRSEDATVYCAKTIILGILPSSGWTPNSDYIIYIGMDVMGQGTVTTVSSGSA	155

Qy 114 SAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLRGG 173
Db 156 SAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGG 215
Qy 174 KYAATSOVLLPSKDVMOGTDDEHVY-----TGSKE 202
Db 216 KYAATSOVLLPSKDVMOGTDDEHVYKQHPNGNKE 250

RESULT 2

US-10-108-260A-4112
; Sequence 4112, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1el full length cDNA
; FILE REFERENCE: HI-A0106
; CURRENT APPLICATION NUMBER: US/10/108,260A
; CURRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4112
; LENGTH: 595
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-108-260A-4112

Query Match 68.3%; Score 727; DB 15; Length 595;
Best Local Similarity 70.7%; Pred. No. 1.7e-45;
Matches 145; Conservative 20; Mismatches 32; Indels 8; Gaps 3;

Qy 5 TSLSLTCAVYGGFSGYWSWIRPPGKLEWIGBHNHSGSTN-YNPSLKSRVTISVDTSK 63
Db 37 SLRLSCAASGTFNFAMHWIRQPPGKLEWISVTSISNGRQKYGESVKGRFTISRDSK 96
Qy 64 NQFSLKLSVTAADTAVYICARGAAEYYYYYGGMDVMGQGTAVTVSSGSASAPTLFPLVS 123
Db 97 NTLFLQMSLRDDTAVYICARGHS-IDNYHYGVDVMGQGTAVTVSSGSASAPTLFPLVS 155
Qy 124 CENSFSDTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 183
Db 156 CENSFSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 215
Qy 184 PSKDVMOGTDDEHVY-----TGSKE 202
Db 216 PSKDVMOGTDDEHVYKQHPNGNKE 240

RESULT 3

US-10-104-047-3224
; Sequence 3224, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20030236392A1el full length cDNA
; FILE REFERENCE: HI-A0105
; CURRENT APPLICATION NUMBER: US/10/104,047
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3224
; LENGTH: 533
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-104-047-3224

Query Match 64.4%; Score 685; DB 15; Length 533;
Best Local Similarity 68.3%; Pred. No. 1.9e-42;
Matches 140; Conservative 15; Mismatches 42; Indels 8; Gaps 3;

Qy 5 TSLSLTCAVYGGFSGYWSWIRPPGKLEWIGBHNHSGSTNYPNPSLKSRVTISVDTSKN 64

Db 36 SLRLSCAASGDFVSSNTWSWVRQSPGKPEWVATMYGCGNTTYAESVKGRFTVSRDGSQN 95
Qy 65 QFSLKLSVTAADTAVYICARGAAEYY-YYYYGMDVMGQGTAVTVSSGSASAPTLFPLVS 123
Db 96 TLYLEMSLRPDDTAVYICVRDHRNYADTSPYGRK-WGQGTAVTVSSGSASAPTLFPLVS 154
Qy 124 CENSFSDTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 183
Db 155 CENSFSDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSOVLL 214
Qy 184 PSKDVMOGTDDEHVY-----TGSKE 202
Db 216 PSKDVMOGTDDEHVYKQHPNGNKE 239

RESULT 4

US-09-972-656-82
; Sequence 82, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 82
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-82

Query Match 58.0%; Score 617; DB 10; Length 229;
Best Local Similarity 62.2%; Pred. No. 8.1e-38;
Matches 125; Conservative 21; Mismatches 45; Indels 10; Gaps 5;

Qy 1 KLPETLSLTCAVYGGFSGYWSWIRPPGKLEWIGBHNHSGSTNYPNPSLKSRVTISVD 60
Db 13 KPSETLSLTCAVYGGFSGYWSWIRPPGKLEWIGBHNHSGSTNYPNPSLKSRVTISVD 72
Qy 61 TSKNQFSLKLSVTAADTAVYICARGAAEYYYYYGG---MDVMGQGTAVTVSSGSASAP 116
Db 73 TSKNQFSLKLSVTAADTAVYICARGWPTVYWGSGYRKPGEYFDYWGQGTAVTVSSASTKGP 132
Qy 117 TLFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLR-GGKY 175
Db 133 SVFPLAPSSKSTSG-GTAALGCLVKDYFPEPVTYSW--NSGALTSGVHTTTPAVLQSSGLY 189
Qy 176 AATSOVLLPSKDVMOGTDDEHV 196
Db 190 SLSSVWTVPSSSL--GTQTVI 208

RESULT 5

US-09-972-656-66
; Sequence 66, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 223


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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-66

Query Match      57.8%; Score 615; DB 10; Length 223;
Best Local Similarity 62.9%; Pred. No. 1.1e-37;
Matches 124; Conservative 22; Mismatches 43; Indels 8; Gaps 5;

QY 1 KLPETLSITCAVYGSFSGYYSWIRQPPGKLEWIGEINHSNSTYNNPSLKSRTVISVD 60
Db 13 KPSETLSITCAVYGSFSGYYSWIRQPPGKLEWIGEINHSNSTYNNPSLKSRTVISVD 72
QY 61 TSKNQFSLKLSVTAADTAATVYTCARGAAEYIIYYGMDVWGQTTVTSSGSASAPTLFP 120
Db 73 TSKNQFSLKLSVTAADTAATVYTCARGARNMRSF--DYWGQGLTVTVSSASTKGPSVFP 130
QY 121 LVSCENSPDTSSTAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLR--GGKYAATS 179
Db 131 LAPSSKSTSG--GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSS 187
QY 180 QVLLPSKDVWGQTDHVV 196
Db 188 VVTVPSSSL--GTQTYI 202

RESULT 6
US-10-309-762-171
; Sequence 171, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXY CARBOXY ANHYDRASE IX
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; PRIOR FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2002-12-02
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-171

Query Match      57.4%; Score 610.5; DB 15; Length 179;
Best Local Similarity 67.6%; Pred. No. 1.9e-37;
Matches 117; Conservative 19; Mismatches 32; Indels 5; Gaps 3;

QY 1 KLPETLSITCAVYGSFSGYYSWIRQPPGKLEWIGEINHSNSTYNNPSLKSRTVISVD 60
Db 7 KPSETLSITCAVYGSFSGYYSWIRQPPGKLEWIGYIYSGNSTYNNPSLKSRTVISVD 66
QY 61 TSKNQFSLKLSVTAADTAATVYTCARG--AAEYIIYYGMDVWGQTTVTSSGSASAPTL 118
Db 67 TSKNQFSLKLSVTAADTAATVYTCARGDQSSSVYIIYYGMDVWGQTTVTSSASTKGPSV 126
QY 119 PVLSCENSPDTSSTAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLR 171
Db 127 PFLAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQ 176

RESULT 7
US-09-972-656-72
; Sequence 72, Application US/09972656
; Publication No. US2003009647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
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; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 72
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-72

Query Match      57.1%; Score 607.5; DB 10; Length 230;
Best Local Similarity 59.8%; Pred. No. 4.1e-37;
Matches 125; Conservative 21; Mismatches 38; Indels 25; Gaps 6;

QY 1 KLPETLSITCAVYGSFSGYYSWIRQPPGKLEWIGEINHSNSTYNNPSLKSRTVISVD 60
Db 13 KPSETLSITCAVYGSFSGYYSWIRQPPGKLEWIGEINHSNSTYNNPSLKSRTVISVD 72
QY 61 TSKNQFSLKLSVTAADTAATVYTCAR-----GAAEYIIYYGMDVWGQTTVTV 108
Db 73 TSKNQFSLKLSVTAADTAATVYTCARDKGRITIFGWGSA-----GFDYWGQGLTVTV 125
QY 109 SSGSASAPTLPLVSCENSPDTSSTAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPS 168
Db 126 SSASTKGPSVFPPLAPSSKSTSG--GTAALGCLVKDYFPEPVTVSW--NSGALTSGVHTPPA 182
QY 169 VLR--GGKYAATSOVLLPSKDVWGQTDHVV 196
Db 183 VLQSSGLYSLSVTVVPSSSL--GTQTYI 209

RESULT 8
US-10-292-088-22
; Sequence 22, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; PRIOR FILING DATE: 2003-03-14
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-22

Query Match      54.9%; Score 584.5; DB 15; Length 464;
Best Local Similarity 62.2%; Pred. No. 4.1e-35;
Matches 117; Conservative 22; Mismatches 42; Indels 7; Gaps 4;

QY 1 KLPETLSITCAVYGSFSGYYSWIRQPPGKLEWIGEINHSNSTYNNPSLKSRTVISVD 60
Db 32 KPSETLSITCAVYGSFSGYYSWIRQPPGKLEWIGEINHSNSTYNNPSLKSRTVISVD 91
QY 61 TSKNQFSLKLSVTAADTAATVYTCARGAAEYIIYYGMDVWGQTTVTSSGSASAPTLFP 120
Db 92 TSKNQFSLKLSVTAADTAATVYTCAR--DGLYRGYGMVWGQTTVTSSASTKGPSVFP 148
QY 121 LVSCENSPDTSSTAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPVLR--GGKYAATS 179
Db 149 LAPCSRSTSE--STAALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSS 205
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Qy 180 QVLLPSKD 187
Db 206 VVTVPSSN 213

RESULT 9
US-10-292-088-86
; Sequence 86, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-86

Query Match 53.6%; Score 570.5; DB 15; Length 466;
Best Local Similarity 61.7%; Pred. No. 4.4e-34;
Matches 116; Conservative 21; Mismatches 46; Indels 5; Gaps 4;

Qy 1 KLPETLSLTCVYGGSGFYWSWIRQPPGKGLEWIGEINHSGSTNNPNSLKSRVTISVD 60
Db 32 KPSETLSLTCVSGGSIRGYWSWIRQPPGKGLEWIGIYYSGSTNNPNSLKSRVTISVD 91
Qy 61 TSKNQFSLKLSVTAADTAVYYCARGAAEYIIYGGMDVWGQGTITVTVSSGSASAPTLFP 120
Db 92 TSKNQFSLKLSVTAADTAVYYCARGGLYDYGW-FAPWGQGLTVTVSSASTKGPVSFP 150
Qy 121 LVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR-GGKYAATS 179
Db 151 LAPCSRSTSE-STAAIGCLVKDYFPEPVTVSW--NSGALTSGVHTTFFPAVLQSSGLYSLS 207
Qy 180 QVLLPSKD 187
Db 206 VVTVPSSN 215

RESULT 10
US-10-292-088-70
; Sequence 70, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-70

Query Match 53.0%; Score 563.5; DB 14; Length 580;
Best Local Similarity 61.1%; Pred. No. 1.8e-33;
Matches 116; Conservative 20; Mismatches 43; Indels 11; Gaps 5;

Qy 1 KLPETLSLTCVYGGSP-SGYWSWIRQPPGKGLEWIGEINHSGSTNNPNSLKSRVTISV 59
Db 13 KPSETLSLTCVSGYSISSGYWIRQPPGKGLEWIGSIYHSGSTYNNPNSLKSRVTISV 72
Qy 60 DTSKNQFSLKLSVTAADTAVYYCARGAAEYIIYGGMDVWGQGTITVTVSSGSASAPTLF 119
Db 73 DTSKNQFSLKLSVTAADTAVYYCARGK-----WSKFDYWGQGLTVTVSSASTKGPVSF 126
Qy 120 PLVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR-GGKYAAT 178
Db 127 PLAPCSRSTSE-STAAIGCLVKDYFPEPVTVSW--NSGALTSGVHTTFFPAVLQSSGLYSLS 183
Qy 179 SQVLLPSKD 188
Db 184 SVTVPSSSL 193

RESULT 12
US-10-310-719-35
; Sequence 35, Application US/10310719
; Publication No. US20030166163A1
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US-10-292-088-70

Query Match 53.3%; Score 567.5; DB 15; Length 466;
Best Local Similarity 61.2%; Pred. No. 7.4e-34;
Matches 115; Conservative 22; Mismatches 46; Indels 5; Gaps 4;

Qy 1 KLPETLSLTCVYGGSGFYWSWIRQPPGKGLEWIGEINHSGSTNNPNSLKSRVTISVD 60
Db 32 KPSETLSLTCVSGGSIRGYWSWIRQPPGKGLEWIGIYYSGSTNNPNSLKSRVTISVD 91
Qy 61 TSKNQFSLKLSVTAADTAVYYCARGAAEYIIYGGMDVWGQGTITVTVSSGSASAPTLFP 120
Db 92 TSKNQFSLKLSVTAADTAVYYCARGGLYDYGW-FAPWGQGLTVTVSSASTKGPVSFP 150
Qy 121 LVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR-GGKYAATS 179
Db 151 LAPCSRSTSE-STAAIGCLVKDYFPEPVTVSW--NSGALTSGVHTTFFPAVLQSSGLYSLS 207
Qy 180 QVLLPSKD 187
Db 208 VVTVPSSN 215

RESULT 11
US-10-310-719-37
; Sequence 37, Application US/10310719
; Publication No. US20030166163A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Immunocytokines With Modulated Selectivity
; FILE REFERENCE: LEX-020
; CURRENT APPLICATION NUMBER: US/10/310,719
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: 60/337,113
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/371,966
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 580
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: di-NHS76(gamma4h) (FN>AQ) -ala-IL2(D20T) heavy chain fused to
; OTHER INFORMATION: IL-2 variant
US-10-310-719-37

Query Match 53.0%; Score 563.5; DB 14; Length 580;
Best Local Similarity 61.1%; Pred. No. 1.8e-33;
Matches 116; Conservative 20; Mismatches 43; Indels 11; Gaps 5;

Qy 1 KLPETLSLTCVYGGSP-SGYWSWIRQPPGKGLEWIGEINHSGSTNNPNSLKSRVTISV 59
Db 13 KPSETLSLTCVSGYSISSGYWIRQPPGKGLEWIGSIYHSGSTYNNPNSLKSRVTISV 72
Qy 60 DTSKNQFSLKLSVTAADTAVYYCARGAAEYIIYGGMDVWGQGTITVTVSSGSASAPTLF 119
Db 73 DTSKNQFSLKLSVTAADTAVYYCARGK-----WSKFDYWGQGLTVTVSSASTKGPVSF 126
Qy 120 PLVSCENSPDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR-GGKYAAT 178
Db 127 PLAPCSRSTSE-STAAIGCLVKDYFPEPVTVSW--NSGALTSGVHTTFFPAVLQSSGLYSLS 183
Qy 179 SQVLLPSKD 188
Db 184 SVTVPSSSL 193

RESULT 12
US-10-310-719-35
; Sequence 35, Application US/10310719
; Publication No. US20030166163A1
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; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-80

Query Match      51.9%; Score 552; DB 10; Length 221;
Best Local Similarity 58.8%; Pred. No. 4.8e-33;
Matches 117; Conservative 21; Mismatches 47; Indels 14; Gaps 6;

Qy 1 KLPETLSLTCVAVGGSPS--GYWWSWIRQPPGKGLEWIGEIINHSSTYNPFLKSRVTIS 58
Db 13 KPSETLSLTCVAVSGSISGGYSWSWIRQPPGKGLEWIGIYIYHSGSTYNPFLKSRVTIS 72
Qy 59 VDTSKNQFSLKLSVTAADTAIVYTCARGAABYYIYYGMDVMWGQGTWTVSSGSAAPT 118
Db 73 VDRSKNQFSLKLSVTAADTAIVYTCARGDWGYF-----DYWGQGTWTVSSASTKGPSV 126
Qy 119 FPLVSCENSPSDTSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGFPSVLR-GGKYAA 177
Db 127 FPLAPSSKSTSG-GTAALGCLVKDYFPEPVTIWSW-NSGALTSGVHTFPAVLQSSGLYSL 183
Qy 178 TSQVLLPSKQVMQGTDEHV 196
Db 184 SSVVTVFSSSL--GTQTVI 200
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Search completed: March 8, 2005, 07:05:53
Job time : 108.196 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 22.2112 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-31
Perfect score: 1064
Sequence: 1 KLPTLSLTCAVYGGFSFGY.....LPSKDVMOGTDEHVVTGSKE 202

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	624.5	58.7	472	3	US-08-793-450-8
2	568	53.4	473	3	US-09-049-672A-4
3	544.5	51.2	172	4	US-09-472-087-7
4	544.5	51.2	172	4	US-09-472-087-86
5	528	49.6	832	3	US-08-630-820-7
6	528	49.6	832	4	US-09-273-453-7
7	516	48.5	429	4	US-09-372-425A-6
8	508	47.7	447	4	US-09-372-425A-2
9	504.5	47.4	467	3	US-08-523-894-8
10	504.5	47.4	467	3	US-08-523-894-10
11	504.5	47.4	467	3	US-08-523-894-12
12	502.5	47.2	123	3	US-08-793-450-4
13	496.5	46.7	476	3	US-08-487-550-12
14	496.5	46.7	476	4	US-09-526-098-12
15	496.5	46.7	476	4	US-09-383-916-12
16	496.5	46.7	476	4	US-09-383-916-12
17	492	46.2	139	4	US-09-800-729-145
18	486.5	45.7	476	3	US-09-203-768A-2
19	486.5	45.7	476	3	US-08-487-550-4
20	486.5	45.7	476	4	US-09-526-098-4
21	483.5	45.4	219	4	US-09-383-916-4
22	471	44.3	122	1	US-09-460-384-37
23	471	44.3	122	1	US-08-360-125-11
24	471	44.3	122	2	US-08-450-578-11
25	471	44.3	122	2	US-09-017-628-11
26	471	44.3	122	2	US-09-014-880-11
27	471	44.3	122	4	US-08-450-363-11
					US-09-467-903-11

28	466.5	43.8	229	2	US-08-887-352B-20	Sequence 20, Appl
29	466.5	43.8	229	3	US-09-109-207C-20	Sequence 20, Appl
30	466.5	43.8	229	3	US-09-296-005-20	Sequence 20, Appl
31	466.5	43.8	229	4	US-09-920-171-20	Sequence 20, Appl
32	466.5	43.8	229	4	US-09-716-028-20	Sequence 20, Appl
33	466.5	43.8	229	4	US-10-113-996-20	Sequence 20, Appl
34	466.5	43.8	229	4	US-08-887-352B-25	Sequence 25, Appl
35	466.5	43.8	229	3	US-09-109-207C-25	Sequence 25, Appl
36	466.5	43.8	229	3	US-09-296-005-25	Sequence 25, Appl
37	466.5	43.8	229	3	US-09-920-171-25	Sequence 25, Appl
38	466.5	43.8	229	4	US-09-716-028-25	Sequence 25, Appl
39	466.5	43.8	229	4	US-10-113-996-25	Sequence 25, Appl
40	466.5	43.8	451	2	US-08-887-352B-14	Sequence 14, Appl
41	466.5	43.8	451	2	US-08-887-352B-16	Sequence 16, Appl
42	466.5	43.8	451	3	US-08-466-151-65	Sequence 65, Appl
43	466.5	43.8	451	3	US-09-109-207C-14	Sequence 14, Appl
44	466.5	43.8	451	3	US-09-109-207C-16	Sequence 16, Appl
45	466.5	43.8	451	3	US-09-296-005-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABIBI, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-793-450-8

Query Match 58.7%; Score 624.5; DB 3; Length 472;
Best Local Similarity 63.3%; Pred. No. 2.1e-49;
Matches 126; Conservative 23; Mismatches 41; Indels 9; Gaps 6;

QY	1	KLPETLSLTCAVYGSFSGYYWMIROPCKGLEWIGEINHSGSTNYNPSLKSRTVISYD	60
Db	32	KPSETLSLTCTCYGGSFSGYYWMIROPCKGLEWIGEINHSGSTNYNPSLKSRTVISYD	91
QY	61	TSKNQFSLKLSVTAADTAVYCYARGAAEYYYYYG--MDVWGQGTTVTVSSGSAAPT	118
Db	92	TSKNQFSLKLSVTAADTAVYCYAR--APEYKWKYHGDWDFPWGGTITTVTVSSASTKGP	150
QY	119	FFLVGENSEPSTSSVAVGCLAQDPLDKITFXWKYKRNSDISTRGFFSVLR--GKYYAA	177
Db	151	FFLAPSSKSTSG--GTAALGCLVKDYFPEPVTWSN--NSGALTSGVHTFPFVQLQSSGLYS	207
QY	178	TSQVLLPSKDVNQGTDEHV	196
Db	208	SSWTVTPSSSL--GTQTVI	224

RESULT 2
 US-09-049-672A-4
 ; Sequence 4, Application US/09049672A
 ; Patent No. 6135941
 ; GENERAL INFORMATION:
 ; APPLICANT: Hillman, Jennifer L.
 ; APPLICANT: Lal, Preeti
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Yue, Henry
 ; APPLICANT: Au-Young, Janice
 ; APPLICANT: Corley, Neil C.
 ; APPLICANT: Guegler, Karl J.
 ; APPLICANT: Baughn, Mariah R.
 ; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
 ; NUMBER OF SEQUENCES: 28
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.
 ; STREET: 3174 Porter Drive
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94304
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: FastSeq for Windows Version 2.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/049,672A
 ; FILING DATE: HEREWITH
 ; CLASSIFICATION: 536
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER:
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cerrione, Michael C
 ; REGISTRATION NUMBER: 39,132
 ; REFERENCE/DOCKET NUMBER: PF-0497 US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-855-0555
 ; TELEFAX: 650-845-4166
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 473 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; IMMEDIATE SOURCE:
 ; LIBRARY: PANCUT01
 ; CLONE: 1513264
 US-09-049-672A-4

Query Match 53.4%; Score 568; DB 3; Length 473;
Best Local Similarity 59.8%; Pred. No. 3.5e-44;

[illegible]

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RESULT 3
US-09-472-087-7
US-09-472-087-7, Application US/09472087
; Sequence 7,
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKS, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOPFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7

```

	Query Match	51.2%	Score 544.5	DB 4	Length 172
	Best Local Similarity	62.4%	Pred. No. 1.3e-42		
	Matches 108	Conservative 22	Mismatches 34	Indels 9	Gaps 4
Qy	1	KLPETLSLTCVAVGGSPS--GYVSWTRPPGKLEWIGEINHSGSTNYNPSLKSERVVIS	58		
Db	7	KPGQLSLTCTVSGGS--SSGGHYSWTRPPGKLEWIGYIYYIGNTVYNPSLKSERVVIS	66		
Qy	59	VDTSKNQFSLKLSVTAADTAVVYCARGAAEYYYYYGMVWGQGTTVTVSSGGSASAPTL	118		
Db	67	VDTSKNQFSLKLSVTAADTAVVYCARDSGD---YYGIDVWGQGTTVTVSSASTKGPSV	122		
Qy	119	FPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNNSDISSTRGPPSVLR	171		
Db	123	FPLAPCSRSSTSE--STAALGVKDYFPEPVTVM--NSGALTSGVHYPFPAVLO	172		

RESULT 4
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY


```
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-12

Query Match          46.7%; Score 496.5; DB 3; Length 476;
Best Local Similarity 52.7%; Pred. No. 1.4e-37;
Matches 108; Conservative 27; Mismatches 53; Indels 17; Gaps 8;

Qy 1 KLPETLSLTCVAVGSGFS-GYYWSWIROPCKGLEWIGE1-NHSGSTYNPNSLKSRVTIS 58
Db 32 KPSETLSLTCVAVGSGISGGYGWGIROPCKGLEWIGSFYSSSGNTYNNPNSLKSOVTIS 91

Qy 59 VDTSKNQPSLKLSSVTAADTAAYVCARGAAEYIIYVGM-----DVMGQGTTVTVSSGS 112
Db 92 TDTSKNQPSLKLNSMTAADTAAYVCVR---DRLFSVVGWVNNWPFVDMGPGVLTVTSSAS 148

Qy 113 ASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNSDISSTRGPPSVLR- 171
Db 149 TKGPSVFLPAPSSKSTSG-GTAALGCLVKDYPPEPTVTSW--NSGALTSGVHTTTPAVLQS 205

Qy 172 GGYAATSVQLLPKSDVMQGTDEHV 196
Db 206 SGLYSLSSVTVTPSSSL--GTQTYI 228

RESULT 14
US-09-526-098-12
; Sequence 12, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-526-098-12

Query Match          46.7%; Score 496.5; DB 4; Length 476;
Best Local Similarity 52.7%; Pred. No. 1.4e-37;
Matches 108; Conservative 27; Mismatches 53; Indels 17; Gaps 8;

Qy 1 KLPETLSLTCVAVGSGFS-GYYWSWIROPCKGLEWIGE1-NHSGSTYNPNSLKSRVTIS 58
Db 32 KPSETLSLTCVAVGSGISGGYGWGIROPCKGLEWIGSFYSSSGNTYNNPNSLKSOVTIS 91

Qy 59 VDTSKNQPSLKLSSVTAADTAAYVCARGAAEYIIYVGM-----DVMGQGTTVTVSSGS 112
Db 92 TDTSKNQPSLKLNSMTAADTAAYVCVR---DRLFSVVGWVNNWPFVDMGPGVLTVTSSAS 148

Qy 113 ASAPTLFPLVSCNSPDSSTSSVAVGCLAQDFLPDXITFXWKYKNSDISSTRGPPSVLR- 171
Db 149 TKGPSVFLPAPSSKSTSG-GTAALGCLVKDYPPEPTVTSW--NSGALTSGVHTTTPAVLQS 205

Qy 172 GGYAATSVQLLPKSDVMQGTDEHV 196
Db 206 SGLYSLSSVTVTPSSSL--GTQTYI 228

RESULT 15
US-09-383-916-12
; Sequence 12, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESS: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 476 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-383-916-12

Query Match          46.7%; Score 496.5; DB 4; Length 476;
Best Local Similarity 52.7%; Pred. No. 1.4e-37;
Matches 108; Conservative 27; Mismatches 53; Indels 17; Gaps 8;

Qy 1 KLPETLSLTCVAVGSGFS-GYYWSWIROPCKGLEWIGE1-NHSGSTYNPNSLKSRVTIS 58
Db 32 KPSETLSLTCVAVGSGISGGYGWGIROPCKGLEWIGSFYSSSGNTYNNPNSLKSOVTIS 91
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Qy	59	VDTSKNQFSLKLSSVTAADTAVYYCARGAAEYYYYYYGM-----DWMGQGTTVTVSSGS	112
Db	92	TDTSKNQFSLKLNSWTAADTAVYYCVR---DRLFSVVGMVYNNWFDYWGPGVLTVSSAS	148
Qy	113	ASAPTLPLVSCENSPSDTSSVAVGCLAQDPLDPXITFXWKYKNNSDISSTRGPPSVLR-	171
Db	149	TKGPSVFPFLAPSSKSTSG-GTAALGCLVKDYFPEPTVSW--NSGALTSGVHTTTPAVLQS	205
Qy	172	GGKYAATSQVLLPSKDVMOGTDEHV	196
Db	206	SGLYSLSSVTVTPSSSL--GIQTYI	228

Search completed: March 8, 2005, 05:54:09
Job time : 23.2112 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.1629 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-32

Perfect score: 752

Sequence: 1 MPVTPGPASISCRSSQSLL.....TASVVCLLSNFPYREAKVQW 143

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	557	74.1	219	2	Pc4203
2	555	73.8	197	2	S29593
3	548	72.9	219	2	S52028
4	543	72.2	135	2	S40342
5	538	71.5	121	2	S40371
6	537	71.4	219	2	S46112
7	535	71.1	217	2	S42772
8	531	70.6	219	2	S38865
9	525	69.8	215	2	J02042
10	525	69.8	225	2	J10029
11	520	69.1	136	2	S40357
12	519	69.0	125	2	S40356
13	509	67.7	215	2	J02044
14	508	67.6	124	2	S03876
15	506	67.3	132	2	S26882
16	502	66.8	112	2	S58207
17	502	66.8	117	1	K2HUGM
18	498	66.2	112	2	S58206
19	494	65.7	215	2	A23746
20	483.5	64.3	126	2	S40339
21	481	64.0	215	2	J02043
22	480.5	63.9	240	2	S06084
23	479.5	63.8	216	2	J02041
24	464	61.7	131	2	S40372
25	463.5	61.6	214	2	S68212
26	463	61.6	113	1	K2HUTW
27	460	61.2	123	2	S40319
28	459.5	61.1	220	2	A31790
29	457.5	60.8	210	2	A36169

30 454 60.4 96 2 S40320 Ig kappa chain - h
31 451 60.0 87 2 S34091 Ig kappa chain v r
32 451 60.0 100 2 S24681 Ig kappa chain - h
33 450.5 59.9 112 1 K2HUML Ig kappa chain v-I
34 450.5 59.9 218 2 JC5810 monoclonal antibod
35 447.5 59.5 218 2 S68241 Ig kappa chain v r
36 447 59.4 114 2 S40375 Ig kappa chain - h
37 432.5 57.5 130 2 S40321 Ig kappa chain - h
38 426 56.6 112 2 F27887 Ig kappa chain v r
39 425 56.5 116 2 S27008 Ig kappa chain v r
40 423.5 56.3 115 1 K2HUCM Ig kappa chain v-I
41 421 56.0 131 2 D29380 Ig kappa chain pre
42 419.5 55.8 140 2 S22658 Ig kappa chain pre
43 415 55.2 112 2 S53750 antibody Fab Jel 1
44 414 55.1 112 2 C26317 Ig kappa chain v r
45 414 55.1 112 2 G26317 Ig kappa chain v r

ALIGNMENTS

RESULT 1

Pc4203

Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000

C:Accession: PC4203

R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.

Gene 173, 257-259, 1996

A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mor

A:Reference number: PC4202; MUID:97082978; PMID:8964510

A:Accession: PC4203

A:Molecule type: mRNA

A:Residues: 1-219 <KWA>

A:Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226

C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:1-112/Domain: V region #status predicted <VRG>

F:113-219/Domain: C region #status predicted <CRG>

Query Match

Best Local Similarity 74.1%; Score 557; DB 2; Length 219;

Matches 103; Conservative 18; Mismatches 22; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLLHSNGYLDWYLRKPGQSPQLLIYLGSNRAGVDPDRFSGS 60

Db 11 LPVSLGDAQASISCRSSQSIHTNGTNTVLEWYLRKPGQSPKLLIYKVSNRFGVDPDRFSGS 70

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVIFPPSDQL 120

Db 71 GSGTDFTLKISRVEADLVGVYCFQSGHVPRTFGGTGKLEIKRADAAPTVSIFPPSSQL 130

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143

Db 131 TSGGASVVCFLNFPKDIINVKW 153

RESULT 2

S29593

Ig kappa chain (WM65) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000

C:Accession: S29593

R:Seymour, R.

submitted to the EMBL Data Library, February 1991

A:Reference number: S29593

A:Accession: S29593

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-197 <SEV>

A:Cross-references: EMBL:X57856; NID:g52588; PIDN:CAA40991.1; PID:g52589

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

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Query Match          73.8%; Score 555; DB 2; Length 197;
Best Local Similarity 74.1%; Pred. No. 1.1e-40;
Matches 106; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 26 IPVTPGESASISCRSSQSLHSGNDTYLWFLQRPQGSPQLLIYRMNLAGVDPDRFSGS 85
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPRLFPGTKVDIKRTVAAPSFIFFPSDEQL 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 86 GSGTSFTLRISRVEAEDVGIFCMQHLIEPYTFGGTKLEIKRADAAPTVSIFPPSDEQL 145
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 146 TSGGASVVCFLNNFYPKDINKW 168
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
S52028
Ig kappa chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S52028
R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994
A;Description: Coordinate expression of antibody subunit genes yields high levels of fun
A;Reference number: S52028
A;Accession: S52028
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <VAN>
A;Cross-references: EMBL:L35138; NID:9522336; PIDN:AAA67525.1; PID:g522337
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match          72.9%; Score 548; DB 2; Length 219;
Best Local Similarity 71.3%; Pred. No. 5e-40;
Matches 102; Conservative 17; Mismatches 24; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 11 LPVSLGDAQASISCRSSQSIHSGNTYLEWYLQKPGQSPKLLIYKNSRFGVDPDRFSGS 70
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPRLFPGTKVDIKRTVAAPSFIFFPSDEQL 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 71 GSGTDFTLKISRVEAEDVGIVCYFCQSGSHVPPTFGGTNLEIKRADAAPTVSIFPPSDEQL 130
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 131 TSGGASVVCFLNNFYPKDINKW 153
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
S40342
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S40342
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40342
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-135 <KLE>
A;Cross-references: UNIPROT:Q8NEK0; EMBL:X72452; NID:g441372; PID:g441373
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;29-108/Domain: immunoglobulin homology <IMM>
```

```
Query Match          72.2%; Score 543; DB 2; Length 135;
Best Local Similarity 93.6%; Pred. No. 8.2e-40;
Matches 102; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 24 LPVTPGEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFSGS 83
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPRLFPGTKVDIKRTVAAPS 109
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 GSGTDFTLKISRVEAEDVGIVCYCMQALQTPRTFGQGTKEIKRTVAAPS 132
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
S40371
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40371
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40371
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-121 <KLE>
A;Cross-references: EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PID:g441431
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;13-92/Domain: immunoglobulin homology <IMM>

Query Match          71.5%; Score 538; DB 2; Length 121;
Best Local Similarity 88.6%; Pred. No. 2e-39;
Matches 101; Conservative 6; Mismatches 7; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 8 LPVTPGEPASISCRSSQSLIYSTGYNDWYLQKPGKSPQLLIYLGSKRAGVDPDRFSGS 67
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPRLFPGTKVDIKRTVAAPSFIFF 114
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 GSGTDFTLKISRVEAEDVGIVYCMQGIQTPTTFGQGTKEIKRTVAAPSFIFF 121
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
S16112
Ig kappa chain V region (G2a) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S16112
R;Vaesen, M.; Froesch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.;
Biochem. Hoppe-Seyler 372, 451-453, 1991
A;Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(
A;Reference number: S16112; MUID:92000313; PMID:1910583
A;Accession: S16112
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-219 <BIT>
A;Cross-references: UNIPROT:Q8VC16; UNIPROT:Q99M37
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match          71.4%; Score 537; DB 2; Length 219;
Best Local Similarity 70.6%; Pred. No. 4.4e-39;
Matches 101; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHSGNYLDWYLQKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 11 LPVSLGDAQASISCRSSQSLHSGNTYLEWYLQKPGQSPKLLIYKNSRFGVDPDRFSGS 70
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 GSGTDFTLKISRVEAEDVGIIYCMQSLQIPRLFPGTKVDIKRTVAAPSFIFFPSDEQL 120
```

Db 71 GSGTDFTLKISRVAEDLVVFCQGTHTVPTFGGTRLEIKRADAAFTVSIFPPSSSEQL 130
Qy 121 KSGTASVVCLLSNFPYKQVQW 143
Db 131 TSGGASVVCFLNNFPYKDVNKW 153

RESULT 7

Ig kappa chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R:Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:G414143; PIDN:CAA53226.1; PID:G414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 71.1%; Score 535; DB 2; Length 217;
Best Local Similarity 69.9%; Pred. No. 6.5e-39;
Matches 100; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSNRASGVDPDRFSGS 60
Db 9 LPVSLGDAQASISCRSSQSLVHTNGNTYLHWYLOKPGSQPKVLIYKVRFSGVDPDRFSGS 68
Qy 61 GSGTDFTLKISRVAEDLVVFCQGTHTVPTFGGTRLEIKRADAAFTVSIFPPSSSEQL 120
Db 69 GSGTDFTLKISRVAEDLVVFCQGTHTVPTFGGTRLEIKRADAAFTVSIFPPSSSEQL 128

Qy 121 KSGTASVVCLLSNFPYKQVQW 143
Db 129 TSGGASVVCFLNNFPYKDVNKW 151

RESULT 8

Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C:Accession: S38865
R:Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38865
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-219 <KIP>
A:Cross-references: EMBL:Z27396; NID:G416538; PIDN:CAA81787.1; PID:G416539
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.6%; Score 531; DB 2; Length 219;
Best Local Similarity 69.9%; Pred. No. 1.5e-38;
Matches 100; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSNRASGVDPDRFSGS 60
Db 11 LSVSLGDAQASISCRSSQSLVHTNGNTYLHWYLOKPGSLPKVLIYKVRFSGVDPDRFSGS 70
Qy 61 GSGTDFTLKISRVAEDLVVFCQGTHTVPTFGGTRLEIKRADAAFTVSIFPPSSSEQL 120
Db 71 GSGTDFTLKISRVAEDLVVFCQGTHTVPTFGGTRLEIKRADAAFTVSIFPPSSSEQL 130

Qy 121 KSGTASVVCLLSNFPYKQVQW 143
Db 131 TSGGASVVCFLNNFPYKDVNKW 153

RESULT 9

Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 69.8%; Score 525; DB 2; Length 215;
Best Local Similarity 72.0%; Pred. No. 4.7e-38;
Matches 103; Conservative 16; Mismatches 20; Indels 4; Gaps 2;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSNRASGVDPDRFSGS 60
Db 11 LSVSLGDAQASISCRSSQSLVHTNGNTYLHWYLOKPGSQPKVLIYKVRFSGVDPDRFSGS 66
Qy 61 GSGTDFTLKISRVAEDLVVFCQGTHTVPTFGGTRLEIKRADAAFTVSIFPPSSSEQL 120
Db 67 GSGTDFTLKISRVAEDLVVFCQGTHTVPTFGGTRLEIKRADAAFTVSIFPPSSSEQL 126

Qy 121 KSGTASVVCLLSNFPYKQVQW 143
Db 127 KSGTASVVCLLSNFPYKQVQW 149

RESULT 10

Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaynard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphory
A:Reference number: JL0029; MUID:88171315; PMID:3127529
A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Cross-references: UNIPROT:Q99M37
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because c
ect except for four positions shown above
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-225/Product: Ig kappa chain #status predicted <ILC>
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <JIR>
F:120-225/Domain: C region #status predicted <COR>

Query Match 69.8%; Score 525; DB 2; Length 225;
Best Local Similarity 68.5%; Pred. No. 4.9e-38;
Matches 98; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGSQPLLIIYLGNSNRASGVDPDRFSGS 60
Db 17 LPVSLGDAQASISCRSSQSLVHTNGNTYLHWYLOKPGSQPKVLIYKVRFSGVDPDRFSGS 76
Qy 61 GSGTDFTLKISRVAEDLVVFCQGTHTVPTFGGTRLEIKRADAAFTVSIFPPSSSEQL 120

Db 77 GSGTDFSLKISRVEAEDLVGVYCFQSSHRVTFGGTKLEIKRADAAPTVSIFFPTSEQL 136
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
Db 137 TSGGASVVCFLNFPKDVNKW 159

RESULT 11

Ig kappa chain V-J-C region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C;Accession: S40357
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40357
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-136 <KLE>
A;Cross-references: UNIPROT:Q8NEK0; EMBL:X72467
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;36-115/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 520; DB 2; Length 136;
Best Local Similarity 92.5%; Pred. No. 7.8e-38;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 60
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 90
Qy 61 GSGTDFTLKISRVEAEDVGVIYCMQSLQIPRLFGPGTKVDIKRTVA 106
Db 91 GSGTDFTLKISRVEAEDVGVIYCMQALQTPWTFGGTKVEIKRTVA 136

RESULT 12

Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40356
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40356
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72466; NID:9441400; PIDN:CAA51134.1; PID:9441401
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;25-104/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 519; DB 2; Length 125;
Best Local Similarity 92.5%; Pred. No. 8.7e-38;
Matches 98; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 60
Db 20 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 79
Qy 61 GSGTDFTLKISRVEAEDVGVIYCMQSLQIPRLFGPGTKVDIKRTVA 106
Db 80 GSGTDFTLKISRVEAEDVGVIYCMQVLIPLTFGGTKVEIKRTVA 125

RESULT 13

JE0244
Ig kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yanagata, F.; Yamaki, H.; Te
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 67.7%; Score 509; DB 2; Length 215;
Best Local Similarity 70.8%; Pred. No. 1.1e-36;
Matches 102; Conservative 16; Mismatches 20; Indels 6; Gaps 3;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 60
Db 11 LSVSPGERATLSCRASQS-VHSN----LAWYQQKPGQAPRLIIYRASTRATGIPARFSGS 65
Qy 61 GSGTDFTLKISRVEAEDVGVIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIPPSDEQ 119
Db 66 GSGTDFTLTISSLSQSEDFALYYCQVNTWPLTFGGTKVEIKRTVAAPSVFIPPSDEQ 125
Qy 120 LKSGTASVVCLLSNFYPREAKVQW 143
Db 126 LKSGTASVVCLLNFPYPREAKVQW 149

RESULT 14

Ig kappa chain V-II region (Inc) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C;Accession: S03876
R;Ferri, G.; Stoppini, M.; Iadarola, P.; Bellotti, V.; Merlini, G.
Biochim. Biophys. Acta 995, 103-108, 1989
A;Title: Structural characterization of kappa II Inc, a new amyloid immunoglobulin.
A;Reference number: S03876; MUID:89194238; PMID:2495028
A;Accession: S03876
A;Molecule type: protein
A;Residues: 1-124 <PER>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 67.6%; Score 508; DB 2; Length 124;
Best Local Similarity 84.2%; Pred. No. 7.6e-37;
Matches 96; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGOSPQLLIYLGNSRAGVDPDRFSGS 60
Db 11 LPVTPGEPASISCRSSQSLHNSGNDYLDWYLOKPGOSPQVIYILGNSRAGVDPDTFSGS 70
Qy 61 GSGTDFTLKISRVEAEDVGVIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFF 114
Db 71 GSGTDFTLTISSVGAEDVGVIYCMQALQTPWTFGGTKVGIKRTVAAPSVFIFF 124

RESULT 15

S26882
Ig kappa chain V region (V607) - human
C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
C;Accession: S26882
R;Weichhold, G.M.; Klobbeck, H.G.; Ohnheiser, R.; Combriato, G.; Zachau, H.G.
Nature 347, 90-92, 1990
A;Title: Megabase inversions in the human genome as physiological events.
A;Reference number: S26882; MUID:90370099; PMID:2118596
A;Accession: S26882

Job time : 10.2129 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 53.4033 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-32
Perfect score: 752
Sequence: 1 MPVTPGPASISCRSSQSL.....TASVVCLLSNFYPREAKVQW 143

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	708	94.1	239	2	Q8NEKO	Q8neko homo sapien
2	681.5	90.6	240	2	Q6PIH6	Q6pih6 homo sapien
3	613	81.5	239	2	Q6P491	Q6p491 homo sapien
4	597	79.4	239	2	Q8TCD0	Q8tcd0 homo sapien
5	538	71.5	219	2	Q65ZC0	Q65zc0 mus musculus
6	525.5	69.9	236	2	Q6PII8	Q6pil8 homo sapien
7	523	69.5	235	2	Q6GMV9	Q6gmv9 homo sapien
8	523	69.5	235	2	Q6PJF2	Q6pjf2 homo sapien
9	507.5	67.5	236	2	Q6P588	Q6p588 homo sapien
10	502	66.8	117	1	KV2E_HUMAN	P06309 homo sapien
11	495.5	65.9	236	2	Q6GMX8	Q6gmx8 homo sapien
12	488.5	65.0	236	2	Q6GMX0	Q6gmx0 homo sapien
13	486.5	64.7	234	2	Q7Z473	Q7z473 homo sapien
14	486.5	64.7	236	2	Q6GMW1	Q6gmw1 homo sapien
15	486	64.6	235	2	Q6GMW0	Q6gmw0 homo sapien
16	477.5	63.5	236	2	Q6PIH7	Q6pih7 homo sapien
17	464.5	61.8	236	2	Q7Z3Y4	Q7z3y4 homo sapien
18	463.5	61.6	236	2	Q6PIT5	Q6pit5 homo sapien
19	463	61.6	113	1	KV2D_HUMAN	P01617 homo sapien
20	456.5	60.7	236	2	Q6GMX9	Q6gmx9 homo sapien
21	450.5	59.9	112	1	KV2C_HUMAN	P01616 homo sapien
22	444.5	59.1	236	2	Q6PIH4	Q6pih4 homo sapien
23	439.5	58.4	238	2	Q66JS7	Q66js7 mus musculus
24	437	58.1	243	2	Q6NTU5	Q6ntu5 xenopus lae
25	423.5	56.3	115	1	KV2A_HUMAN	P01614 homo sapien
26	416.5	55.4	236	2	Q7TS98	Q7ts98 mus musculus
27	416.5	55.4	237	2	Q7SZ36	Q7sz36 xenopus lae
28	415.5	55.3	241	2	Q63ZX4	Q63zx4 mus musculus
29	411	54.7	113	1	KV2B_HUMAN	P01615 homo sapien
30	407	54.1	113	1	KV2E_MOUSE	P03976 mus musculus
31	405	53.9	113	1	KV2G_MOUSE	P01631 mus musculus

32	403	53.6	248	2	Q65ZQ7	Q65zq7 mus sp. b3(
33	400	53.2	113	1	KV2F_MOUSE	P01630 mus musculus
34	395	52.5	133	1	KV2F_HUMAN	P06310 homo sapien
35	381	50.7	112	2	Q6LEM8	Q6lem8 mus musculus
36	378.5	50.3	114	2	Q9UL80	Q9ul80 homo sapien
37	377	50.1	112	1	KV2D_MOUSE	P01629 mus musculus
38	374	49.7	113	1	KV2C_MOUSE	P01628 mus musculus
39	368	48.9	112	1	KV2A_MOUSE	P01626 mus musculus
40	352.5	46.9	108	1	KV1_CANFA	P01618 canis faml1
41	351	46.7	120	1	KV2B_MOUSE	P01627 mus musculus
42	343.5	45.7	134	1	KV4C_HUMAN	P06314 homo sapien
43	341.5	45.4	114	1	KV4A_HUMAN	P01625 homo sapien
44	337.5	44.9	236	2	Q8NEJ1	Q8nej1 homo sapien
45	337	44.8	133	1	KV4B_HUMAN	P06313 homo sapien

ALIGNMENTS

RESULT 1

ID	Q8NEKO	PRELIMINARY;	PRT;	239 AA.
AC	Q8NEKO;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DE	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RA	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC030814; AAH30814.1; -			
DR	PIR; S23638; S23638.			
DR	PIR; S34091; S34091.			
DR	PIR; S40342; S40342.			
DR	PIR; S40357; S40357.			
DR	HSSP; P01834; 117Z.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig cl.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig v.			
DR	Pfam; PF07654; C1-set; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;

Query Match 94.1%; Score 708; DB 2; Length 239;
Best Local Similarity 93.0%; Pred. No. 2.8e-64;
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPVTPGPASISCRSSQSLHSNGYNYLDWYLQKPGSPQLLIYLGNSRASGVDPDFSGS 60
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
31 LPVTPGPASISCRSSQSLHSNGYNYLDWYLQKPGSPQLLIYLGNSRASGVDPDFSGS 90
QY 61 GSGTDFTLKISRVEADVGIYCMQSLQI-PRLFPGPTKVDIKRTVAAPSVFIIPPSPDEQL 120
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
91 GSGTDFTLKISRVEADVGIYCMQSLQI-PRLFPGPTKVDIKRTVAAPSVFIIPPSPDEQL 150
QY 121 KSGTASVVCLLSNFYPREAKVQW 143
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 KSGTASVVCLLSNFYPREAKVQW 173

RESULT 2
Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; -.
DR HSSP; P01837; 1KB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
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DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

Query Match 90.6%; Score 681.5; DB 2; Length 240;
Best Local Similarity 90.3%; Pred. No. 1.5e-61;
Matches 130; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 1 MPVTPGPASISCRSSQSLHSNGYNYLDWYLQKPGSPQLLIYLGNSRASGVDPDFSGS 60
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
31 LSVTPGPASISCRSSQSLHSNGYNYLDWYLQKPGSPQLLIYLGNSRASGVDPDFSGS 90
QY 61 GSGTDFTLKISRVEADVGIYCMQSLQI-PRLFPGPTKVDIKRTVAAPSVFIIPPSPDEQ 119
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
91 GSGTDFTLKISRVEADVGIYCMQSLQI-PRLFPGPTKVDIKRTVAAPSVFIIPPSPDEQ 150
QY 120 KSGTASVVCLLSNFYPREAKVQW 143
DB : |||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 KSGTASVVCLLSNFYPREAKVQW 174

RESULT 3
Q6P491 PRELIMINARY; PRT; 239 AA.
AC Q6P491;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Tohiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063599; AAH63599.1; -.
DR HSSP; P01837; 1KC0.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGV; 1.
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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26245 MW; CD71313DDFFD358B3 CRC64;

Query Match 81.5%; Score 613; DB 2; Length 239;
Best Local Similarity 82.4%; Pred. No. 1.6e-54;
Matches 117; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

QY 2 PVTGEPASISCRSSQSLHNSGNYLDWYKQKQSPQLLIYLGSNRASGVDPDRFSGS 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 32 PVTLGQPASISCRSSQSLHNSGNYLDWYKQKQSPQLLIYKISNRASGVDPDRFSGS 91
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 62 SGTDFTLKISRVEADVGIYCMQSLQIPRLFGPQTKVDIKRTVAAPSVFIFPPSDQLK 121
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 92 AGTDFTLKISRVEADVGIYCMQSLQIPRLFGPQTKVDIKRTVAAPSVFIFPPSDQLK 151
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 122 SGTASVWCLLSNFYPREKQVQW 143
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 152 SGTASVWCLLSNFYPREKQVQW 173
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
Q8TCD0 PRELIMINARY; PRT; 239 AA.
ID Q8TCD0
AC Q8TCD0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=24388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marzina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalski A., Smailus D.E., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC022362; AAH22362.1; -.
DR PIR; S22658; S22658.
DR PIR; S34095; S34095.
DR PIR; S40324; S40324.
DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSRF; P01834; I172.
InterPro; IPR007110; Ig-like.
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DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 79.4%; Score 597; DB 2; Length 239;
Best Local Similarity 78.3%; Pred. No. 6.9e-53;
Matches 112; Conservative 16; Mismatches 15; Indels 0; Gaps 0;

QY 1 MPVTGEPASISCRSSQSLHNSGNYLDWYKQKQSPQLLIYLGSNRASGVDPDRFSGS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 31 LPVTLGQPASISCRSTQSLVSDGNTYLNWFQRPQSPRLIYKVSNRDSGVDPDRFSGS 90
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPQTKVDIKRTVAAPSVFIFPPSDQL 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 91 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPQTKVDIKRTVAAPSVFIFPPSDQL 150
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

QY 121 KSGTASVWCLLSNFYPREKQVQW 143
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 151 KSGTASVWCLLSNFYPREKQVQW 173
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 5
Q65ZC0 PRELIMINARY; PRT; 219 AA.
ID Q65ZC0
AC Q65ZC0;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Kappa light chain C region (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/c; TISSUE=Spleen;
RX MEDLINE=96319505; PubMed=8768802;
RA Kipp B., Schlaak M., Becker W.M.;
RT "Cloning and expression of a recombinant mouse Fab-fragment
RT recognizing a defined linear epitope of Chironomus thummi major
RT allergen Chi t.1.";
RL Int. Arch. Allergy Immunol. 110:348-353(1996).
DR EMBL; Z37499; CAA85724.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
FT NON TER 1 219
FT NON TER 219 219
SQ SEQUENCE 219 AA; 23944 MW; 7E1B82A14EAF8445 CRC64;

Query Match 71.5%; Score 538; DB 2; Length 219;
Best Local Similarity 70.6%; Pred. No. 6.9e-47;
Matches 101; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

QY 1 MPVTGEPASISCRSSQSLHNSGNYLDWYKQKQSPQLLIYLGSNRASGVDPDRFSGS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 11 LSVSLGDAQSISCRSSQSLVHTNGTYLHWYKQKGLSPKLLIYVSNRDSGVDPDRFSGS 70
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
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Db 31 LSLSPGERAALSCRASQSV-----NSKYLAWYQKPGQAPRLMYAASIRATGIPDRFSGS 86
Qy 61 GSGTDFTLKISRVAEDVGIIYCMQSLQIPLRFGGTKVDIKRTVAAPSVFIFFPSDBQL 120
Db 87 GSGTDFTLTISRLSESDPALYFCQQYGTGTSPLTFGGGKVEIKRTVAAPSVFIFFPSDBQL 146
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 147 KSGTASVVCLLNNFPYPREAKVQW 169

RESULT 8
Q6PJF2 PRELIMINARY; PRT; 235 AA.
AC Q6PJF2
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 69.5%; Score 523; DB 2; Length 235;
Best Local Similarity 69.9%; Pred. No. 2.6e-45;
Matches 100; Conservative 18; Mismatches 21; Indels 4; Gaps 1;

Qy 1 MPVTGEPASISCRSSQSLHNSNGYNLDWYLPKQPSQLLIYIGSNRSGVDPDRFSGS 60
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Db 31 LSLSPGERATLSCRASQIVSSA-----YLAWTQQKPGQAPRLMFGSSSRATGIPDRFSGS 86
Qy 61 GSGTDFTLKISRVAEDVGIIYCMQSLQIPLRFGGTKVDIKRTVAAPSVFIFFPSDBQL 120
Db 87 GSGTDFTLTISRLSPEDFAVYVCOQYGSQGTGFGTKVDIKRTVAAPSVFIFFPSDBQL 146
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 147 KSGTASVVCLLNNFPYPREAKVQW 169

RESULT 9
Q6P5S8 PRELIMINARY; PRT; 236 AA.
AC Q6P5S8
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; IKCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BBE4FF5F27 CRC64;

Query Match 67.5%; Score 507.5; DB 2; Length 236;
Best Local Similarity 69.5%; Pred. No. 1e-43;
Matches 98; Conservative 20; Mismatches 18; Indels 5; Gaps 2;
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Qy 4 TPGPASISCRSSOSLLHSNGYNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFSGS 63
Db 34 SPGERATLSKRSASQTVFSS-----HLAWYQQRPGQAPRLIIYAGSSRATGIPDRFSGSG 89
Qy 64 TDFTLKISRVEADVGIYCMQSLQIPRL-FPGTKVDIKRTVAAPSVFPPPSDEQLKS 122
Db 90 TDFTLITITRIEPEDFAVYFCQOYGTSPSLTFGGGTRVEIKRTVAAPSVFPPPSDEQLKS 149
Qy 123 GTASVCLLSNFYFREAKVOW 143
Db 150 GTASVCLLNNFYFREAKVOW 170

RESULT 10
KV2E HUMAN
ID _KV2E_HUMAN STANDARD; PRT; 117 AA.
AC P06309;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region GM607 precursor (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84191506; PubMed=6325927;
RA Klobbeck H.G., Solomon A., Zachau H.G.;
RT "Contribution of human V kappa II germ-line genes to light-chain
RT diversity.";
RL Nature 309:73-76(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z00009; -; NOT_ANNOTATED_CDS.
DR PIR; A01889; K2HUGM.
DR HSP; Q99M37; 1191.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT NON_TER 1
FT SIGNAL <1 4
FT CHAIN 5 117 Ig kappa chain V-II region GM607.
FT DOMAIN 5 27 Framework-1.
FT DOMAIN 28 43 Complementarity-determining-1.
FT DOMAIN 44 58 Framework-2.
FT DOMAIN 59 65 Complementarity-determining-2.
FT DOMAIN 66 97 Framework-3.
FT DOMAIN 98 106 Complementarity-determining-3.
FT DOMAIN 107 116 Framework-4.
FT DISULFID 27 97 By similarity.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12664 MW; 92C57DC719B558B1 CRC64;

Query Match 66.8%; Score 502; DB 1; Length 117;
Best Local Similarity 91.3%; Pred. No. 1.6e-43;
Matches 94; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSOSLLHSNGYNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFSGS 60
:
```

```
Db 15 LPVTPGPASISCRSSOSLLHSNGYNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFSGS 74
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRL-FPGTKVDIKR 103
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 75 GSGTDFTLKISRVEADVGIYCMQSLQIPRL-FPGTKVDIKR 117
|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
Q6GMX8
ID Q6GMX8 PRELIMINARY; PRT; 236 AA.
AC Q6GMX8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=42398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RX Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073764; AAH73764.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-Bet; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 65.9%; Score 495.5; DB 2; Length 236;
Best Local Similarity 68.8%; Pred. No. 1.7e-42;
Matches 95; Conservative 15; Mismatches 23; Indels 5; Gaps 1;

Qy 6 GEPASISCRSSOSLLHSNGYNYLDWYLOKPGQSPQLLIYLGNSRASGVDPDRFSGSGT 65
Db 38 GDRVTITCRASQGI-----SSWLAWYQQRPGQAPRLIIYAGSSRATGIPDRFSGSGT 92
Qy 66 FTLKISRVEADVGIYCMQSLQIPRL-FPGTKVDIKRTVAAPSVFPPPSDEQLKS 125
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Db 91 FTLISCLQSDFAFYCYQQYYTPWTFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTA 150
QY 126 SVVCLLSNFFYPREAKVQW 143
Db 151 SVVCLLNNFFYPREAKVQW 168

RESULT 14
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC Q6GMW1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG1; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFEGA087AFAC437 CRC64;

Query Match 64.7%; Score 486.5; DB 2; Length 236;
Best Local Similarity 68.1%; Pred. No. 1.4e-41;
Matches 94; Conservative 14; Mismatches 25; Indels 5; Gaps 1;

QY 6 GEPASISCRSSQSLHNSGNYLDWYLOKPGSQSPQLLIYLGNSRASGVDFRFGSGGSTD 65
Db 38 GDRVITITRASQGI-----SNDLGWYQOKKAPKPLLIYAASSLQSGVPRFSGSGGSTD 92
QY 66 FTLKISRVEADVGIYYCMQSLQIPFLRFGPGTKVDIKRTVAAPSVFIFPPSDEQLKSGTA 125
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Db 93 FTLTISLQSDFAFYCYQQYYTPWTFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTA 152
QY 126 SVVCLLSNFFYPREAKVQW 143
Db 153 SVVCLLNNFFYPREAKVQW 170

RESULT 15
Q6GMW0 PRELIMINARY; PRT; 235 AA.
AC Q6GMW0
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match 64.6%; Score 486; DB 2; Length 235;
Best Local Similarity 65.3%; Pred. No. 1.6e-41;
Matches 94; Conservative 23; Mismatches 21; Indels 6; Gaps 2;

QY 1 MPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGSQSPQLLIYLGNSRASGVDFRFGSGS 60
Db 31 LSVSPGGRATLSCRASQSI-----SNNLAWYQORPGQAPRLLIYGAASSRVGTGPRFSGS 85
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[illegible]

Search completed: March 8, 2005, 06:35:52
Job time : 54.4033 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 66.2987 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-32

Perfect score: 752

Sequence: 1 MPVTPGPASISCRSSQSL.....TASVVCLLSNFYPREAKVQW 143

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752	100.0	143	2 AAY34313	Aay34313 Igm antib
2	720	95.7	239	3 AAY82616	Aay82616 Human PTH
3	719	95.6	238	8 ADL93653	Adl93653 Human CD4
4	713	94.8	239	3 AAY82618	Aay82618 Human PTH
5	712	94.7	238	8 ADL93649	Adl93649 Human CD4
6	712	94.7	238	8 ADL93654	Adl93654 Human CD4
7	712	94.7	239	7 ADE28461	Ade28461 Human ant
8	710	94.4	239	7 ADE28405	Ade28405 Human ant
9	709	94.3	238	8 ADL93650	Adl93650 Human CD4
10	709	94.3	239	7 ADE28465	Ade28465 Human ant
11	707	94.0	239	7 ADE28521	Ade28521 Human ant
12	707	94.0	239	7 ADE28397	Ade28397 Human ant
13	707	94.0	239	7 ADE28477	Ade28477 Human ant
14	705	93.8	239	3 AAY82611	Aay82611 Human PTH
15	704	93.6	219	8 ADL16817	Adl16817 Human bre
16	702	93.4	239	3 AAY82615	Aay82615 Human PTH
17	702	93.4	239	7 ADE28421	Ade28421 Human ant
18	701.5	93.3	237	8 ADL93657	Adl93657 Human CD4
19	697	92.7	239	3 AAY82617	Aay82617 Human PTH
20	695	92.4	148	2 AAY34309	Aay34309 Igm antib
21	695	92.4	219	7 ADJ32150	Adj32150 Human int
22	694	92.3	238	8 ADL93652	Adl93652 Human CD4
23	693.5	92.2	237	8 ADL93658	Adl93658 Human CD4
24	693.5	92.2	237	8 ADL93651	Adl93651 Human CD4
25	693	92.2	239	6 ABR48456	AbR48456 Human Cal

ALIGNMENTS

RESULT 1

AAY34313

ID AAY34313 standard; protein; 143 AA.

AC AAY34313;

DT 19-NOV-1999 (first entry)

DE Igm antibody CEM 13.12 kappa chain sequence.

KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

FN WO9945031-A2.

PD 10-SEP-1999.

PF 03-MAR-1999; 99WO-US004583.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

PA (ABGE-) ABGENIX INC.

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;

DR WPI; 1999-540816/45.

DR N-PSDB; AAZ20414.

PT New monoclonal antibody, used for treating e.g. graft versus host

PT disease, cancers, autoimmune diseases and inflammatory diseases.

PS Claim 61; Fig 28; 245pp; English.

XX This sequence represents the kappa chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAb) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 MAb
CC by the Igm MAb ABX-CBL, providing that the antibody is not CBL1. The MAb
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 143 AA;

Query Match 100.0%; Score 752; DB 2; Length 143;
Best Local Similarity 100.0%; Pred. No. 6.1e-55;
Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLLHSNGYNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60
Db 1 MPVTPGEPASISCRSSQSLLHSNGYNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 120
Db 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 120

Qy 121 KSGTASVVCLLSNFYPREKQVQW 143
Db 121 KSGTASVVCLLSNFYPREKQVQW 143

RESULT 2
AAy82616
ID AAy82616 standard; protein; 239 AA.
XX
AC AAy82616;
XX
XX 02-AUG-2000 (first entry)
XX
DE Human PTHrP monoclonal antibody clone 2G4-12-20 protein SEQ ID NO:16.
XX
KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;
KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;
KW antiarthritic; cytostatic; antiinflammatory.
XX
OS Homo sapiens.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 5 /label= Val, Ala, Asp, Gly
FT FT Misc-difference 13 /note= "possibly Leu"
FT FT Misc-difference 25 /label= Ile, Thr, Asn, Ser
FT FT Misc-difference 27 /label= Phe, Ser, Tyr, Cys
FT FT Misc-difference 216 /note= "possible Val"
XX
XX JP2000080100-A.
FN
XX
XX 21-MAR-2000.
PD
XX
XX 12-OCT-1998; 98JP-00304793.
PF
XX
XX 17-JUN-1998; 98JP-00188196.
PR
XX 26-JUN-1998; 98JP-00196729.
PR
XX
XX (NIBS) JAPAN TOBACCO INC.
PA
XX
XX WPI; 2000-286723/25.
DR
XX N-PSDB; AAA13926.
DR
XX
PT A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain.
XX
XX Claim 31; Page 48-49; 88pp; Japanese.
PS
XX The present invention describes a human monoclonal antibody to

CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC its fragments, following the stimulation of PTHrP has the following
CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC the release of calcium from bone; or (c) inhibits elevation of blood
CC calcium content. The monoclonal antibody can be used in the treatment of
CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC antiinflammatory activities. The present sequence represents a human
CC PTHrP monoclonal antibody clone protein sequence from the present
XX invention
XX
SQ Sequence 239 AA;

Query Match 95.7%; Score 720; DB 3; Length 239;
Best Local Similarity 94.4%; Pred. No. 4.8e-52;
Matches 135; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLLHSNGYNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60
Db 31 LPVTPGEPASISCRSSQSLLHSNGYNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 120
Db 91 GSGTDFTLKISRVEADVGIYCMQALQTPFTFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 150

Qy 121 KSGTASVVCLLSNFYPREKQVQW 143
Db 151 KSGTASVVCLLSNFYPREKQVQW 173

RESULT 3
ADL93653
ID ADL93653 standard; protein; 238 AA.
XX
AC ADL93653;
XX
XX 17-JUN-2004 (first entry)
DT
XX
DE Human CD44-binding antibody light chain BE-D7-kappa-light SEQ ID NO:148.
XX
KW Human; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;
KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX
OS Homo sapiens.
XX
XX WO2004024750-A2.
FN
XX
XX 25-MAR-2004.
PD
XX
XX 15-SEP-2003; 2003WO-US029318.
PF
XX
XX 13-SEP-2002; 2002US-0410758P.
PR
XX 09-MAY-2003; 2003US-0469123P.
PR
XX
XX (DYAX-) DYAX CORP.
PA
XX
XX Rondon IJ, Edge A, Baribault Kent R;
PI
XX
XX WPI; 2004-270003/25.
DR
XX
PT New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX
XX Disclosure; SEQ ID NO 148; 128pp; English.

PF 15-SEP-2003; 2003WO-US029318.

```
XX 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX (DYAX-) DYAX CORP.
XX Rondon IJ, Edge A, Baribault Kent R;
XX WPI; 2004-270003/25.
XX New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX Disclosure; SEQ ID NO 144; 128pp; English.
XX The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CDR3 of the LC variable domain sequence. A protein of the invention has
CC cytotatic, antiinflammatory, immunosuppressive, antiarthritic,
CC antirheumatic, dermatological, vasotrophic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a human CD44-binding
CC antibody light chain.
XX Sequence 238 AA;
Query Match 94.7%; Score 712; DB 8; Length 238;
Best Local Similarity 93.7%; Pred. No. 2.2e-51;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGOSPQLLYLGSNRASGVDPDRSGS 60
DB 30 LPVTPGPASISCRSSQSLHSGNYLDWYLOKPGOSPQLLYLGSNRASGVDPDRSGS 89
QY 61 GSGTDFTLKISRVEADVGIYQCWSLIQIRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
DB 90 GSGTDFTLKISRVEADVGIYQCWSLIQIRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 149
QY 121 KSGTASVVCLLSNFYPREAKVQW 143
DB 150 KSGTASVVCLLSNFYPREAKVQW 172
RESULT 6
ADL93654
ID ADL93654 standard; protein; 238 AA.
XX ADL93654;
XX 17-JUN-2004 (first entry)
XX Human CD44-binding antibody light chain BE-H10-kappa-light SEQ ID NO:149.
XX human; CD44; light chain immunoglobulin variable domain;
XX heavy chain immunoglobulin variable domain; immunoglobulin; cytotatic;
XX antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
XX dermatological; vasotrophic; neuroprotective; antibody therapy;
XX inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
XX graft versus host response; multiple sclerosis; neoplastic disorder;
XX cancer; antibody.
XX Homo sapiens.
XX OS
XX WO2004024750-A2.
XX 25-MAR-2004.
XX PD
```

```
XX 15-SEP-2003; 2003WO-US029318.
XX 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX (DYAX-) DYAX CORP.
XX Rondon IJ, Edge A, Baribault Kent R;
XX WPI; 2004-270003/25.
XX New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX Disclosure; SEQ ID NO 149; 128pp; English.
XX The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CDR3 of the LC variable domain sequence. A protein of the invention has
CC cytotatic, antiinflammatory, immunosuppressive, antiarthritic,
CC antirheumatic, dermatological, vasotrophic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a human CD44-binding
CC antibody light chain.
XX Sequence 238 AA;
Query Match 94.7%; Score 712; DB 8; Length 238;
Best Local Similarity 93.7%; Pred. No. 2.2e-51;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 1 MPVTPGPASISCRSSQSLHSGNYLDWYLOKPGOSPQLLYLGSNRASGVDPDRSGS 60
DB 30 LPVTPGPASISCRSSQSLHSGNYLDWYLOKPGOSPQLLYLGSNRASGVDPDRSGS 89
QY 61 GSGTDFTLKISRVEADVGIYQCWSLIQIRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
DB 90 GSGTDFTLKISRVEADVGIYQCWSLIQIRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 149
QY 121 KSGTASVVCLLSNFYPREAKVQW 143
DB 150 KSGTASVVCLLSNFYPREAKVQW 172
RESULT 7
ADE28461
ID ADE28461 standard; protein; 239 AA.
XX ADE28461;
XX 29-JAN-2004 (first entry)
XX Human anti-CD40 antibody 23-28-1 variable region light chain protein.
XX anti-CD40 monoclonal antibody; CD40; cytotatic; virucide; antibacterial;
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
XX bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
XX human; variable region light chain; 23-28-1.
XX Homo sapiens.
XX OS
XX WO2003040170-A2.
XX 15-MAY-2003.
XX PD
```


XX 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX (DYAX-) DYAX CORP.
XX Rondon IJ, Edge A, Baribault Kent R;
PI WPI; 2004-270003/25.
XX
XX New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX
XX Disclosure; SEQ ID NO 145; 128pp; English.
XX
XX The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CD83 of the LC variable domain sequence. A protein of the invention has
CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a human CD44-binding
CC antibody light chain.
XX
SQ Sequence 238 AA;
Query Match 94.3%; Score 709; DB 8; Length 238;
Best Local Similarity 93.0%; Pred. No. 4e-51;
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRAGVDPDRFSGS 60
Db 30 LPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRAGVDPDRFSGS 89
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLPGGPKVDIKRTVAAPSVFIPPSPDEQL 120
Db 90 GSGTDFTLKISRVEADVGIYCMQALQTPWTFGQTKLEIKRTVAAPSVFIPPSPDEQL 149
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
Db 150 KSGTASVVCLLNNFYPREAKVQW 172
RESULT 10
ADE28465
ID ADE28465 standard; protein; 239 AA.
XX ADE28465;
XX 29-JAN-2004 (first entry)
XX Human anti-CD40 antibody 23-28-1 full length light chain protein.
DE anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; light chain; 23-28-1.
XX Homo sapiens.
OS WO2003040170-A2.
XX 15-MAY-2003.
XX 08-NOV-2002; 2002WO-US036107.
XX 08-NOV-2002; 2002WO-US036107.
XX

PR 09-NOV-2001; 2001US-0348980P.
XX (PFIZ) PFIZER PROD INC.
PA (ABGE-) ABGENIX INC.
XX Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
PI WPI; 2003-441521/41.
XX N-PSDB; ADE28464.
XX
XX New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX
XX Claim 7; SEQ ID NO 72; 177pp; English.
XX
XX The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody full length light chain protein of the invention.
XX
SQ Sequence 239 AA;
Query Match 94.3%; Score 709; DB 7; Length 239;
Best Local Similarity 93.0%; Pred. No. 4e-51;
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRAGVDPDRFSGS 60
Db 31 LPVTPGPASISCRSSQSLHNSGNYLDWYLOKPGSPQLLIYLGSNRAGVDPDRFSGS 90
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLPGGPKVDIKRTVAAPSVFIPPSPDEQL 120
Db 91 GSGTDFTLKISRVEADVGIYCMQALQTPRTFGQTKVEIKRTVAAPSVFIPPSPDEQL 150
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
Db 151 KSGTASVVCLLNNFYPREAKVQW 173
RESULT 11
ADE28521
ID ADE28521 standard; protein; 239 AA.
XX ADE28521;
XX 29-JAN-2004 (first entry)
XX Human anti-CD40 antibody 23-29-1L-R174K mutant VL light chain protein.
DE anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
XX immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; light chain; mutein; mutant; 23-29-1L-R174K.
XX Homo sapiens.
OS WO2003040170-A2.
XX 15-MAY-2003.
XX 08-NOV-2002; 2002WO-US036107.
XX 09-NOV-2001; 2001US-0348980P.
XX


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XX WPI; 2003-441521/41.
DR N-PSDB; ADE28476.
XX
PT New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX
XX Claim 1; SEQ ID NO 84; 177pp; English.
XX
XX The invention relates to a novel chimeric or human monoclonal antibody or
XX its antigen-binding portion that specifically binds to and activates
XX human CD40. The anti-CD40 antibody of the invention demonstrates
XX cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
XX activities and may be useful for treating a hyperproliferative disorder
XX such as cancer, viral and bacterial infection or genetic, primary or
XX combined immunodeficiency conditions including neutropenia or HIV
XX infection. The anti-CD40 antibodies may also be useful for detecting CD40
XX in a biological sample in vitro or in vivo, as well as during gene
XX therapy procedures. The current sequence is that of the human anti-CD40
XX antibody variable region light chain protein of the invention.
XX
SQ Sequence 239 AA;
Query Match 94.0%; Score 707; DB 7; Length 239;
Best Local Similarity 93.7%; Pred. No. 5.9e-51;
Matches 134; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 90
Qy 61 GSGTDFTLKISRVEADVGIYQCWSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 91 GSGTDFTLKISRVEADVGIYQCWSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 150
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 151 KSGTASVVCLLSNFPYPREAKVQW 173
RESULT 14
AAV82611
ID AAV82611 standard; protein; 239 AA.
XX
AC AAV82611;
XX
XX 02-AUG-2000 (first entry)
XX
XX Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.
XX
XX Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
XX hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
XX fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;
XX systemic inflammatory response syndrome; SIRS; hypophosphataemia;
XX antiarthritic; cytostatic; antiinflammatory.
XX
XX Homo sapiens.
XX
XX JP2000080100-A.
XX
XX 21-MAR-2000.
XX
XX 12-OCT-1998; 98JP-00304793.
XX
XX 17-JUN-1998; 98JP-00188196.
XX
XX 26-JUN-1998; 98JP-00196729.
XX
XX (NISR ) JAPAN TOBACCO INC.
XX
XX WPI; 2000-286723/25.
DR N-PSDB; AAA13921.

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XX A human monoclonal antibody to parathyroid hormone related protein. -
PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
PT including metastasis, and pain.
XX
XX Claim 31; Page 34-35; 88pp; Japanese.
XX
XX The present invention describes a human monoclonal antibody to
XX parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX its fragments, following the stimulation of PTHrP has the following
XX properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX the release of calcium from bone; or (c) inhibits elevation of blood
XX calcium content. The monoclonal antibody can be used in the treatment of
XX hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX diseases and gingiva, sepsis, systemic inflammatory response syndrome
XX (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX antiinflammatory activities. The present sequence represents a human
XX PTHrP monoclonal antibody clone protein sequence from the present
XX invention
XX
SQ Sequence 239 AA;
Query Match 93.8%; Score 705; DB 3; Length 239;
Best Local Similarity 92.3%; Pred. No. 8.6e-51;
Matches 132; Conservative 7; Mismatches 4; Indels 0; Gaps 0;
Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 60
Db 31 LPVTPGEPATISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGSRASGVDPDRFSGS 90
Qy 61 GSGTDFTLKISRVEADVGIYQCWSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 120
Db 91 GSGTDFTLKISRVEADVGIYQCWSLQIPRLFGPGTKVDIKRTVAAPSVFIPPPSDEQL 150
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 151 KSGTASVVCLLSNFPYPREAKVQW 173
RESULT 15
ADR16817
ID ADR16817 standard; protein; 219 AA.
XX
XX ADR16817;
XX
XX 21-OCT-2004 (first entry)
XX
XX Human breast cancer-specific antibody Fab fragment, Fab14.6.19 #2.
XX
XX Breast cancer; diagnosis; therapy; human; antibody; Fab 14.6.19.
XX
XX Homo sapiens.
XX
XX US2004151724-A1.
XX
XX 05-AUG-2004.
XX
XX 30-OCT-2003; 2003US-00698041.
XX
XX 31-OCT-2002; 2002US-0423052P.
XX
XX (CORO/) CORONELLA-WOOD J.
XX
XX Coronella-Wood J;
XX
XX WPI; 2004-570704/55.
DR N-PSDB; ADR16814.
XX
XX New isolated polynucleotides encoding breast cancer-specific antibody Fab
XX fragments 14.6.19 and 14.6.20, useful as clinical reagents for diagnosing
XX or treating breast cancer.

```

PS Claim 8; SEQ ID NO 4; 36pp; English.
XX
CC The invention provides a breast cancer-specific antibody fragment
CC polynucleotide and its corresponding polypeptide. The invention is useful
CC as clinical reagents for the diagnosis and therapy of breast cancer. The
CC present sequence is human breast cancer-specific antibody Fab fragment,
CC Fab14.6.19.
XX
SQ Sequence 219 AA;
Query Match 93.6%; Score 704; DB 8; Length 219;
Best Local Similarity 91.6%; Pred. No. 9.5e-51;
Matches 131; Conservative 7; Mismatches 5; Indels 0; Gaps 0;
Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRAGVDPDRFSGS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
11 LPVTPGEPASISCRSSQSLHNSGNYLDWYLQKPGQSPQLLIYLGSNRAGVDPDRFSGS 70
Qy 61 GSGTDPTLKISRVEADGVYCYCMQSLQIPRLPGPGTKVDIKRTVAAPSVFIAPPDDEQL 120
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
71 GSGTDPTLKISRVEADGVYCYCMQSLQIPRTFGQGTREIKRTVAAPSVFIAPPDDEQL 130
Qy 121 KSGTASVVCLLSNFPYPAKQVQW 143
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
131 KSGTASVVCLLSNFPYPAKQVQW 153

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Job time : 66.2987 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 75.8864 Seconds
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620.051 Million cell updates/sec

Title: US-09-784-950-32

Perfect score: 752

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Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubaa/US06_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	719	95.6	238	16	US-10-663-244-148 Sequence 148, App
2	712	94.7	238	16	US-10-663-244-144 Sequence 144, App
3	712	94.7	238	16	US-10-663-244-149 Sequence 149, App
4	710	94.4	239	15	US-10-292-088-40 Sequence 40, Appl
5	710	94.4	239	15	US-10-292-088-16 Sequence 16, Appl
6	709	94.3	238	16	US-10-663-244-145 Sequence 145, App
7	709	94.3	239	15	US-10-292-088-56 Sequence 56, Appl
8	707	94.0	239	15	US-10-292-088-8 Sequence 8, Appl
9	707	94.0	239	15	US-10-292-088-80 Sequence 80, Appl
10	707	94.0	239	15	US-10-292-088-102 Sequence 102, App
11	704	93.6	219	16	US-10-698-041-4 Sequence 4, Appl
12	702	93.4	239	15	US-10-292-088-32 Sequence 32, Appl
13	701.5	93.3	237	16	US-10-663-244-152 Sequence 152, App

14	695	92.4	219	10	US-09-972-656-104 Sequence 104, App
15	694	92.3	238	16	US-10-663-244-147 Sequence 147, App
16	693.5	92.2	237	16	US-10-663-244-146 Sequence 146, App
17	693.5	92.2	237	16	US-10-663-244-153 Sequence 153, App
18	693	92.2	239	10	US-09-992-600A-8 Sequence 8, Appl
19	693	92.2	239	10	US-09-924-340-8 Sequence 8, Appl
20	693	92.2	239	10	US-09-992-095B-8 Sequence 8, Appl
21	693	92.2	239	10	US-09-999-570-8 Sequence 8, Appl
22	693	92.2	239	14	US-10-000-489-8 Sequence 8, Appl
23	693	92.2	239	14	US-10-000-986-8 Sequence 8, Appl
24	693	92.2	239	14	US-10-154-678-8 Sequence 8, Appl
25	693	92.2	239	17	US-10-838-854-8 Sequence 8, Appl
26	692	92.0	239	15	US-10-292-088-64 Sequence 64, Appl
27	684	91.0	239	15	US-10-108-260A-4028 Sequence 4028, App
28	682.5	90.8	220	9	US-09-822-698A-24 Sequence 24, Appl
29	677	90.0	247	15	US-10-466-164-69 Sequence 69, Appl
30	666	88.6	219	10	US-09-972-656-94 Sequence 94, Appl
31	666	88.6	219	10	US-09-972-656-106 Sequence 106, App
32	658	87.5	133	14	US-10-153-382-39 Sequence 39, Appl
33	656	87.2	239	15	US-10-404-724-12 Sequence 12, Appl
34	656	87.2	239	17	US-10-816-276-8 Sequence 8, Appl
35	654	87.0	239	15	US-10-404-724-49 Sequence 49, Appl
36	654	87.0	239	17	US-10-816-276-45 Sequence 45, Appl
37	646	85.9	239	15	US-10-404-724-41 Sequence 41, Appl
38	646	85.9	239	15	US-10-404-724-45 Sequence 45, Appl
39	646	85.9	239	17	US-10-816-276-37 Sequence 37, Appl
40	646	85.9	239	17	US-10-816-276-41 Sequence 41, Appl
41	644	85.6	239	15	US-10-404-724-43 Sequence 43, Appl
42	644	85.6	239	15	US-10-404-724-47 Sequence 47, Appl
43	644	85.6	239	17	US-10-816-276-39 Sequence 39, Appl
44	644	85.6	239	17	US-10-816-276-43 Sequence 43, Appl
45	636	84.6	239	15	US-10-404-724-10 Sequence 10, Appl

ALIGNMENTS

RESULT 1

US-10-663-244-148
; Sequence 148, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-148

Query Match 95.6%; Score 719; DB 16; Length 238;

Best Local Similarity 94.4%; Pred. No. 1.7e-49;

Matches 135; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSNGYLDWYLPKPGSPQLLYLGSNRASGVDPDFSGS 60

Db 30 LPVTPGPASISCRSSQSLHSNGYLDWYLPKPGSPQLLYLGSNRASGVDPDFSGS 89

Qy 61 GSGTDFTLKTSRVEAEVGIYCMQSLQIPALFPGTKVDIKRTVAAPSVFIIPDSDEL 120

```
Db 90 GSGTDFTLKISRVEAEDGVVYCMQALQTPTFGGTVKEIKRTVAAPSFIIPPSPDEQL 149
Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 150 KSGTASVVCLLSNFPYREAKVQW 172

RESULT 2
US-10-663-244-144
; Sequence 144, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-144

Query Match 94.7%; Score 712; DB 16; Length 238;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIIPPSPDEQL 120
Db 90 GSGTDFTLKISRVEAEDGVVYCMQALQTPTFGGTVKEIKRTVAAPSFIIPPSPDEQL 149

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 150 KSGTASVVCLLSNFPYREAKVQW 172

RESULT 3
US-10-663-244-144
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-144

Query Match 94.7%; Score 712; DB 16; Length 238;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIIPPSPDEQL 120
Db 90 GSGTDFTLKISRVEAEDGVVYCMQALQTPTFGGTVKEIKRTVAAPSFIIPPSPDEQL 149

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 150 KSGTASVVCLLSNFPYREAKVQW 172

RESULT 3
US-10-663-244-149
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; PRIOR FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149

Query Match 94.7%; Score 712; DB 15; Length 239;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIIPPSPDEQL 120
Db 91 GSGTDFTLKISRVEAEDGVVYCMQVLTPTFTFGPGTKVDIKRTVAAPSFIIPPSPDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 5
US-10-292-088-16
; Sequence 16, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
```

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; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149

Query Match 94.7%; Score 712; DB 16; Length 238;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIIPPSPDEQL 120
Db 90 GSGTDFTLKISRVEAEDGVVYCMQALQTPTFGGTVKEIKRTVAAPSFIIPPSPDEQL 149

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 150 KSGTASVVCLLSNFPYREAKVQW 172

RESULT 4
US-10-292-088-40
; Sequence 40, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-40

Query Match 94.7%; Score 712; DB 15; Length 239;
Best Local Similarity 93.7%; Pred. No. 6.1e-49;
Matches 134; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 60
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPOLLIYLGNSRAGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEAEDGVVYCMQSLQIPRLFGPGTKVDIKRTVAAPSFIIPPSPDEQL 120
Db 91 GSGTDFTLKISRVEAEDGVVYCMQVLTPTFTFGPGTKVDIKRTVAAPSFIIPPSPDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 5
US-10-292-088-16
; Sequence 16, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
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; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-16

Query Match          94.4%; Score 710; DB 15; Length 239;
Best Local Similarity 93.0%; Pred. No. 8.8e-49;
Matches 133; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGGTVKVDIKRTVAAPSVFIFFPSDEQL 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 91 GSGTDFTLKISRVEADVGVVYCMQALQTPRTFGGTVKVEIKRTVAAPSVFIFFPSDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 151 KSGTASVVCLLNFPYREAKVQW 173

RESULT 6
US-10-663-244-145
; Sequence 145, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; FILE OF INVENTION: CD44 LIGANDS
; TITLE OF INVENTION: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-145

Query Match          94.3%; Score 709; DB 16; Length 238;
Best Local Similarity 93.0%; Pred. No. 1.1e-48;
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGGTVKVDIKRTVAAPSVFIFFPSDEQL 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 90 GSGTDFTLKISRVEADVGVVYCMQALQTPRTFGGTVKLEIKRTVAAPSVFIFFPSDEQL 149

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 150 KSGTASVVCLLNFPYREAKVQW 172

RESULT 7
```

```
US-10-292-088-56
; Sequence 56, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-56

Query Match          94.3%; Score 709; DB 15; Length 239;
Best Local Similarity 93.0%; Pred. No. 1.1e-48;
Matches 133; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGGTVKVDIKRTVAAPSVFIFFPSDEQL 120
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 91 GSGTDFTLKISRVEADVGVVYCMQALQTPRTFGGTVKVEIKRTVAAPSVFIFFPSDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 151 KSGTASVVCLLNFPYREAKVQW 173

RESULT 8
US-10-292-088-8
; Sequence 8, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-8

Query Match          94.0%; Score 707; DB 15; Length 239;
Best Local Similarity 92.3%; Pred. No. 1.5e-48;
Matches 132; Conservative 8; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 60
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLRKPGQSPQLLIYLGSRASGVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGGTVKVDIKRTVAAPSVFIFFPSDEQL 120
```



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; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-32

Query Match      93.4%; Score 702; DB 15; Length 239;
Best Local Similarity 91.6%; Pred. No. 3.8e-48;
Matches 131; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLPKPGSPQLLIYLGNSRAGVDPDRFSGS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
31 LPVTPGEPASISCRSSQSLHNSGNYLDWYLPKPGSPQLLIYLGNSRAGVDPDRFSGS 90
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQL 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
91 GSGTDFTLKISRVEADVGIYCMQALQTPYSFGQGTKEIKRTVAAPSVFIFFPSDEQL 150
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
151 KSGTASVVCLLSNFPYPREAKVQW 173

RESULT 13
US-10-663-244-152
; Sequence 152, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Kent, Rachel Baribault
; APPLICANT: Edge, Albert
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-152

Query Match      93.3%; Score 701.5; DB 16; Length 237;
Best Local Similarity 93.0%; Pred. No. 4.1e-48;
Matches 133; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLPKPGSPQLLIYLGNSRAGVDPDRFSGS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLPKPGSPQLLIYLGNSRAGVDPDRFSGS 89
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQL 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
90 GSGTDFTLKISRVEADVGIYCMQALQTP-TFGGTKVEIKRTVAAPSVFIFFPSDEQL 148
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
149 KSGTASVVCLLSNFPYPREAKVQW 171

RESULT 14
US-09-972-656-104
; Sequence 104, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
```

```
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 104
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-104

Query Match      92.4%; Score 695; DB 10; Length 219;
Best Local Similarity 90.2%; Pred. No. 1.3e-47;
Matches 129; Conservative 9; Mismatches 5; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLPKPGSPQLLIYLGNSRAGVDPDRFSGS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
11 LPVTPGEPASISCRSSQSLHNSGNYLDWYLPKPGSPQLLIYLGNSRAGVDPDRFSGS 70
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQL 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
71 GSGTDFTLKISRVEADVGIYCMQALQTPRTFGQGTKEIKRTVAAPSVFIFFPSDEQL 130
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
131 KSGTASVVCLLSNFPYPREAKVQW 153

RESULT 15
US-10-663-244-147
; Sequence 147, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Kent, Rachel Baribault
; APPLICANT: Edge, Albert
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 147
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-147

Query Match      92.3%; Score 694; DB 16; Length 238;
Best Local Similarity 91.6%; Pred. No. 1.6e-47;
Matches 131; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLPKPGSPQLLIYLGNSRAGVDPDRFSGS 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
30 LPVTPGEPASISCRSSQSLHNSGNYLDWYLPKPGSPQLLIYLGNSRAGVDPDRFSGS 89
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQL 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
90 GSGTDFTLKISRVEADVGIYCMQALQTP-TFGGTKVEIKRTVAAPSVFIFFPSDEQL 149
Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
150 KSGTASVVCLLSNFPYPREAKVQW 172

Search completed: March 8, 2005, 07:05:54
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Job time : 76.8864 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 15.7238 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-32

Perfect score: 752

Sequence: 1 MPVTPGPASISCRSSQSLL.....TASVVCLLSNFPYREAKVQW 143

Scoring table:

BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	693	92.2	239	4	US-10-000-489-8
2	658	87.5	133	4	US-09-472-087-26
3	658	87.5	133	4	US-09-472-087-116
4	618	82.2	238	4	US-09-698-705-10
5	612	81.4	239	3	US-08-487-550-6
6	612	81.4	239	4	US-09-526-098-6
7	612	81.4	239	4	US-09-383-916-6
8	587	78.1	218	4	US-09-698-705-12
9	586	77.9	242	1	US-08-398-613A-56
10	586	77.9	242	1	US-08-398-612A-56
11	586	77.9	242	1	US-08-398-611A-56
12	586	77.9	242	2	US-08-491-334A-56
13	586	77.9	242	3	US-09-027-449-42
14	586	77.9	242	3	US-08-804-444A-42
15	586	77.9	242	3	US-09-026-985-42
16	586	77.9	242	4	US-09-121-952A-42
17	586	77.9	242	4	US-09-234-340A-42
18	561	74.6	139	4	US-09-472-087-25
19	561	74.6	139	4	US-09-472-087-114
20	555	73.8	222	4	US-09-479-614-26
21	555	73.8	242	4	US-09-479-614-20
22	552	73.4	238	3	US-09-192-545-4
23	547	72.7	173	5	PCT-US91-02942-3
24	547	72.7	173	5	PCT-US91-02946-3
25	544.5	72.4	146	4	US-09-472-087-21
26	544.5	72.4	146	4	US-09-472-087-93
27	542.5	72.1	240	4	US-09-301-593-36

28	542	72.1	216	4	US-09-254-180C-132	Sequence 132, Appl
29	542	72.1	216	4	US-09-254-180C-183	Sequence 183, Appl
30	540	71.8	216	4	US-09-254-180C-182	Sequence 182, Appl
31	538.5	71.6	226	4	US-09-456-090A-38	Sequence 38, Appl
32	538.5	71.6	226	4	US-09-453-234-38	Sequence 38, Appl
33	538	71.5	239	4	US-09-627-896B-22	Sequence 22, Appl
34	537	71.4	219	3	US-09-027-449-72	Sequence 72, Appl
35	537	71.4	219	3	US-09-026-985-72	Sequence 72, Appl
36	537	71.4	219	4	US-09-121-952A-72	Sequence 72, Appl
37	537	71.4	219	4	US-09-234-340A-72	Sequence 72, Appl
38	537	71.4	242	3	US-09-027-449-51	Sequence 51, Appl
39	537	71.4	242	3	US-09-027-449-56	Sequence 56, Appl
40	537	71.4	242	3	US-09-027-449-62	Sequence 62, Appl
41	537	71.4	242	3	US-08-804-444A-51	Sequence 51, Appl
42	537	71.4	242	3	US-08-804-444A-56	Sequence 56, Appl
43	537	71.4	242	3	US-09-026-985-51	Sequence 51, Appl
44	537	71.4	242	3	US-09-026-985-56	Sequence 56, Appl
45	537	71.4	242	3	US-09-026-985-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-10-000-489-8
; Sequence 8, Application US/10000489
; Patent No. 6794363
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.USE.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: 1..20
US-10-000-489-8

Query Match 92.2%; Score 693; DB 4; Length 239;
Best Local Similarity 91.6%; Pred. No. 4.1e-60;
Matches 131; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

Qy	1	MPVTPGPASISCRSSQSLLHSNGYNYLDWYLPKQSGSPQLLIYLGSRASGVDPDRFSGS	60
Db	31	LPVTPGPASISCRSSQSLLHVGQSNYLDWYLPKQSGSPQLLIYLGSRASGVDPDRFSGS	90
Qy	61	GSQTDFTLKISRVAEDVGIYCMOSLOIPRLFGPGTKVDIKRTVAAPSVFIPEPSDQL	120
Db	91	GSQTDFTLKISRVAEDVGVYCMQALQTPFTFGPTRVDIKRTVAAPSVFIPEPSDQL	150
Qy	121	KSGTASVVCLLSNFPYREAKVQW	143
Db	151	KSGTASVVCLLSNFPYREAKVQW	173

RESULT 2
US-09-472-087-26
; Sequence 26, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-26

Query Match 87.5%; Score 658; DB 4; Length 133;
Best Local Similarity 93.2%; Pred. No. 5.4e-57;
Matches 124; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PGEPAISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGSGT 64
Db 1 PGEPAISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGSGT 60

Qy 65 DFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQLKSGT 124
Db 61 DFTLKISRVEADVGIYCMQALQTLPTLFTGGTKVEIKRTVAAPSVFIFFPSDEQLKSGT 120

Qy 125 ASVVCLLSNFYPR 137
Db 121 ASVVCLLSNFYPR 133

RESULT 3
US-09-472-087-116
; Sequence 116, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILEEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 116
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-116

Query Match 87.5%; Score 658; DB 4; Length 133;
Best Local Similarity 93.2%; Pred. No. 5.4e-57;
Matches 124; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PGEPAISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGSGT 64
Db 1 PGEPAISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGSGT 60

Qy 65 DFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQLKSGT 124
Db 61 DFTLKISRVEADVGIYCMQALQTLPTLFTGGTKVEIKRTVAAPSVFIFFPSDEQLKSGT 120

Qy 125 ASVVCLLSNFYPR 137
Db 121 ASVVCLLSNFYPR 133

RESULT 4
US-09-698-705-10
; Sequence 10, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koeppe, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P1777R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 10
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-10

Query Match 82.2%; Score 618; DB 4; Length 238;
Best Local Similarity 81.8%; Pred. No. 8.9e-53;
Matches 117; Conservative 12; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
Db 30 VPVTPGESVSIKSSKSLHNSGNTLYLWFLQPGSPQLLIYRMSNLASGVDPDRFSGS 89

Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQL 120
Db 90 GSGTAPTLRISRVEADVGIYCMQALQTLPTLFTGGTKVEIKRTVAAPSVFIFFPSDEQL 149

Qy 121 KSGTASVVCLLSNFYPR 143
Db 150 KSGTASVVCLLSNFYPR 172

RESULT 5
US-08-487-550-6
; Sequence 6, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF."
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA

;; COUNTRY: USA
;; ZIP: 22314
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA: US/08/487,550
;; APPLICATION NUMBER: US/08/487,550
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-131
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6620
;; TELEFAX: 703-836-2021
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 239 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-487-550-6

Query Match 81.4%; Score 612; DB 3; Length 239;
Best Local Similarity 81.1%; Pred. No. 3.4e-52;
Matches 116; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
Db 31 LPITGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVSNRDGSVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVAEDVGIIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQL 120
Db 91 GAGTDFTLKISAVEAEDVGIVFCGGTPTPTFGGKTVEIKRTVAAPSVFIFFPSDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 6
US-09-526-098-6
; Sequence 6, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:

;; APPLICATION NUMBER: US 08/487,550
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-131
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6620
;; TELEFAX: 703-836-2021
;; INFORMATION FOR SEQ ID NO: 6:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 239 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-09-526-098-6

Query Match 81.4%; Score 612; DB 4; Length 239;
Best Local Similarity 81.1%; Pred. No. 3.4e-52;
Matches 116; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MPVTGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
Db 31 LPITGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVSNRDGSVDPDRFSGS 90

Qy 61 GSGTDFTLKISRVAEDVGIIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPSDEQL 120
Db 91 GAGTDFTLKISAVEAEDVGIVFCGGTPTPTFGGKTVEIKRTVAAPSVFIFFPSDEQL 150

Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 151 KSGTASVVCLLSNFPYREAKVQW 173

RESULT 7
US-09-383-916-6
; Sequence 6, Application US/09383916
; Patent No. 670654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:

LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-6

Query Match 81.4%; Score 612; DB 4; Length 239;
Best Local Similarity 81.1%; Pred. No. 3.4e-52;
Matches 116; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYVLPKPGQSPQLLIYLGNSRAGVDPDFSGS 60
Db 31 LPITPGEPASISCRSSQSLHSGNDTFLSWYQKPGQPRLLIYKVNRSQGVDPDFSGS 90
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIRLFGPGTKVDIKRTVAAPSFIIPPSPDEQL 120
Db 91 GAGTDFTLKISRVEADVGVFCQGTPTPTFGGKVEIKRTVAAPSFIIPPSPDEQL 150
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
Db 151 KSGTASVVCLLNNFYPREAKVQW 173

RESULT 8

US-09-698-705-12
Sequence 12, Application US/09698705
Patent No. 6824780

GENERAL INFORMATION:
APPLICANT: Devaux, B.

APPLICANT: Keller, G.

APPLICANT: Koepfen, H.

APPLICANT: Laaky, L.

TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
FILE REFERENCE: P1777R1

CURRENT APPLICATION NUMBER: US/09/698,705
CURRENT FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/162,558

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60/182,872

PRIOR FILING DATE: 2000-02-16

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 12

LENGTH: 218

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: sequence is chimeric mouse/human

US-09-698-705-12

Query Match 78.1%; Score 587; DB 4; Length 218;
Best Local Similarity 78.3%; Pred. No. 8.6e-50;
Matches 112; Conservative 13; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYVLPKPGQSPQLLIYLGNSRAGVDPDFSGS 60
Db 11 LSVTIGQPASISCRSSQSLHSDCKTYLWLLQRPQSPKRLIYLVSTLDSGVDPDFSGS 70
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIRLFGPGTKVDIKRTVAAPSFIIPPSPDEQL 120
Db 71 GSGTDFTLKISRVEADVGVYVYQGTHTFPTFGGKVEIKRTVAAPSFIIPPSPDEQL 130
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
Db 131 KSGTASVVCLLNNFYPREAKVQW 153

RESULT 9

US-08-398-613A-56

Sequence 56, Application US/08398613A

Patent No. 5677426

GENERAL INFORMATION:

APPLICANT: Fong, Sherman

APPLICANT: Hebert, Caroline Alice

APPLICANT: Kim, Kyung Jin
APPLICANT: Leong, Steven R.
TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory I
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/398,613A

FILING DATE: 01-MAR-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/205864

FILING DATE: 03-MAR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Fitts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 874P1-3

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1489

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 242 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-398-613A-56

Query Match 77.9%; Score 586; DB 1; Length 242;

Best Local Similarity 76.9%; Pred. No. 1.2e-49;

Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGPASISCRSSQSLHSGNYLDWYVLPKPGQSPQLLIYLGNSRAGVDPDFSGS 60
Db 34 LPVSLGQASISCRSSQSLVHGIGNTYLVWYLPKPGQSPKLLIYKVNRSQGVDPDFSGS 93
Qy 61 GSGTDFTLKISRVEADVGIYCMQSLQIRLFGPGTKVDIKRTVAAPSFIIPPSPDEQL 120
Db 94 GSGTDFTLRISRVEADLGLYFCQSSTHVLPTFGAGTKLKLKRAVAAPTFFIPPSSEQL 153
Qy 121 KSGTASVVCLLSNFYPREAKVQW 143
Db 154 KSGTASVVCLLNNFYPREAKVQW 176

RESULT 10

US-08-398-612A-56

Sequence 56, Application US/08398612A

Patent No. 5686070

GENERAL INFORMATION:

APPLICANT: Doershuk, Claire M.

APPLICANT: Fong, Sherman

APPLICANT: Hebert, Caroline Alice

APPLICANT: Kim, Kyung Jin

APPLICANT: Leong, Steven R.

TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for

TITLE OF INVENTION: Treatment of Inflammatory Disorders

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California


```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/398,611A
FILING DATE: 01-Mar-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205864
FILING DATE: 03-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Love, Richard B.
REGISTRATION NUMBER: 34,659
REFERENCE/DOCKET NUMBER: P0874P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-5530
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 242 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-398-611A-56

Query Match          77.9%; Score 586; DB 1; Length 242;
Best Local Similarity 76.3%; Pred. No. 1.2e-49;
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0

QY      1  MPVTPGEPASISCRSSQLHSGNYLDWYLOKPGOSPOLLIIYLGSNRAGSVDPDRFSGS 60
DB      34  LPVSLGDAQISCRSSQSLVHGNTYLLHWYLOKPGOSPKLLIYKVNRRSGVDPDRFSGS 93
QY      61  GSGTDTFLKISRVEADVGIIYQMSQLQIPRLFGPGTKVDIKRTVAAPSVFIFFPPSDQL 120
DB      94  GSGTDTFLAIRVEADGLGYFCQSQTHVPLTFGAGTKLELKRAVAAPTVFIFPPSSSQL 153
QY      121 KSGTASVWCLLSNFYPREAKVQW 143
DB      154 KSGTASVWCLLNFFYPREAKVQW 176

RESULT 12
US-08-491-334A-56
; Sequence 56, Application US/08491334A
; Patent No. 5874080
; GENERAL INFORMATION:
; APPLICANT: Hebert, Caroline A.
; APPLICANT: Kabakoff, Rhona C.
; APPLICANT: Moore, Mark W.
; TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
; TITLE OF INVENTION: Disorders and Asthma
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,334A
; FILING DATE: 27-Jun-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-Mar-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:

```

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; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-491-334A-56

Query Match 77.9%; Score 586; DB 2; Length 242;
Best Local Similarity 76.9%; Pred. No. 1.2e-49;
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
Db 34 LPVSLGDAQSISCRSSQSLVHGIGNTYLVHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFSGS 93

Qy 61 GSGTDFTLKISRVEAEDVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 120
Db 94 GSGTDFTLRISRVEAEDLGLYFCQSQSTHVPLTFGAGTKLELKRVAAPTTFVIFPPSSEQL 153

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 154 KSGTASVVCLLNFPYPREAKVQW 176

RESULT 13
US-09-027-449-42
; Sequence 42, Application US/09027449
; Patent No. 6025158
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/027,449
; FILING DATE: 20-Feb-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/074,330
; FILING DATE: 22-Jan-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/038,664
; FILING DATE: 21-Feb-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P108R3-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-491-334A-56
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; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-027-449-42

Query Match 77.9%; Score 586; DB 3; Length 242;
Best Local Similarity 76.9%; Pred. No. 1.2e-49;
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
Db 34 LPVSLGDAQSISCRSSQSLVHGIGNTYLVHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFSGS 93

Qy 61 GSGTDFTLKISRVEAEDVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 120
Db 94 GSGTDFTLRISRVEAEDLGLYFCQSQSTHVPLTFGAGTKLELKRVAAPTTFVIFPPSSEQL 153

Qy 121 KSGTASVVCLLSNFPYPREAKVQW 143
Db 154 KSGTASVVCLLNFPYPREAKVQW 176

RESULT 14
US-08-804-444A-42
; Sequence 42, Application US/0880444A
; Patent No. 6117980
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania N
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/804,44A
; FILING DATE: 21-Feb-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-804-444A-42

Query Match 77.9%; Score 586; DB 3; Length 242;
Best Local Similarity 76.9%; Pred. No. 1.2e-49;
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGNYLDWYLOKPGQSPQLLIYLGNSRAGVDPDRFSGS 60
Db 34 LPVSLGDAQSISCRSSQSLVHGIGNTYLVHWYLOKPGQSPKLLIYKVSNRFSGVDPDRFSGS 93

Qy 61 GSGTDFTLKISRVEAEDVGIYCMQSLQIPRLFGPGTKVDIKRTVAAPSVFIFFPPSDEQL 120
Db 94 GSGTDFTLRISRVEAEDLGLYFCQSQSTHVPLTFGAGTKLELKRVAAPTTFVIFPPSSEQL 153
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Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 154 KSGTASVVCLLNFPYREAKVQW 176

RESULT 15

US-09-026-985-42
; Sequence 42, Application US/09026985
; Patent No. 6133426
; GENERAL INFORMATION:
; APPLICANT: Gonzalez, Tania R.
; APPLICANT: Leong, Steven R.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/026,985
; FILING DATE: 20-Feb-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P1085R3-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5530
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-026-985-42

Query Match 77.9%; Score 586; DB 3; Length 242;
Best Local Similarity 76.9%; Pred. No. 1.2e-49;
Matches 110; Conservative 15; Mismatches 18; Indels 0; Gaps 0;

Qy 1 MPVTPGEPASISCRSSQSLHNSGVNYLDWYLQKPGQSPQLLIYLGSNRAGVDPDRFSGS 60
Db 34 LPVSLGQDASISCRSSQSLVHGIGNTYLHWYLQKPGQSPKLLIYKVENRFGVDPDRFSGS 93
Qy 61 GSGTDFTLKISRVAEDVGIYYCMQSLQIPRLFGEGTKVDIKRTVAAPSVEIFPPPSDEQL 120
Db 94 GSGTDFTLRISRVAEDILGLYFCQSQSTHVPLTFCAGTKLELKRVAAPTVEIFPPPSDEQL 153
Qy 121 KSGTASVVCLLSNFPYREAKVQW 143
Db 154 KSGTASVVCLLNFPYREAKVQW 176

Search completed: March 8, 2005, 05:54:09
Job time : 15.7238 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 13.5032 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-33
Perfect score: 998
Sequence: 1 SETLSLTCVAVGSGFSGYW.....YAATSQVLLPSKDVMOQTDE 190
Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	902	90.4	231	2 B23746	Ig Fab region IV-J
2	678.5	68.0	627	2 S14683	Ig mu chain precur
3	556.5	55.8	143	2 B49028	Ig heavy chain V-I
4	535.5	53.7	592	2 S25705	Ig mu chain - shee
5	519	52.0	140	2 S78052	Ig heavy chain pre
6	517.5	51.9	140	2 A49045	Ig heavy chain V r
7	506	50.7	126	2 S47010	Ig heavy chain V4.
8	503.5	50.5	288	2 S29690	Ig heavy chain VDJ
9	492.5	49.3	220	2 A49444	Ig gamma-1 heavy c
10	470	47.1	139	2 S31586	Ig heavy chain V r
11	461	46.2	146	1 GHUR2	Ig heavy chain pre
12	451	45.2	106	2 S37454	Ig mu chain - huma
13	450.5	45.1	130	2 S31690	Ig heavy chain V r
14	450.5	45.1	140	2 I37782	Ig variable region
15	449	45.0	122	2 JL0047	Ig heavy chain V r
16	443	44.4	97	2 S26898	Ig heavy chain V r
17	440	44.1	97	2 S26805	Ig heavy chain V r
18	437	43.8	130	2 S30534	Ig heavy chain V r
19	436	43.7	568	2 A34891	Ig heavy chain pre
20	434.5	43.5	155	2 S31511	Ig heavy chain - h
21	434	43.5	97	2 S14474	Ig heavy chain V r
22	433.5	43.4	155	2 S31512	Ig heavy chain - h
23	433	43.4	97	2 S26806	Ig heavy chain V r
24	433	43.4	97	2 G34964	Ig heavy chain V-I
25	433	43.4	452	1 MHU	Ig mu chain C regi
26	433	43.4	453	2 S37768	Ig mu chain C regi
27	433	43.4	473	1 MHUM	Ig mu chain C regi
28	433	43.4	474	2 S15590	Ig heavy chain - h
29	431	43.2	137	2 S31676	Ig heavy chain V r

RESULT 1
B23746
Ig Fab region IV-J(H4)-C (KAU cold agglutinin) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: B23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin C region: immunoglobulin homology
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: B23746
A:Status: preliminary
A:Molecule type: protein
C:Residues: 1-231 <L80>
C:Superfamily: immunoglobulin C region: immunoglobulin homology
F:140-209/Domain: immunoglobulin homology <IM>

Query Match 90.4%; Score 902; DB 2; Length 231;
Best Local Similarity 92.1%; Pred. No. 4e-64;
Matches 175; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Qy 1 SETLSLTCVAVGSGFSGYWSWIRQPKGLEWGEINHSSTNYNPSLKSRVTISVDTS 60
Db 14 SETLSLTCVAVGSGFSDYWSWIRQPKGLEWGEINHSSTNYNPSLKSRVTISVDTS 73
Qy 61 KNQFSLKLSSTVAADTAVVYCARGGTTVPDPAFDWGGTWTVTYSSGSASAPTLFPLVSC 120
Db 74 KNQFSLKLSSTVAADTAVVYCRRPHTSGHYWYWGQSTLVTYSSGSASAPTLFPLVSC 133
Qy 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGKYAATSQVLLP 180
Db 134 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGKYAATSQVLLP 193
Qy 181 SKDVMQGTDE 190
Db 194 SKDVMQGTDE 203

RESULT 2
S14683
Ig mu chain precursor, membrane-bound (clone 201) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
C:Accession: S14683; S08047
R:Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
Nucleic Acids Res. 18, 4278, 1990
A:Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain.
A:Reference number: S14683; MUID:90332450; PMID:2115996
A:Accession: S14683
A:Molecule type: mRNA
A:Residues: 1-627 <FRI>
A:Cross-references: EMBL:X17115; NID:G33450; PIDN:CAA34971.1; PID:G33451

30	430.5	43.1	114	2	I72667	cold agglutinin FS
31	427.5	42.8	116	2	S37456	Ig mu chain - huma
32	427.5	42.8	135	2	S78051	Ig heavy chain pre
33	425.5	42.6	139	2	S31696	Ig heavy chain V r
34	425.5	42.6	147	2	S13519	Ig heavy chain V r
35	422	42.3	129	2	S44114	Ig heavy chain V r
36	421	42.2	470	2	S22080	Ig heavy chain pre
37	420	42.1	118	2	S20780	Ig heavy chain V r
38	419.5	42.0	123	2	S30530	Ig heavy chain V r
39	418	41.9	145	2	S78055	Ig heavy chain pre
40	416.5	41.7	134	2	S54906	Ig heavy chain V r
41	410	41.1	110	2	S44110	Ig heavy chain V-D
42	409.5	41.0	121	2	S44113	Ig heavy chain V r
43	408	40.9	97	2	JH0428	Ig gamma chain V r
44	408	40.9	118	2	S24443	Ig heavy chain V r
45	407.5	40.8	146	2	S09711	Ig heavy chain V r

ALIGNMENTS

C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;1-15/Domain: signal sequence #status predicted <STG>
F;16-627/Product: Ig mu chain #status predicted <MAP>
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match	68.0%	Score 678.5;	DB 2;	Length 627;
Best Local Similarity	66.7%	Pred. No. 5.2e-46;		
Matches 134; Conservative	20;	Mismatches 34;	Indels 13;	Gaps 2

QY 3 TSLTCAVYGGFSGYYWSWIRQPPGKGLEWIGE-INHSGSTNYNPSLKSRVTISVDTSK 61

db 36 SVKVSCASCGTFSSYAISWVROAPGCGLEWMGGIPIPIFGTANYAOKFOGRVTTITADEST 95

62 NOFSIKLSSVTAADTAVYCARGGT^{VT}TFDA-----FDIWGGTMT^{TV}SSGSA 109

96 95 94 93 92 91 90 89 88 87 86 85 84 83 82 81 80 79 78 77 76 75 74 73 72 71 70 69 68 67 66 65 64 63 62 61 60 59 58 57 56 55 54 53 52 51 50 49 48 47 46 45 44 43 42 41 40 39 38 37 36 35 34 33 32 31 30 29 28 27 26 25 24 23 22 21 20 19 18 17 16 15 14 13 12 11 10 9 8 7 6 5 4 3 2 1

0- 11 A SIX DTF EBT VSCENQDCNTGCI/VCCY NADREY DDCTEEBGLVWVNINCYT COTTCCEBDUUT BOC 169

100

[illegible]

RESULT 3

B49028
Ig heavy chain V-IV region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: B49028

R. J. Immunol. 21, 2355-2363, 1991
R.Timmers, E.; Kenter, M.; Thompson, A.; Kraakman, M.E.; Berman, J.E.; Alt, F.W.; Schuurder
A Title: Diversity of immunoglobulin heavy chain gene segment rearrangement in B lymphoblastoid cell lines
Mol. Cell. Probes 7, 191-198, 1993

A;Reference Number: A43028; NUID:32008140; PMID:1513343
A;Accession: B49028

A;Status: preliminary

A;Molecule type: mRNA
A:Residues: 1-143 CTM-

A;References: 1-143 <IMS>
A;Cross-references: GB:S64473; NID:q236906; PIDN:AAB20012.1; PID:q236907

A;Experimental source: X-linked agammaglobulinemia patients, B lymphoblastoid cell lines

A;Note: sequence extracted from NCBI backbone (NCBIN:64473, NCBIIP:64472)
C;Superfamily: immunoglobulin V region; immunoglobulin homolour

C: Keywords: heterotetramer; immunoglobulin C/superfamily; immunoglobulin V region; immunoglobulin homology

F;15-97/Domain: immunoglobulin homology <IMM>

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 68. *Chrysomelidae*
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Query Match 55.8%; Score 556.5; DB 2; Length 143;
Best Local Similarity 84.5%; Pred. No. 4.3e-37;
Matches 109; Conservative 1; Mismatches 10; Indels 9; Gaps 1

QV 1 SETLSLTCVYGGSFSGYYWSWIROPFGKGLEWIGEINHSGSTNYPNPSLKSRVTISVDTS 60

db 15 SETLSITCAVYGGSESGYVWSWITROPCKGREWITGETNHSGSTNYNPST.KSRVTTSVDTS 74

61 KNQFSLKISSVTARNDAVVVCAPGCTTVEEA-----EDTWCGGTWTVSSCSA 111

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RESULT 4

S25705
Ig mu chain - sheep
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-JUL-1999
C;Accession: S25705

R;Patri, S.; Nau, F.

RESULT 6

Ig heavy chain V region (anti-B cell autoantibody) - human (fragment)
A;Accession: A49045
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
R;Accession: A49045
R;Grillot-Courvalin, C.; Brouet, J.C.; Piller, F.; Rasseenti, L.Z.; Labaume, S.; Silverma
Bur, J. Immunol. 22, 1781-1788, 1992
A;Title: An anti-B cell autoantibody from Wiskott-Aldrich syndrome which recognizes i bl
A;Reference number: A49045; MUID:92324290; PMID:1623923
A;Accession: A49045
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-140 <GRI>
A;Cross-references: GB:539381; NID:G250899; PIDN:AAB22441.1; PID:G250900
A;Note: sequence extracted from NCBI backbone (NCBIN:108088, NCRIP:108089)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;34-116/Domain: immunoglobulin homology <IMM>

Query Match 51.9%; Score 517.5; DB 2; Length 140;
Best Local Similarity 91.6%; Pred. No. 5e-34;
Matches 98; Conservative 3; Mismatches 5; Indels 1; Gaps 1;
Qy 1 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISDTS 60
Db 34 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISDTS 93
Qy 61 KNQPSLKLSSVTAADTAVYVCARGTWTFF-DAFDIWGQGTMTVSS 106
Db 94 KNQPSLKLSSVTAADTAVYVCARGGPAATIVESFDYWGQGTMTVSS 140

RESULT 7

S47010
Ig heavy chain V4.21-UniqueJ5 region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S47010
R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.
submitted to the EMBL Data Library, July 1994
A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin
A;Reference number: S47009
A;Accession: S47010
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-126 <MAH>
A;Cross-references: EMBL:Z35492; NID:G517254; PIDN:CAA84625.1; PID:G517255
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
P;15-97/Domain: immunoglobulin homology <IMM>

Query Match 50.7%; Score 506; DB 2; Length 126;
Best Local Similarity 87.5%; Pred. No. 3.6e-33;
Matches 98; Conservative 3; Mismatches 5; Indels 6; Gaps 1;
Qy 1 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISDTS 60
Db 15 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISDTS 74
Qy 61 KNQPSLKLSSVTAADTAVYVCARGG-----TTTTFDAFDIWGQGTMTVSS 106
Db 75 KNQPSLKLSSVTAADTAVYVCARGGQCPKASCYTKNWFDPWGQGTMTVSS 126

RESULT 8

S29690
Ig heavy chain VDJ region - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000
C;Accession: S29690
R;Dammers, P.M.; Bos, N.A.; Kroese, F.G.M.
submitted to the EMBL Data Library, October 1992

A;Description: Analysis of the rat B cell repertoire: cloning of rat Vh genes.
A;Reference number: S29690
A;Accession: S29690
A;Molecule type: mRNA
A;Residues: 1-288 <DAM>
A;Cross-references: EMBL:X68782; NID:G56442; PID:gi334294
A;Experimental source: strain DZB
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;12-95/Domain: immunoglobulin homology <IMM>

Query Match 50.5%; Score 503.5; DB 2; Length 288;
Best Local Similarity 51.1%; Pred. No. 1.4e-32;
Matches 97; Conservative 36; Mismatches 52; Indels 5; Gaps 3;
Qy 3 TSLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEIN-HSGSTNNPNSLKSRTVISDTSK 61
Db 14 SVKISKASGYTFTDYMHVWVQRPQGLVWIGRINPANGNTEYAEKFKSRATLTADKSS 73
Qy 62 NQPSLKLSSVTAADTAVYVCARGTWTFFDAFDIWGQGTMTVSSGSASAPTLPLVSC 121
Db 74 NTAYMQLSLTSEDATYFCTIWTGV---PPDYWGQGVMTVSSQSSTPLVPLVSC 130
Qy 122 NSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDI--SSTRGFPVLGGKYAATSQVLLP 180
Db 131 SPUSDENLVAMGCLARDFLPSSISFSWNYQNTEVMOGVTFPTLTGDKTATTSQVLLS 190
Qy 181 SKDVMOQTDE 190
Db 191 AKNVLEGSDE 200

RESULT 9

A49444
Ig gamma-1 heavy chain (New) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999
C;Accession: A49444
R;Saul, F.A.; Poljak, R.J.
Proteins 14, 363-371, 1992
A;Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res
A;Reference number: A49444; MUID:93066153; PMID:1438175
A;Accession: A49444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-220 <SAU>
A;Note: sequence modified after extraction from NCBI backbone
A;Note: this sequence report includes corrections based on crystal structure refinement
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
P;137-202/Domain: immunoglobulin homology <IMM>

Query Match 49.3%; Score 492.5; DB 2; Length 220;
Best Local Similarity 51.9%; Pred. No. 7.8e-32;
Matches 99; Conservative 32; Mismatches 44; Indels 15; Gaps 5;
Qy 1 SETLSLTCAVYGGSFSGYYSWIRQPPGKGLEWIGEINHGSGTNNPNSLKSRTVISDTS 60
Db 15 SQTLSLTCTVSGTSDDDYWTWYRQPPGKLEWIGYVFTGTTLLDPSLRGRVTMLVNTS 74
Qy 61 KNQPSLKLSSVTAADTAVYCAR-----GGTTFDAFDIWGQGTMTVSSGSASAPTLFP 116
Db 75 KNQPSLKLSSVTAADTAVYCARLTIAGG-----IDVMGQGSGLVTVSSASTGPSVFP 127
Qy 117 LVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPVLGR-GGKYAATS 175
Db 128 LAPSSKSTSG-GTAAUGCLVKDIFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSS 184
Qy 176 QVLLPSKSDV 184
Db 185 VVTVPSSSL 193

Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes expressed by h
A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: J37782
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140 <RES>
A;Cross-references: EMBL:X67906; NID:G33582; PIDN:CAA48104.1; PID:G33583
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;46-128/Domain: immunoglobulin homology <IMM>

Query Match 45.1%; Score 450.5; DB 2; Length 140;
Best Local Similarity 82.2%; Pred. No. 9.7e-29;
Matches 88; Conservative 5; Mismatches 13; Indels 1; Gaps 1;
Qy 1 SETLSLTCVYGGSFSGYYWIRQPPGKGLWIGINHSNSTNPNPSLKSRTVISVDT 60
Db 34 SETLSLTCVGGGSISSYYWIRQPPGKGLWIGIYYSGSTNPNPSLKSRTVISVDT 93
Qy 61 KNQPSLKLSSVTAADTAVYTCARGTTFDA-PDINGQGTMTVSS 106
Db 94 KNQPSLKLSSVTAADTAVYTCARHNSSSWYGRYFDYWGQGLTVSS 140

RESULT 15

JL0047
Ig heavy chain V region precursor (clone cR18) - human
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 16-Aug-1996
C;Accession: JL0047
R;Baer, R.; Forster, A.; Lavenir, I.; Rabbitts, T.H.
J. Exp. Med. 187, 2011-2016, 1988
A;Title: Immunoglobulin V-H genes are transcribed by T cells in association with a new S
A;Reference number: JL0047; MUID:88258392; PMID:3133445
A;Accession: JL0047
A;Molecule type: mRNA
A;Residues: 1-122 <BAE>
A;Experimental source: T-cell line RPMI 8402
A;Note: the authors translated the reading frame which extends to the stop codon; the se
A;Note: this sequence belongs to the VH II subgroup
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;23-105/Domain: immunoglobulin homology <IMM>

Query Match 45.0%; Score 449; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SETLSLTCVYGGSFSGYYWIRQPPGKGLWIGINHSNSTNPNPSLKSRTVISVDT 60
Db 23 SETLSLTCVYGGSFSGYYWIRQPPGKGLWIGIYYSGSTNPNPSLKSRTVISVDT 82
Qy 61 KNQPSLKLSSVTAADTAVYTCARG 84
Db 83 KNQPSLKLSSVTAADTAVYTCARG 106

Search completed: March 8, 2005, 06:39:27
Job time : 14.5532 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 70.9554 Seconds

(without alignments)

1371.214 Million cell updates/sec

Title: US-09-784-950-33

Perfect score: 998

Sequence: 1 SETLSLCAVYGGSFSGYV.....YAATSOVLPSKDVMOQTDE 190

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_crembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	900.5	90.2	595	2	Q8WUX4	Q8WUX4	homo sapien
2	900.5	90.2	597	2	Q6GMX5	Q6GMX5	homo sapien
3	900.5	90.2	597	2	Q9BU10	Q9BU10	homo sapien
4	900.5	90.2	625	2	Q96AA6	Q96AA6	homo sapien
5	894.5	89.6	597	2	Q9BQ88	Q9BQ88	homo sapien
6	851	85.3	620	2	Q96EY0	Q96EY0	homo sapien
7	733	73.4	606	2	Q6GMX2	Q6GMX2	homo sapien
8	713	71.4	613	2	Q8WUK1	Q8WUK1	homo sapien
9	698.5	70.0	597	2	Q96BB9	Q96BB9	homo sapien
10	572	57.3	465	2	Q6GMX6	Q6GMX6	homo sapien
11	553.5	55.5	476	2	Q6GMX1	Q6GMX1	homo sapien
12	530.5	53.2	576	2	Q6P4I8	Q6P4I8	homo sapien
13	527.5	52.9	477	2	Q6GMX7	Q6GMX7	homo sapien
14	512.5	51.4	613	2	Q8VCX7	Q8VCX7	mus musculus
15	492.5	49.3	478	2	Q72379	Q72379	homo sapien
16	490.5	49.1	496	2	Q96KX8	Q96KX8	homo sapien
17	485	48.6	473	2	Q8TC63	Q8TC63	homo sapien
18	484	48.5	614	2	Q7TMT6	Q7TMT6	mus musculus
19	475	47.6	478	2	Q6NYH3	Q6NYH3	homo sapien
20	475	47.6	492	2	Q72374	Q72374	homo sapien
21	474.5	47.5	476	2	Q6MZX7	Q6MZX7	homo sapien
22	465	46.6	150	2	Q95973	Q95973	homo sapien
23	461	46.2	146	1	HV21_HUMAN	HV21_HUMAN	homo sapien
24	460.5	46.1	479	2	Q9NM22	Q9NM22	mus musculus
25	442	44.3	116	2	Q7Z3Y6	Q7Z3Y6	homo sapien
26	433	43.4	454	1	MUC_HUMAN	MUC_HUMAN	homo sapien
27	428.5	42.9	605	2	Q6GN83	Q6GN83	homo sapien
28	417.5	41.8	119	2	Q9UL73	Q9UL73	homo sapien
29	417	41.8	593	2	Q6INM5	Q6INM5	homo sapien
30	414.5	41.5	470	2	Q6PJA4	Q6PJA4	homo sapien
31	410.5	41.1	614	2	Q6DDQ7	Q6DDQ7	homo sapien

Query Match

90.2%; Score 900.5; DB 2; Length 595;

32	410	41.1	482	2	Q91X92	Q91X92	mus musculus
33	399	40.0	572	2	Q66IQ7	Q66IQ7	homo sapien
34	397	39.8	139	2	Q86SX2	Q86SX2	homo sapien
35	397	39.8	465	2	Q6PC4	Q6PC4	homo sapien
36	395.5	39.6	478	2	Q6PI81	Q6PI81	homo sapien
37	393	39.4	225	2	Q6PAF5	Q6PAF5	homo sapien
38	385	38.6	482	2	Q8K172	Q8K172	mus musculus
39	384.5	38.5	464	2	Q6MZU6	Q6MZU6	homo sapien
40	383.5	38.4	129	1	HV2F_HUMAN	HV2F_HUMAN	homo sapien
41	383.5	38.4	466	2	Q6IN78	Q6IN78	homo sapien
42	383.5	38.4	480	2	Q6N094	Q6N094	homo sapien
43	383	38.4	473	2	Q6P055	Q6P055	homo sapien
44	383	38.4	493	2	Q6GMX2	Q6GMX2	homo sapien
45	380.5	38.1	472	2	Q6N089	Q6N089	homo sapien

ALIGNMENTS

RESULT 1

Q8WUX4	PRELIMINARY;	PRT;	595 AA.
AC	Q8WUX4;		
DT	01-MAR-2002 (TrEMBLrel. 20, Created)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)		
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)		
DE	Hypothetical protein.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lymph;		
RX	MEDLINE=32388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,		
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).		
RN	[2]		
RC	TISSUE=Lymph;		
RA	Strausberg R.;		
RA	Submitted (DSC-2001) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; BC019235; AAH19235.2; -		
DR	PIR; G34964; G34964.		
DR	HSSP; P01861; 1ADQ.		
DR	Pfam; PF07654; Cl-set; 4.		
DR	SMART; SM00409; IG; 2.		
DR	SMART; SM00407; IGL; 4.		
DR	SMART; SM00406; IGV; 1.		
DR	PROSITE; PS00835; IG LIKE; 5.		
DR	PROSITE; PS00290; IG MHC; UNKNOWN_3.		
KW	Hypothetical protein.		
SQ	SEQUENCE 595 AA; 65290 MW; 0D4B50776545714E CRC64;		

Best Local Similarity 89.8%; Pred. No. 2.3e-72;
Matches 176; Conservative 2; Mismatches 11; Indels 7; Gaps 2;

QY 1 SETLSLTCVYGGSGFYGWSWIRQPGKLEWIGEHSGSTNYPNPSLKSRTVISVDT 60
DB 41 SETLSLTCVYGGSGFYGWSWIRQPGKLEWIGEHSGSTNYPNPSLKSRTVISVDT 100
QY 61 KNQFSLKLSVTAADTAIVYCAR-----GGTTVTFDAFDIWGGTMTVTVSSGSASAPTL 114
DB 101 KKQLSLKLSVNAADTAIVYCARVITRASPGTDGRY-GMDVWGQGTTVTVSSGSASAPTL 159
QY 115 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGGKYAAT 174
DB 160 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGGKYAAT 219
QY 175 SQVLLPSKDVMOGTDE 190
DB 220 SQVLLPSKDVMOGTDE 235

RESULT 2
Q6GMX5 ID Q6GMX5 PRELIMINARY; PRT; 597 AA.
AC Q6GMX5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC073767; AAH73767.1; -.
DR InterPro; IPR003599; IG-like.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 4.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_Like; 5.

DR PROSITE; PS00290; IG.MHC; UNKNOWN 3.
KW Hypothetical protein_
SQ SEQUENCE 597 AA; 65304 MW; 2A1E75F6AED85230 CRC64;

Query Match 90.2%; Score 900.5; DB 2; Length 597;
Best Local Similarity 89.8%; Pred. No. 2.3e-72;
Matches 176; Conservative 2; Mismatches 11; Indels 7; Gaps 2;

QY 1 SETLSLTCVYGGSGFYGWSWIRQPGKLEWIGEHSGSTNYPNPSLKSRTVISVDT 60
DB 34 SETLSLTCVYGGSGFYGWSWIRQPGKLEWIGEHSGSTNYPNPSLKSRTVISVDT 93
QY 61 KNQFSLKLSVTAADTAIVYCAR-----GGTTVTFDAFDIWGGTMTVTVSSGSASAPTL 114
DB 94 KKQLSLKLSVNAADTAIVYCARVITRASPGTDGRY-GMDVWGQGTTVTVSSGSASAPTL 152
QY 115 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGGKYAAT 174
DB 153 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGGKYAAT 212
QY 175 SQVLLPSKDVMOGTDE 190
DB 213 SQVLLPSKDVMOGTDE 228

RESULT 3
Q9BU10 ID Q9BU10 PRELIMINARY; PRT; 597 AA.
AC Q9BU10;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC002963; AAH02963.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG.MHC.
DR InterPro; IPR003596; IG.v.
DR Pfam; PF07654; Cl-set; 4.

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DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65274 MW; 2DAFA8FB7E055851 CRC64;

Query Match 90.2%; Score 900.5; DB 2; Length 597;
Best Local Similarity 89.8%; Pred. No. 2.3e-72;
Matches 176; Conservative 2; Mismatches 11; Indels 7; Gaps 2;

Qy 1 SETLSLTCVYGGSFSGYVSWIRQPPGKGLWIEINHGSGTNYNPSLKSRTVISVDT 60
Db 34 SETLSLTCVYGGSFSGYVSWIRQPPGKGLWIEINHGSGTNYNPSLKSRTVISVDT 93
Qy 61 KNQPSLKLSSVTAADTAVYCAR-----GGTTTFDAFDIWGQGTWTVSSGSASAPTL 114
Db 94 KKQLSLKLSSVNAADTAVYCARVITRASPGTDGRY-GMDVMGQGTTVTVSSGSASAPTL 152
Qy 115 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKGYAAT 174
Db 153 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKGYAAT 212
Qy 175 SQVLLPSKDVMOQGTDE 190
Db 213 SQVLLPSKDVMOQGTDE 228

RESULT 4
Q96AA6 PRELIMINARY; PRT; 625 AA.
AC Q96AA6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC017356; AAH17356.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01861; 1ADQ.
DR DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG.cl.

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DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 625 AA; 68610 MW; F62FAB3ADE7ECBFE CRC64;

Query Match 90.2%; Score 900.5; DB 2; Length 625;
Best Local Similarity 89.8%; Pred. No. 2.5e-72;
Matches 176; Conservative 2; Mismatches 11; Indels 7; Gaps 2;

Qy 1 SETLSLTCVYGGSFSGYVSWIRQPPGKGLWIEINHGSGTNYNPSLKSRTVISVDT 60
Db 41 SETLSLTCVYGGSFSGYVSWIRQPPGKGLWIEINHGSGTNYNPSLKSRTVISVDT 100
Qy 61 KNQPSLKLSSVTAADTAVYCAR-----GGTTTFDAFDIWGQGTWTVSSGSASAPTL 114
Db 101 KKQLSLKLSSVNAADTAVYCARVITRASPGTDGRY-GMDVMGQGTTVTVSSGSASAPTL 159
Qy 115 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKGYAAT 174
Db 160 FPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGKGYAAT 219
Qy 175 SQVLLPSKDVMOQGTDE 190
Db 220 SQVLLPSKDVMOQGTDE 235

RESULT 5
Q9BQB8 PRELIMINARY; PRT; 597 AA.
ID Q9BQB8
AC Q9BQB8;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.

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DR HSSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65300 MW; 2DAPAD50A6375851 CRC64;

Query Match      89.6%; Score 894.5; DB 2; Length 597;
Best Local Similarity 89.3%; Pred. No. 8.1e-72;
Matches 175; Conservative 2; Mismatches 12; Indels 7; Gaps 2;

QY 1 SETLSLTCVYGGSGFYGSWIRQPGKGLWIGINHSSTNPNLSKSRVTISVDTS 60
   |||||
Db 34 SETLSLTCGVYGGSGFYGSWIRQPGKGLWIGINHSSTNPNLSKSRVTISVDTS 93
   |||||

QY 61 KNQFSLKLSVTAADTAIVYCAR-----GGTTVTFDAFDIWGGQTMVTIVSSGSASAPTL 114
   |||||
Db 94 KKQLSLKLSVNADTAIVYCARVITRASPTDQRY-GMDVWGQGTIVTVSSGSASAPTL 152
   |||||

QY 115 PPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGKYAAT 174
   |||||
Db 153 PPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGKYAAT 212
   |||||

QY 175 SQVLLPSKDVMOQGTDE 190
   |||||
Db 213 SQVLLPSKDVMOQGTDE 228
   |||||

RESULT 6
Q96EY0
ID Q96EY0 PRELIMINARY; PRT; 620 AA.
AC Q96EY0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUB=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.;
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
SEQUENCE FROM N.A.
TISSUB=Primary B-Cells;
RA Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
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DR EMBL; BC011857; AAH11857.2; -.
DR PIR; S15590; S15590.
DR HSSP; P01820; IG7J.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00407; IGV; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 620 AA; 68125 MW; 990A1A4A6E8FF27B CRC64;

Query Match      85.3%; Score 851; DB 2; Length 620;
Best Local Similarity 87.9%; Pred. No. 6.9e-68;
Matches 167; Conservative 3; Mismatches 20; Indels 0; Gaps 0;

QY 1 SETLSLTCVYGGSGFYGSWIRQPGKGLWIGINHSSTNPNLSKSRVTISVDTS 60
   |||||
Db 41 SETLSLTCVTGGSSISYIWSWIRQPGKGLWIGRIYTSNSTNPNLSKSRVTISVDTS 100
   |||||

QY 61 KNQFSLKLSVTAADTAIVYCARGGTTVTFDAFDIWGGQTMVTIVSSGSASAPTLFPLVSC 120
   |||||
Db 101 KNQFSLKLSVTAADTAIVYCARQWELPTVGLFYWGQGLTVTVSSGSASAPTLFPLVSC 160
   |||||

QY 121 ENSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGKYAATSOVLLP 180
   |||||
Db 161 ENSPSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGFPSPVLRGGKYAATSOVLLP 220
   |||||

QY 181 SKDVMOQGTDE 190
   |||||
Db 221 SKDVMOQGTDE 230
   |||||

RESULT 7
Q6GMV2
ID Q6GMV2 PRELIMINARY; PRT; 606 AA.
AC Q6GMV2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
[1]
SEQUENCE FROM N.A.
TISSUB=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
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RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., McKernan K.J., Abranson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL EMBL; BC015760; AAH15760.1; -.
DR PIR; S05271; S05271.
DR PIR; S24260; S24260.
DR HSP; P01861; IADQ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8EC263D9 CRC64;

Query Match 70.08; Score 698.5; DB 2; Length 597;
Best Local Similarity 73.11; Pred. No. 3.4e-54;
Matches 141; Conservative 16; Mismatches 31; Indels 5; Gaps 3;

QY 3 TSLTCAVYGGSGFYGSYWSWIRQPPGKLEWIGINHS-GSTWYNPSLKSRTVISVDTSK 61
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 36 SLRLSCAAGFSFSSYAMWVRQAPGKLEWVSAGSGGTYADSVKGRFTISRNSR 95
QY 62 NQPSLKLSVTAADTAVYYCA---RG-GTTVTDFADFWGQGMVTVSSGSASAPTLFPL 117
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 96 DTLYLQWNSLRAEDTAVYYCAKDPGRYSAGSNVTREDYWGQGLTVTVSSGSASAPTLFPL 155
QY 118 VSCNSPDSSTSSVAVGCLAQDFLPSITFSWKYKNNSDISSTRGFPVLRGGKYAATSQV 177
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 156 VSCNSPDSSTSSVAVGCLAQDFLPSITFSWKYKNNSDISSTRGFPVLRGGKYAATSQV 215
QY 178 LLPSKQVMQGTDE 190
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 216 LLPSKQVMQGTDE 228

RESULT 10
Q6GMX6 PRELIMINARY; PRT; 465 AA.
AC Q6GMX6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RC MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner C.M., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dlatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., McKernan K.J., Abranson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;

Query Match 57.31; Score 572; DB 2; Length 465;
Best Local Similarity 62.7%; Pred. No. 6e-43;
Matches 116; Conservative 18; Mismatches 43; Indels 8; Gaps 4;

QY 1 SETLSITCAVYGGSGFYGSYWSWIRQPPGKLEWIGINHS-GSTWYNPSLKSRTVISVDTS 60
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 34 SETLSITCTVSGSGISGYYSWIRQPPGKLEWIGIRIYTSGSTWYNPSLKSRTVISVDTS 93
QY 61 KNQFSLKLSVTAADTAVYYCARGTTVTFDAFDWQGMVTVSSGSASAPTLFPLVSC 120
DB :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 94 KNQFSLKLSVTAADTAVYYCARG---RPTFYDYGQGLTVTVSSASTKGPVFPPLAPS 149
QY 121 ENSPSPDSTSSVAVGCLAQDFLPSITFSWKYKNNSDISSTRGFPVLR-GGKYAATSQVLL 179
DB :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 150 SKSTSG-GTAAIGCLVQDYFPEPTVTSW--NSGALTSGVHTTFFAVLQSSGLYSLSSVTV 206
QY 180 PSKDV 184
DB :|||:
DB 207 PSSSL 211

RESULT 11
Q6GMX1 PRELIMINARY; PRT; 476 AA.
AC Q6GMX1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073765; AAH73765.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 2.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00409; Ig; 4.
DR SMART; SM00407; IgC1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 477 AA; 51631 MW; 9FE59C09C50CFF85 CRC64;

Query Match 52.9%; Score 527.5; DB 2; Length 477;
Best Local Similarity 58.5%; Pred. No. 6.2e-39;
Matches 113; Conservative 22; Mismatches 43; Indels 15; Gaps 7;

Qy 1 SETLSLTCVAVYGGSGFYVSWIRQPPGKLEWIGIENHSGSTYVNSLSKRVTSVDTSS 60
Db 34 SETLSLTCVAVYGGSGFYVSWIRQPPGKLEWIGIENHSGSTYVNSLSKRVTSVDTSS 93
Qy 61 KNQSLKLSVTAADTAVYVCARGGTTVTPD-AFDINGQGTMTVTVSSGSASAPTLPLVLS 119
Db 94 KNQSLKLSVTAADTAVYVCARGGTTVTPD-AFDINGQGTMTVTVSSGSASAPTLPLVLS 149
Qy 120 KNSFSDTSSVAVGCLAQDFLPD---SIFTSWKYKNSDISSTRGFP--SVLRGGKYAAT 174
Db 150 LDSTPQD-GNVVAVACLQVGFPPQPLSVTVNSESQN---VTARNPPPSQDASGDLTYS 204
Qy 175 SQVLLPSKDVNQG 187
Db 205 SQLTLPTAQCPDG 217
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RESULT 14
O8VCX7 PRELIMINARY; PRT; 613 AA.
ID Q8VCX7
AC Q8VCX7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Igh-6 protein.
DE Name=Igh-6;
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
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RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Salivary gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAH18315.1; -.
DR FIR; C30562; C30562.
DR HSP; P01751; Ia6W.
DR MGD; MGI:96448; Igh-6.
DR GO; GO:0019815; C:B-cell receptor complex; IDA.
DR GO; GO:0009897; C:external side of plasma membrane; IDA.
DR GO; GO:0042571; C:immunoglobulin complex, circulating; IDA.
DR GO; GO:0003823; P:antigen binding; IDA.
DR GO; GO:0030333; P:antigen processing; IDA.
DR GO; GO:0045022; P:early endosome to late endosome transport; IDA.
DR GO; GO:0016064; P:humoral defense mechanism (sensu Vertebrata); IDA.
DR GO; GO:0050871; P:positive regulation of B-cell activation; IDA.
DR GO; GO:0030890; P:positive regulation of B-cell proliferation; IDA.
DR GO; GO:0045807; P:positive regulation of endocytosis; IDA.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;
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Query Match 51.4%; Score 512.5; DB 2; Length 613;
Best Local Similarity 52.6%; Pred. No. 1.9e-37;
Matches 100; Conservative 34; Mismatches 51; Indels 5; Gaps 3;

Qy 3 TSLTLCVAVYGGSGFYVSWIRQPPGKLEWIGIENHSGSTYVNSLSKRVTSVDTSS 61
Db 36 SVKISCATGTYTSSYVWIEWKORPGHGLEWIGIENHSGSTYVNSLSKRVTSVDTSS 95
Qy 62 NQFSLKLSVTAADTAVYVCARGGTTVTPD-AFDINGQGTMTVTVSSGSASAPTLPLVLS 121
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 88.0892 Seconds

(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-33

Perfect score: 998

Sequence: 1 SETLSLTCVVGSGFSGYY.....YAATSOVLLPSKDVMOQTDE 190

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	998	100.0	190	2	AAV34304	Aay34304 Igm antib
2	919	92.1	205	2	AAV34299	Aay34299 Igm antib
3	898	90.0	202	2	AAV34303	Aay34303 Igm antib
4	880.5	88.2	197	2	AAV34300	Aay34300 Igm antib
5	720	72.1	596	4	AAW23924	Aam23924 Human EST
6	717	71.8	223	2	AAV08598	Aay08598 Anti-huma
7	712.5	71.4	228	8	ADL70776	Adl70776 Anti-TNPa
8	711	71.2	223	8	ADL70773	Adl70773 Anti-TNPa
9	693.5	69.5	266	8	ADF69305	Adf69305 Human lun
10	689	69.0	588	2	AAW71880	Aaw71880 Anti-huma
11	689	69.0	588	3	AAW12917	Aab12917 Anti-huma
12	686	68.7	595	7	ADM05427	Adm05427 Human pro
13	678.5	68.0	627	7	ADE97370	Ade97370 Human imm
14	675	67.6	588	2	AAW71881	Aaw71881 Anti-huma
15	675	67.6	588	3	AAW12918	Aab12918 Anti-huma
16	673.5	67.5	199	2	AAV34302	Aay34302 Igm antib
17	673.5	67.5	203	2	AAV34301	Aay34301 Igm antib
18	666	66.7	533	7	ADB65070	Adb65070 Human pro
19	662.5	66.4	570	8	ADR19329	Adr19329 Chimeric
20	656	65.7	571	8	ADP84970	Adp84970 Chimeric
21	655	65.6	569	8	ADR19330	Adr19330 Chimeric
22	634.5	63.6	450	6	ABP96294	Abp96294 4A5-3.1.1
23	624	62.5	229	7	ADJ32128	Adj32128 Human int
24	623	62.4	223	7	ADJ32112	Adj32112 Human int
25	620.5	62.2	462	3	AAW26684	Aaw26684 Human imm

26	617.5	61.9	453	6	ABP96295	Abp96295 4A5-3.1.1
27	616.5	61.8	230	7	ADJ32118	Adj32118 Human int
28	599.5	60.1	472	2	AAW93166	Aaw93166 Anti-rhes
29	590	59.1	537	3	RAY96290	Ray96290 Human IGF
30	584.5	58.6	466	7	ADE28479	Ade28479 Human ant
31	581.5	58.3	466	7	ADE28471	Ade28471 Human ant
32	579.5	58.1	580	6	AAO30915	Aao30915 di-NHS76
33	575	57.6	580	6	AAO30913	Aao30913 di-NHS76
34	570.5	57.2	466	7	ADE28419	Ade28419 Human ant
35	564.5	56.6	464	7	ADE28411	Ade28411 Human ant
36	560.5	56.2	446	8	ADK52356	Adk52356 Human ant
37	556	55.7	221	7	ADJ32126	Adj32126 Human int
38	553	55.4	473	4	ABW36206	Abw36206 Human imm
39	551	55.2	241	8	ADS84467	Ads84467 Human ant
40	551	55.2	241	8	ADR68609	Adr68609 Human ant
41	547	54.8	241	8	ADS84432	Ads84432 Human ant
42	547	54.8	241	8	ADR68574	Adr68574 Human ant
43	540	54.1	239	8	ADS84461	Ads84461 Human ant
44	540	54.1	239	8	ADR68603	Adr68603 Human ant
45	539	54.0	241	8	ADS84449	Ads84449 Human ant

ALIGNMENTS

RESULT 1
AAV34304
ID AAY34304 standard; protein; 190 AA.
XX
AC AAY34304;
XX
DT 19-NOV-1999 (first entry)
XX
DE Igm antibody CEM 13.5 heavy chain sequence.
XX
KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
PN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
XX
PR 03-FEB-1999; 99US-00244253.
XX
(ABGE-) ABGENIX INC.
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
WPI; 1999-540816/45.
DR N-PSDB; AAZ20405.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
Claim 60; Fig 29; 245pp; English.
CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the Igm Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
CC can selectively kill activated T-cells, activated B-cells or treating or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes. e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
 XX
 SQ Sequence 190 AA;
 Query Match 100.0%; Score 998; DB 2; Length 190;
 Best Local Similarity 100.0%; Pred. No. 2.7e-63;
 Matches 190; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SETLSLTCAYVGSFSGYYSWIRQPPGKLEWIGEHSGSTNPNPSLKSRTVISVDTS 60
 |||||
 DB 1 SETLSLTCAYVGSFSGYYSWIRQPPGKLEWIGEHSGSTNPNPSLKSRTVISVDTS 60
 |||||
 QY 61 KNQPSLKLSSVTAAADTAVVYCARGTTVTDFADIMGQGTMTVTSSGASAPTLFPLVSC 120
 |||||
 DB 61 KNQPSLKLSSVTAAADTAVVYCARGTTVTDFADIMGQGTMTVTSSGASAPTLFPLVSC 120
 |||||
 QY 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSQVLLP 180
 |||||
 DB 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSQVLLP 180
 |||||
 QY 181 SKDVMQGTDE 190
 |||||
 DB 181 SKDVMQGTDE 190
 |||||
 RESULT 2
 AAY34299
 ID AAY34299 standard; protein; 205 AA.
 AC
 XX AAY34299;
 XX
 DT 19-NOV-1999 (first entry)
 XX
 DE Igm antibody CEM 10.1 C3 heavy chain sequence.
 XX
 KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 150
 FT /label= unknown
 FT /note= "encoded by TYC"
 FT
 XX WO9945031-A2.
 XX
 XX 10-SEP-1999.
 XX
 PF 03-MAR-1999; 99WO-US004583.
 XX
 PR 03-MAR-1998; 98US-00034607.
 PR 03-FEB-1999; 99US-00244253.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;
 XX
 XX WPI; 1999-540816/45.
 DR N-PSDB; AAZ20400.
 XX
 XX New monoclonal antibody, used for treating e.g. graft versus host
 PT disease, cancers, autoimmune diseases and inflammatory diseases.
 PT
 PS Claim 60; Fig 24; 245pp; English.
 XX
 CC This sequence represents the heavy chain of an antibody of the invention.
 CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
 CC complement and a variable region that binds to the epitope on CD147 bound

CC by the Igm MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
 CC can selectively kill activated T-cells, activated B-cells or resting or
 CC activated monocytes. The products and methods can be used for treating
 CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
 CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
 CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
 CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
 XX
 SQ Sequence 205 AA;
 Query Match 92.1%; Score 919; DB 2; Length 205;
 Best Local Similarity 93.2%; Pred. No. 1.2e-57;
 Matches 179; Conservative 3; Mismatches 8; Indels 2; Gaps 1;
 QY 1 SETLSLTCAYVGSFSGYYSWIRQPPGKLEWIGEHSGSTNPNPSLKSRTVISVDTS 60
 |||||
 DB 6 SETLSLTCAYVGSFSGYYSWIRQPPGKLEWIGEHSGSTNPNPSLKSRTVISVDTS 65
 |||||
 QY 61 KNQPSLKLSSVTAAADTAVVYCARGTTVTDFADIMGQGTMTVTSSGASAPTLFPLV 118
 |||||
 DB 66 KNQPSLKLSSVTAAADTAVVYCARGTTTEYYYYYGMVWGQTTVTSSGASAPTLFPLV 125
 |||||
 QY 119 SCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPVLRGGKYAATSQVL 178
 |||||
 DB 126 SCENSPDSTSSVAVGCLAQDFLPDXITFSWKYKNNSDISSTRGFPVLRGGKYAATSQVL 185
 |||||
 QY 179 LPSKDVMOGTDE 190
 |||||
 DB 186 LPSKDVMOGTDE 197
 |||||
 RESULT 3
 AAY34303
 ID AAY34303 standard; protein; 202 AA.
 AC
 XX AAY34303;
 XX
 DT 19-NOV-1999 (first entry)
 XX
 DE Igm antibody CEM 13.12 heavy chain sequence.
 XX
 KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
 KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
 KW organ transplant rejection disease; lymphoma; pancreatic disease;
 KW autoimmune disease; inflammatory disease; arthritis; binding site.
 XX
 OS Homo sapiens.
 XX
 PH Key Location/Qualifiers
 FT Misc-difference 147
 FT /label= unknown
 FT /note= "encoded by TYC"
 FT Misc-difference 151
 FT /label= unknown
 FT /note= "encoded by TYC"
 XX
 XX WO9945031-A2.
 XX
 XX 10-SEP-1999.
 XX
 PF 03-MAR-1999; 99WO-US004583.
 XX
 PR 03-MAR-1998; 98US-00034607.
 PR 03-FEB-1999; 99US-00244253.
 XX
 PA (ABGE-) ABGENIX INC.
 XX
 XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
 PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;
 XX
 XX WPI; 1999-540816/45.
 DR N-PSDB; AAZ20404.

```
XX New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
XX Claim 60; Fig 28; 245pp; English.
XX
XX This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 202 AA;

Query Match 90.0%; Score 898; DB 2; Length 202;
Best Local Similarity 92.1%; Pred. No. 3.6e-56;
Matches 176; Conservative 3; Mismatches 10; Indels 2; Gaps 1;

Qy 2 ETLSLTCAVYGSFSGYVWSIRPPGKGLWIGETINHSNSTNPNLSKSRVTISVDTSK 61
Db 4 ETLSLTCAVYGSFSGYVWSIRPPGKGLWIGETINHSNSTNPNLSKSRVTISVDTSK 63
Qy 62 NQPSLKLSSVTAADTAVYVCARGGTTVTFDAF--DIMGGQTMVTVSSGSASAPTLFPLVS 119
Db 64 NQPSLKLSSVTAADTAVYVCARGAEEYVYVGGMDVMGQGTTVTVSSGSASAPTLFPLVS 123
Qy 120 CENSPTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFPSVLRGGKYAATSQVLL 179
Db 124 CENSPTSSTSSVAVGCLAQDFLPDXITFPKWKYKNNSDISSTRGPFPSVLRGGKYAATSQVLL 183
Qy 180 PSKDVMOGTDE 190
Db 184 PSKDVMOGTDE 194

RESULT 4
AAY34300
ID AAY34300 standard; protein; 197 AA.
AC AAY34300;
XX
XX 19-NOV-1999 (first entry)
XX
XX IgM antibody CEM 10.1 G10 heavy chain sequence.
XX
XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
XX activated B-cell; monocyte; graft versus host disease; therapy; cancer;
XX organ transplant rejection disease; lymphoma; pancreatic disease;
XX autoimmune disease; inflammatory disease; arthritis; binding site.
XX
XX Homo sapiens.
XX
XX WO9945031-A2.
XX
XX 10-SEP-1999.
XX
XX 03-MAR-1999; 99WO-US004583.
XX
XX 03-MAR-1998; 98US-00034607.
XX 03-FEB-1999; 99US-00244253.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
XX Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
XX WPI; 1999-540816/45.

DR N-PSDB; AAZ20401.
XX New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
XX Claim 60; Fig 25; 245pp; English.
XX
XX This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 197 AA;

Query Match 88.2%; Score 880.5; DB 2; Length 197;
Best Local Similarity 90.6%; Pred. No. 6.1e-55;
Matches 173; Conservative 3; Mismatches 12; Indels 3; Gaps 2;

Qy 1 SETLSLTCAVYGSFSGYVWSIRPPGKGLWIGETINHSNSTNPNLSKSRVTISVDTS 60
Db 5 SETLSLTCTVYSGGSISSYYWNIRPPGKGLWIGETIYVYSGNSTNPNLSKSRVTISVDTS 64
Qy 61 KNQPSLKLSSVTAADTAVYVCARG-GTTVTDFADIMGGQTMVTVSSGSASAPTLFPLVS 119
Db 65 KNQPSLKLSSVTAADTAVYVCARDRGVAT--GFDYMGQGTTLVTVSSGSASAPTLFPLVS 122
Qy 120 CENSPTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFPSVLRGGKYAATSQVLL 179
Db 123 CENSPTSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPFPSVLRGGKYAATSQVLL 182
Qy 180 PSKDVMOGTDE 190
Db 183 PSKDVMOGTDE 193

RESULT 5
AAM23924
ID AAM23924 standard; protein; 596 AA.
AC AAM23924;
XX
XX 12-OCT-2001 (first entry)
XX
XX Human EST encoded protein SEQ ID NO: 1449.
XX
XX Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse;
XX tomato; monkey; dog; sea urchin; expressed sequence tag; EST;
XX diagnostics; forensic test; gene mapping; genetic disorder; biodiversity;
XX gene therapy; nutrition.
XX
XX Homo sapiens.
XX
XX WO200154477-A2.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-US002687.
XX
XX 25-JAN-2000; 2000US-00491404.
XX 17-JUL-2000; 2000US-00617746.
XX 03-AUG-2000; 2000US-00631451.
XX 15-SEP-2000; 2000US-00663870.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Qian XB, Wang Z, Chen R, Asundi V;
```

PI Cao Y, Drmanac RA, Zhang J, Werhman T;
XX WPI; 2001-476164/51.
DR N-PSDB; AAH98583.
XX Isolated polypeptide for treatment of diseases, diagnostics, raising
PT antibodies and research use.
XX
XX Claim 20; Page 1011-1012; 1275pp; English.
XX
XX The present invention provides the protein and coding sequences of novel
CC proteins from a variety of organisms, including human, dog, cat, horse,
CC cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea
CC urchin and tomato. These were derived from expressed sequence tags (ESTs)
CC from the organism of interest. They can be used in diagnostics,
CC forensics, gene mapping, identification of mutations, to assess
CC biodiversity and for nutritional purposes. The present sequence is a
CC protein of the invention
XX
XX Sequence 596 AA;

Query Match 72.1%; Score 720; DB 4; Length 596;
Best Local Similarity 73.4%; Pred. No. 4.9e-43;
Matches 141; Conservative 16; Mismatches 31; Indels 4; Gaps 2;
Qy 3 TSLTCAVYGGSGFYWMIROPPGKGLWIGIBNHSG-STNYPNPKSRVTISVDTSK 61
Db 36 SLRLSCAAGFTFSYGMHVRQAPGKGLVWVRINTDGSSTSYADSVKGRFTISRDNK 95
Qy 62 NQPSLKLSVTAADTAVYYCARG---GTTVTFDADIWGGQTMVTVSSGSASAPTLPLV 118
Db 96 NTLYLQWNSLRAEDTAVYYCARADNCSSCYKCFDYWGQGLTVTVSSGSASAPTLPLV 155
Qy 119 SCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLRGKGYAATSOVL 178
Db 156 SCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLRGKGYAATSOVL 215
Qy 179 LPKSKDVMQGTDE 190
Db 216 LPKSKDVMQGTDE 227

RESULT 6
AAV08598
ID AAY08598 standard; protein; 223 AA.
XX
AC AAY08598;
XX
XX 05-AUG-1999 (first entry)
XX
XX Anti-human TNF-alpha monoclonal antibody H-chain protein.
XX
XX Monoclonal antibody; H chain; heavy chain; anti-human; TNF-alpha;
KW tumour necrosis factor; light chain; L chain.
XX
XX Homo sapiens.
XX
XX JP11127855-A.
PN
XX 18-MAY-1999.
PD
XX 27-OCT-1997; 97JP-00293994.
PF
XX 27-OCT-1997; 97JP-00293994.
PR
XX (NIHA) JAPAN ENERGY CORP.
XX
XX WPI; 1999-350318/30.
DR
DR N-PSDB; AAX77407.
XX
XX Recombinant anti-human TNF-alpha human monoclonal antibody - produced
PT stably with a high purity, and in large amounts.
XX

PS Claim 3; Page 12-13; 22pp; Japanese.
XX
XX This invention describes novel recombinant anti-human TNF-alpha human
CC monoclonal antibody consisting of a heavy (H) chain and a light (L)
CC chain. The recombinant anti-human TNF-alpha human monoclonal antibody can
CC be produced stably in a high purity and in a large amount
XX
XX Sequence 223 AA;
Query Match 71.8%; Score 717; DB 2; Length 223;
Best Local Similarity 75.1%; Pred. No. 2.9e-43;
Matches 142; Conservative 14; Mismatches 29; Indels 4; Gaps 2;
Qy 3 TSLTCAVYGGSGFYWMIROPPGKGLWIGIBNHSGSTN-YNPSLKSRVTISVDTSK 61
Db 17 SLRLSCAAGFTFSYGMHVRQAPGKGLWVAVISYDGSNKYADSVKGRFTISRDNK 76
Qy 62 NQPSLKLSVTAADTAVYYCARGTTVTFDADIWGGQTMVTVSSGSASAPTLPLVSC 121
Db 77 NTLYLQWNSLRAEDTAVYYCAKDSGDL---AFDIWGQGTMTVTSSGSASAPTLPLVSC 133
Qy 122 NSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLRGKGYAATSOVLPS 181
Db 134 NSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLRGKGYAATSOVLPS 193
Qy 182 KDVNQGTDE 190
Db 194 KDVNQGTDE 202
RESULT 7
ADL70776
ID ADL70776 standard; protein; 228 AA.
XX
AC ADL70776;
XX
XX 03-JUN-2004 (first entry)
XX
XX Anti-TNFalpha antibody VH region, SEQ ID 49.
XX
XX Immunosuppressive; Haemostatic; Antiallergic; Antiasthmatic;
KW Dermatological; Antiinflammatory; Antibacterial; Vasotropic;
KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnary;
KW Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antiatherosclerotic;
KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory; transferrin;
KW Tf; transferrin fusion protein; Tf fusion protein; anti-TNFalpha;
KW antibody; VH region.
XX
XX Unidentified.
XX
XX WO2004020588-A2.
PN
XX 11-MAR-2004.
PD
XX 28-AUG-2003; 2003WO-US026779.
PF
XX 30-AUG-2002; 2002US-0406977P.
PR
XX 10-MAR-2003; 2003US-00384060.
PR
XX 09-JUL-2003; 2003US-0485404P.
XX
XX (BIOR-) BIOREXIS PHARM CORP.
PA
XX Prior CP, Turner AJ, Sadeghi H;
PI
XX WPI; 2004-239175/22.
DR
XX Novel library containing several fusion proteins each of which comprises
PT first transferrin polypeptide fused to at least one second peptide,
PT useful for screening for transferrin fusion protein having the particular
PT activity.
XX
XX Example 8; SEQ ID NO 49; 243pp; English.
PS
XX

CC The present invention relates to a library (I) of modified fusion
 CC proteins of transferrin (Tf) and therapeutic proteins with increased
 CC serum half-life or serum stability. Preferred fusion proteins include
 CC those modified so that the Tf moiety exhibits no or reduced
 CC glycosylation, iron binding and/or Tf receptor binding. The transferrin
 CC fusion proteins are useful for treating, preventing or ameliorating
 CC disorders or diseases of endocrine system, nervous system, immune system,
 CC respiratory system, cardiovascular system, diseases and/or disorders
 CC relating to cell proliferation, and/or diseases or disorders relating to
 CC blood. The modified fusion proteins are useful in diagnosis, prognosis,
 CC prevention and/or treatment of autoimmune disorders; diseases and
 CC disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia
 CC and thrombocytopenia); allergic reactions such as allergic asthma,
 CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and
 CC eczema; inflammatory conditions e.g., inflammation associated with
 CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
 CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders
 CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel
 CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
 CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
 CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The
 CC fusion protein is also useful as an adjuvant to enhance antibacterial or
 CC antifungal immune responses, antiparasitic immune responses, etc. The
 CC fusion protein is also useful for treating monoclonal gammopathy of
 CC undetermined significance (MGUS), Waldenström's disease, plasmacytomas,
 CC adult respiratory distress syndrome, for stimulating wound repair, for
 CC preventing or treating infections of joints, bones, skin, etc. The fusion
 CC protein is also useful for treating or preventing thrombosis, myocardial
 CC infarction, cancers, thrombocytopenia, sickle cell anaemia,
 CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
 CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf
 CC and a specific example of a SCA that can be fused to Tf is anti-tumour
 CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence
 CC from an anti-TNFalpha antibody.

XX Sequence 228 AA;

Query Match 71.4%; Score 712.5; DB 8; Length 228;
 Best Local Similarity 73.1%; Pred. No. 6.2e-43;
 Matches 144; Conservative 13; Mismatches 25; Indels 15; Gaps 3;
 QY 3 TSLTCAVYGGFSGYYSWIRQPGKLEWTEIN-HSGSTNTNPSLKSRTVTSVDTSK 61
 Db 17 SLRUSCAASGFTFSYVWVRQAPGKLEWVSGISGGGYSYVADSVKGRFTISRDNM 76
 QY 62 NQFSLKLSVTAADTAVYTCAR-----GGTTVTDFADTWGGTQVTVYSSGSASAPT 113
 Db 77 NTVLYQWNSLRADTAVYTCALNSRLSGGT-----FDIWGGTQVTVYSSGSASAPT 130
 QY 114 LPPLVSCNSPDSSTSSAVGCLAQDFLPDSITFSWKYKXNDSISSTRGFPVLRGGKYAA 173
 Db 131 LPPLVSCNSPDSSTSSAVGCLAQDFLPDSITFSWKYKXNDSISSTRGFPVLRGGKYAA 190
 QY 174 TSQVLLPSKDVWQGTDE 190
 Db 191 TSQVLLPSKDVWQGTDE 207

RESULT 8

ADL70773

ID ADL70773 standard; protein; 223 AA.

XX AC ADL70773;

XX DT 03-JUN-2004 (first entry)

XX DE Anti-TNFalpha antibody VH region, SEQ ID 46.

XX Immunosuppressive; Haemostatic; Antiallergic; Antiaesthetic;
 KW Dermatological; Antinflammatory; Antibacterial; Vasotropic;
 KW Nephrotropic; Neuroprotective; Cytostatic; Cerebroprotective; Vulnary;
 KW Antiparkinsonian; Nootropic; Cardiant; Antianaemic; Antiatherosclerotic;
 KW Thrombolytic; Anticoagulant; Gastrointestinal; Respiratory;

KW Tf: transferrin fusion protein; Tf fusion protein; anti-TNFalpha;
 XX antibody; VH region.

XX Unidentified.

XX WO2004020588-A2.

XX PD 11-MAR-2004.

XX 28-AUG-2003; 2003WO-US026779.

XX 30-AUG-2002; 2002US-0406977P.

XX 10-MAR-2003; 2003US-00384060.

XX 09-JUL-2003; 2003US-0485404P.

XX (BIOR-) BIOREXIS PHARM CORP.

XX Prior CP, Turner AJ, Sadeghi H;

XX WPI; 2004-239175/22.

XX Novel library containing several fusion proteins each of which comprises
 PT first transferrin polypeptide fused to at least one second peptide,
 PT useful for screening for transferrin fusion protein having the particular
 PT activity.

XX Example 8; SEQ ID NO 46; 243pp; English.

CC The present invention relates to a library (I) of modified fusion
 CC proteins of transferrin (Tf) and therapeutic proteins with increased
 CC serum half-life or serum stability. Preferred fusion proteins include
 CC those modified so that the Tf moiety exhibits no or reduced
 CC glycosylation, iron binding and/or Tf receptor binding. The transferrin
 CC fusion proteins are useful for treating, preventing or ameliorating
 CC disorders or diseases of endocrine system, nervous system, immune system,
 CC respiratory system, cardiovascular system, diseases and/or disorders
 CC relating to cell proliferation, and/or diseases or disorders relating to
 CC blood. The modified fusion proteins are useful in diagnosis, prognosis,
 CC prevention and/or treatment of autoimmune disorders; diseases and
 CC disorders of haematopoietic cells (e.g., leukopenia, neutropenia, anaemia
 CC and thrombocytopenia); allergic reactions such as allergic asthma,
 CC anaphylaxis, IgE-mediated allergic reactions such as asthma, rhinitis and
 CC eczema; inflammatory conditions e.g., inflammation associated with
 CC infection (e.g., septic shock, sepsis), ischaemia-reperfusion injury,
 CC nephritis, Crohn's disease, multiple sclerosis, respiratory disorders
 CC (asthma and allergy), gastrointestinal disorders (inflammatory bowel
 CC disease), cancers (e.g., gastric, ovarian, lung, bladder), CNS disorders
 CC (multiple sclerosis, stroke, traumatic brain injury, neurodegenerative
 CC disorders such as Parkinson's disease, Alzheimer's disease), etc. The
 CC fusion protein is also useful as an adjuvant to enhance antibacterial or
 CC antifungal immune responses, antiparasitic immune responses, etc. The
 CC fusion protein is also useful for treating monoclonal gammopathy of
 CC undetermined significance (MGUS), Waldenström's disease, plasmacytomas,
 CC adult respiratory distress syndrome, for stimulating wound repair, for
 CC preventing or treating infections of joints, bones, skin, etc. The fusion
 CC protein is also useful for treating or preventing thrombosis, myocardial
 CC infarction, cancers, thrombocytopenia, sickle cell anaemia,
 CC glomerulonephritis, cardiac arrest, edema, pulmonary embolism,
 CC atherosclerosis, etc. Single chain antibodies (SCA) can be fused to Tf
 CC and a specific example of a SCA that can be fused to Tf is anti-tumour
 CC necrosis factor (TNF) alpha. The present sequence is a VH region sequence
 CC from an anti-TNFalpha antibody.

XX Sequence 223 AA;

Query Match 71.2%; Score 711; DB 8; Length 223;

Best Local Similarity 74.6%; Pred. No. 7.7e-43;

Matches 141; Conservative 14; Mismatches 30; Indels 4; Gaps 2;

OY 3 TSLTCAVYGGFSGYYSWIRQPGKLEWTEIN-HSGSTNTNPSLKSRTVTSVDTSK 61

Db 17 SLRUSCAASGFTFSYVWVRQAPGKLEWVSGISGGGYSYVADSVKGRFTISRDNM 76

Qy 62 NQFSLKLSVTAADTAVYTCARGGTTVTDFADFWGQGTWTVTVSSGSASAPTLPLVSC 121
Db 77 NTLYLQWNSLRAEDTAVYTCARGGDL---AFDIWGQGTWTVTVSSGSASAPTLPLVSC 133
Qy 122 NSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQVLLPS 181
Db 134 NSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQVLLPS 193
Qy 182 KDVMQGTDE 190
Db 194 KDVMQGTDE 202
RESULT 9
ADF69305
ID ADF69305 standard; protein; 266 AA.
AC ADF69305;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human lung specific protein sequence SEQ ID NO:62.
XX
KW human; lung specific nucleic acid; lung specific protein; lung cancer;
KW cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003102137-A2.
XX
PD 11-DEC-2003.
XX
XX 30-MAY-2003; 2003WO-US016810.
XX
PR 31-MAY-2002; 2002US-0385301P.
XX
PA (DIAD-) DIADEXUS INC.
XX
PI Chen S, Macina RA, Sun Y, Liu C, Turner LR;
XX
DR WPI; 2004-053457/05.
XX
XX New human lung specific nucleic acid, useful for preparing a composition
PT for diagnosing or treating lung cancer.
PT
XX Claim 11; SEQ ID NO 62; 221pp; English.
XX
CC The present invention describes a human lung specific nucleic acid
CC molecule. Also described: (1) a method for determining the presence of a
CC lung specific nucleic acid (LSNA) in a sample; (2) a vector comprising
CC the nucleic acid molecule; (3) a host cell comprising the vector; (4) a
CC method for producing a polypeptide encoded by the nucleic acid molecule;
CC (5) a polypeptide encoded by the nucleic acid molecule; (6) an antibody
CC or its fragment that specifically binds to the polypeptide; (7) a method
CC for determining the presence of a lung specific protein in a sample; (8)
CC a method for diagnosing and monitoring the presence and metastases of
CC lung cancer in a patient; (9) a kit for detecting a risk of cancer or
CC presence of cancer in a patient comprising a means for determining the
CC presence the nucleic acid molecule or polypeptide in a sample of a
CC patient; (10) a method of treating a patient with lung cancer; and (11) a
CC vaccine comprising the polypeptide or the nucleic acid encoding the
CC polypeptide. Human LSNA molecules and related proteins have cytostatic
CC activity, and can be used in gene therapy. They are useful for preparing
CC a composition for diagnosing or treating lung cancer. The present
CC sequence represents a human lung specific protein, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 266 AA;

Query Match 69.5%; Score 693.5; DB 8; Length 266;
Best Local Similarity 72.6%; Pred. No. 1.6e-41;
Matches 138; Conservative 16; Mismatches 35; Indels 1; Gaps 1;

Qy 2 ETLSLTCVYGGSPGSGYVWIRQPPGKGLWIGBINHSGS-TNYPNLSKSRVTISVDT 60
Db 27 ESLKISCKSGSYFTSYWIGVQRQMPGKGLWGLIYPGDSDRYSFQGVITISADKS 86
Qy 61 KNQFSLKLSVTAADTAVYTCARGGTTVTDFADFWGQGTWTVTVSSGSASAPTLPLVSC 120
Db 87 ISTAYLQWNSLRAEDTAVYTCARGGDL---AFDIWGQGTWTVTVSSGSASAPTLPLVSC 146
Qy 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQVLLP 180
Db 147 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLRGGKYAATSQVLLP 206
Qy 181 SKDVMQGTDE 190
Db 207 SKDVMQGTDE 216
RESULT 10
AAW71880
ID AAW71880 standard; protein; 588 AA.
XX
AC AAW71880;
XX
DT 18-JAN-1999 (first entry)
XX
DE Anti-human Fas humanised antibody CH11 heavy chain HmuH.
XX
KW Humanised antibody; Fas; CH11; monoclonal antibody; MAb; apoptosis;
KW autoimmune disease; rheumatoid arthritis; therapy; human;
KW antibody engineering.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..19
FT /label= Sig_peptide
FT Protein 20..588
FT /label= Mat_protein
FT Region 50..54
FT /label= CDR1
FT /note= "complementarity determining region 1 from CH11
FT heavy chain"
FT Region 69..84
FT /label= CDR2
FT /note= "complementarity determining region 2 from CH11
FT heavy chain"
FT Region 118..124
FT /label= CDR3
FT /note= "complementarity determining region 3 from CH11
FT heavy chain"
XX
PN EP866131-A2.
XX
XX 23-SEP-1998.
XX
XX 20-MAR-1998; 98EP-00302113.
XX
XX 21-MAR-1997; 97JP-00067938.
XX (SANY) SANKYO CO LTD.
PI Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;
XX
XX WPI; 1998-482965/42.
DR N-PSDB; AAV61363.
XX
PT Production of anti-Fas protein humanised antibodies - for use in inducing
PT apoptosis on Fas expressing cells in the treatment of auto-immune
XX diseases, especially rheumatoid arthritis.
XX Claim 21; Page 105-107; 187pp; English.
XX


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FT Region 118..124
FT /label= CDR3
FT /note= "complementarity determining region 3 from .CH11
FT heavy chain"
PN EP866131-A2.
XX
XX
XX 23-SEP-1998.
PD
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XX 20-MAR-1998; 98EP-00302113.
PF
XX
XX 21-MAR-1997; 97JP-00067938.
PR
XX
XX (SANY ) SANKYO CO LTD.
PA
XX
XX Serizawa N, Haruyama H, Takahashi T, Nakahara K, Yonehara S;
XX WPI; 1998-482965/42.
XX N-PSDB; AAV61364.
DR
DR
XX
XX
XX Production of anti-Fas protein humanised antibodies - for use in inducing
PT apoptosis on Fas expressing cells in the treatment of auto-immune
PT diseases, especially rheumatoid arthritis.
XX
XX
XX Claim 22; Page 111-113; 187pp; English.
PS
XX
XX This is the amino acid sequence of a humanised anti-Fas antibody CH11
CC heavy chain, designated HmuM. HmuM is based on the heavy chain (see
CC AA71888) of murine anti-human Fas monoclonal antibody CH11. The
CC humanised sequence was designed following selection of donor residues
CC from CH11 to be grafted onto acceptor molecule 21.28*CL. 2 Heavy chain
CC sequences (see AA71880-81) have been designed, and each can be used in
CC combination with any of 4 light chain sequences (see AA71876-79) to
CC provide novel, claimed humanised CH11 IGM antibodies that lack a J chain.
CC These humanised anti-human Fas antibodies are capable of inducing
CC apoptosis in cells expressing Fas (e.g. synovocytes) and are useful in
CC the treatment of autoimmune disease and chronic rheumatoid arthritis. DNA
CC sequences encoding the humanised antibodies are claimed, as are vectors
CC such as pHmuM1-1 including the HmuM nucleotide sequence (see AAV61364),
CC and host cells such as Escherichia coli pHmuM1-1 (FERM BP-5864)
XX
XX Sequence 588 AA;
SQ
Query Match 67.6%; Score 675; DB 2; Length 588;
Best Local Similarity 69.3%; Pred. No. 7.6e-40;
Matches 131; Conservative 22; Mismatches 30; Indels 6; Gaps 2;
QY 3 TSLTCAVYGGSFSGYYSWIRQPPGKLEWIGEI-NHSGSTNYNPSLKSRVTISVDTSK 61
Db 36 SVKVSCKASGYTFDYNHWHVQAHGKSLWVGYYIPYNGGTGYNQKPKSKATLTVDNSA 95
QY 62 NQFSLKLSSTVAADTAVVYCARGGTTVTDFADIWGQGTMTVTVSSGSASAPTLPLVSC 121
Db 96 STAYMELSLSESDTAVYICAR-----SYIAMDYWGQGTTLTVSSGSASAPTLPLVSC 150
QY 122 NSPSTSSVAVGCLAQDFLPDSITFSWKYKKNDSISSTRGPPSVLRGGKYAATSOVLPS 181
Db 151 NSPSTSSVAVGCLAQDFLPDSITFSWKYKKNDSISSTRGPPSVLRGGKYAATSOVLPS 210
QY 182 KDVNQGTDE 190
Db 211 KDVNQGTDE 219
RESULT 15
AAB12918
ID AAB12918 standard; protein; 588 AA.
XX
XX AAB12918;
AC
XX
XX 16-NOV-2000 (first entry)
DT
XX
XX Anti-human Fas immunoglobulin M heavy chain protein sequence SEQ ID #88.
```

```
XX
XX Antirheumatic agent; immunoglobulin M; IgM; apoptosis inducer;
KW immunosuppression; autoimmune disease; treatment; rheumatism;
KW anti-Fas antibody.
XX
XX Synthetic.
XX
XX JP2000154149-A.
PN
XX
XX 06-JUN-2000.
PD
XX
XX 17-SEP-1999; 99JP-00263984.
PF
XX
XX 18-SEP-1998; 98JP-00264598.
PR
XX
XX (SANY ) SANKYO CO LTD.
PA
XX
XX WPI; 2000-454476/40.
XX N-PSDB; AAA78272.
DR
DR
XX
XX
XX Anti-human Fas humanizing antibody-containing antirheumatic agents.
PT
XX
XX Claim 1; Page 80-81; 109pp; Japanese.
PS
XX
XX The present invention relates to antirheumatic agents which comprise as
CC active ingredients an immunoglobulin M (IgM) protein. The IgM protein
CC does not include a J segment, has apoptosis inducing activity, and
CC consists of a light and heavy chain polypeptide produced synthetically.
CC The agents of the invention exhibit antirheumatic and immunosuppressive
CC activity and can be used to treat autoimmune diseases, especially
CC rheumatism. The IgM molecule used in the invention has human Fas-antigen
CC binding properties. Included in the invention are nucleotide sequences of
CC the IgM light and heavy chains (see AAA78267-A78272) and the
CC corresponding protein sequences (see AAB12913-B12918 and AAB12919), and
CC nucleotide sequences of the humanised anti-human Fas Ig CH11 (see
CC AA78202-A78206) and protein sequences (see AAB12908-B12910). Also
CC included are anti-human Fas antibody CDR peptides (AAB12902-B12907).
CC Primers specific for the anti-human Fas antibody, light, heavy and kappa
CC chains used in the invention are represented by sequences AAA78213-
CC A78266. Primers used for sequencing the human Ig DNA used in the
CC invention are represented by sequences AAA78277-A78318 and AAA78335-
CC A78337, while humanised anti-Fas Ig DNA sequencing primers are
CC represented by sequences AAA78321-A78334 and AAA78338-A78367. Primer
CC sequences AAA78207-A78212 are specific for murine Ig DNA, and are used in
CC the production of the agent of the invention
XX
XX Sequence 588 AA;
SQ
Query Match 67.6%; Score 675; DB 3; Length 588;
Best Local Similarity 69.3%; Pred. No. 7.6e-40;
Matches 131; Conservative 22; Mismatches 30; Indels 6; Gaps 2;
QY 3 TSLTCAVYGGSFSGYYSWIRQPPGKLEWIGEI-NHSGSTNYNPSLKSRVTISVDTSK 61
Db 36 SVKVSCKASGYTFDYNHWHVQAHGKSLWVGYYIPYNGGTGYNQKPKSKATLTVDNSA 95
QY 62 NQFSLKLSSTVAADTAVVYCARGGTTVTDFADIWGQGTMTVTVSSGSASAPTLPLVSC 121
Db 96 STAYMELSLSESDTAVYICAR-----SYIAMDYWGQGTTLTVSSGSASAPTLPLVSC 150
QY 122 NSPSTSSVAVGCLAQDFLPDSITFSWKYKKNDSISSTRGPPSVLRGGKYAATSOVLPS 181
Db 151 NSPSTSSVAVGCLAQDFLPDSITFSWKYKKNDSISSTRGPPSVLRGGKYAATSOVLPS 210
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Db 211 KDVNQGTDE 219
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 100.828 Seconds
(without alignments)
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Title: US-09-784-950-33

Perfect score: 998

Sequence: 1 SEILSLTCAVYGSFSGYV.....YAATSVQLFSDVMQGTDE 190

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Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	686	68.7	595	15	US-10-108-260A-4112
2	678.5	68.0	627	13	US-10-047-542-47
3	666	66.7	533	15	US-10-104-047-3224
4	624	62.5	229	10	US-09-972-656-82
5	623	62.4	223	10	US-09-972-656-66
6	616.5	61.8	230	10	US-09-972-656-72
7	584.5	58.6	466	15	US-10-292-088-86
8	581.5	58.3	466	15	US-10-292-088-70
9	579.5	58.1	580	14	US-10-310-719-37
10	575	57.6	580	14	US-10-310-719-35
11	570.5	57.2	466	15	US-10-292-088-30
12	564.5	56.6	464	15	US-10-292-088-22
13	556	55.7	221	10	US-09-972-656-80
14					Sequence 4112, Ap
15					Sequence 47, Appl
16					Sequence 3224, Ap
17					Sequence 82, Appl
18					Sequence 66, Appl
19					Sequence 72, Appl
20					Sequence 86, Appl
21					Sequence 70, Appl
22					Sequence 37, Appl
23					Sequence 35, Appl
24					Sequence 30, Appl
25					Sequence 28, Appl

14	555.5	55.7	179	15	US-10-309-762-171	Sequence 171, App
15	551	55.2	241	16	US-10-684-109-106	Sequence 106, App
16	547	54.8	241	16	US-10-684-109-71	Sequence 71, Appl
17	540	54.1	239	16	US-10-684-109-100	Sequence 100, App
18	539	54.0	241	16	US-10-684-109-88	Sequence 88, Appl
19	526	52.7	173	15	US-10-309-762-173	Sequence 173, App
20	521.5	52.3	193	15	US-10-264-049-4331	Sequence 4331, Ap
21	518	51.9	119	14	US-10-078-958-3	Sequence 3, Appli
22	515.5	51.7	172	14	US-10-153-382-21	Sequence 21, Appl
23	515	51.6	152	9	US-09-187-693-68	Sequence 68, Appl
24	512.5	51.4	125	15	US-10-371-942-110	Sequence 110, App
25	512	51.3	235	16	US-10-684-109-112	Sequence 112, App
26	511.5	51.3	254	10	US-09-880-748-1659	Sequence 1659, Ap
27	511.5	51.3	254	15	US-10-293-418-1659	Sequence 1659, Ap
28	511	51.2	122	15	US-10-360-828-63	Sequence 63, Appl
29	511	51.2	229	9	US-09-974-449-37	Sequence 37, Appl
30	509.5	51.1	120	14	US-10-078-958-4	Sequence 4, Appli
31	509	51.0	250	14	US-10-194-975-110	Sequence 110, App
32	504.5	50.6	487	9	US-09-800-729-145	Sequence 145, App
33	504.5	50.6	487	11	US-09-833-245-2194	Sequence 2194, Ap
34	504	50.5	249	10	US-09-880-748-1321	Sequence 1321, Ap
35	504	50.5	249	15	US-10-293-418-1321	Sequence 1321, Ap
36	504	50.5	253	10	US-09-880-748-1333	Sequence 1333, Ap
37	504	50.5	253	15	US-10-293-418-1333	Sequence 1333, Ap
38	499.5	50.1	476	9	US-09-758-173-12	Sequence 12, Appl
39	499.5	50.1	476	9	US-09-948-429B-12	Sequence 12, Appl
40	499.5	50.1	476	13	US-10-124-905-12	Sequence 12, Appl
41	499.5	50.1	476	14	US-10-124-807-12	Sequence 12, Appl
42	499.5	50.1	476	14	US-10-291-532-12	Sequence 12, Appl
43	497.5	49.8	250	10	US-09-880-748-1413	Sequence 1413, Ap
44	497.5	49.8	250	15	US-10-293-418-1413	Sequence 1413, Ap
45	496.5	49.7	476	9	US-09-758-173-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1

US-10-108-260A-4112

; Sequence 4112, Application US/10108260A

; Publication No. US20040005560A1

; GENERAL INFORMATION:

; APPLICANT: HELIX RESEARCH INSTITUTE

; TITLE OF INVENTION: No. US20040005560A1el full length cDNA

; FILE REFERENCE: HI-A0106

; CURRENT APPLICATION NUMBER: US/10/108,260A

; CURRENT FILING DATE: 2002-03-27

; NUMBER OF SEQ ID NOS: 5458

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4112

; LENGTH: 595

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-108-260A-4112

Query Match 68.7%; Score 686; DB 15; Length 595;

Best Local Similarity 71.6%; Pred. No. 5.9e-44;

Matches 136; Conservative 17; Mismatches 35; Indels 2; Gaps 2;

Qy	3	TLSLTCAVYGSFSGYVMSWTRPPGKGLWIGWGHNSGTSN--YNPSLKSRVTISVDTSK	61
Db	37	SLRLSCAASGFTFSNFAMHWVRQAPGKGLVSTVSISSNGRKYYGESVKGRTISRDSK	96
Qy	62	NQFSLKSSVTAADTAVYVYARGGTTVTFFD--AFDIWGQGTMTVTVSSSGSASAPTLPPLVSC	120
Db	97	NTLFLQWGLSLREDTAVYVYARGHSIDNYHYGVGVWQGTVTTVSSSGSASAPTLPPLVSC	156
Qy	121	ENSPDSTSSVAVGCLAQDFLPDSITTFSWKYKNSDISSTRGFPSPVLRGGKYAATSQVLLP	180
Db	157	ENSPDSTSSVAVGCLAQDFLPDSITTFSWKYKNSDISSTRGFPSPVLRGGKYAATSQVLLP	216
Qy	181	SKDVMQGTDE	190

Db 217 SKDVMQGTDE 226

RESULT 2

US-10-047-542-47

Sequence 47, Application US/10047542

Publication No. US20020168367A1

GENERAL INFORMATION:

APPLICANT: LARRICK, JAMES W.

APPLICANT: WYCOFF, KEITH L.

TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL

FILE REFERENCE: 030905.0004.C1P1

CURRENT APPLICATION NUMBER: US/10/047,542

CURRENT FILING DATE: 2001-10-26

PRIOR APPLICATION NUMBER: PCT/US01/13932

PRIOR FILING DATE: 2001-04-28

PRIOR APPLICATION NUMBER: 60/200,298

PRIOR FILING DATE: 2000-04-28

NUMBER OF SEQ ID NOS: 101

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 47

LENGTH: 627

TYPE: PRT

ORGANISM: Homo sapiens

US-10-047-542-47

Query Match 68.0%; Score 678.5; DB 13; Length 627;

Best Local Similarity 66.7%; Pred. No. 2.3e-43;

Matches 134; Conservative 20; Mismatches 34; Indels 13; Gaps 2;

QY 3 TSLSLTCAVYGGSFSGYVSWIRQPPGKGLWIGI- INHSGSTNPNPGLKSRVTISVDTSK 61

Db 36 SVKVSCKASGGTFSYAISWVRQAPGGGLEWGGIIPFGTANYAOKFQGRVITADEST 95

QY 62 NQFSLKLSVTAADTAVYVCARGGTTVTFDA-----FDWGGTMTVTVSSGSA 109

Db 96 STAYMELSLRLSEDTAVYCAKTIIGLPGYSSGWYPNSDYVYGGMDVWGGTMTVTVSSGSA 155

QY 110 SAPFLPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRG 169

Db 156 SAPFLPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRG 215

QY 170 KYAATSOVLLPSKDVMOGTDE 190

Db 216 KYAATSOVLLPSKDVMOGTDE 236

RESULT 3

US-10-104-047-3224

Sequence 3224, Application US/10104047

Publication No. US20030236392A1

GENERAL INFORMATION:

APPLICANT: HELIX RESEARCH INSTITUTE

TITLE OF INVENTION: NO. US20030236392A1el full length cDNA

FILE REFERENCE: HI-A0105

CURRENT APPLICATION NUMBER: US/10/104,047

CURRENT FILING DATE: 2002-03-25

PRIOR APPLICATION NUMBER:

PRIOR FILING DATE:

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 3224

LENGTH: 533

TYPE: PRT

ORGANISM: Homo sapiens

US-10-104-047-3224

Query Match 66.7%; Score 666; DB 15; Length 533;

Best Local Similarity 70.5%; Pred. No. 1.7e-42;

Matches 134; Conservative 13; Mismatches 41; Indels 2; Gaps 1;

QY 3 TSLSLTCAVYGGSFSGYVSWIRQPPGKGLWIGI- INHSGSTNPNPGLKSRVTISVDTSKN 62

Db 36 SLRLSCAASGFDVSSNYSWVRQSPGKGPSEWATMYGGCTTYAESVKGRFTVSRDGSQN 95

QY 63 QPSLKLSVTAADTAVYVCARGGTTV--TFDAFDWGGTMTVTVSSGSAASAPTLFPLVSC 120

Db 96 TLYLEMSLSRDPDTAVYVCVRDHRNYADTSPYGRKWGGTLVTVSSGSAASAPTLFPLVSC 155

QY 121 ENSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGKYAATSQVLLP 180

Db 156 ENSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVLRGKYAATSQVLLP 215

QY 181 SKDVMQGTDE 190

Db 216 SKDVMQGTDE 225

RESULT 4

US-09-972-656-82

Sequence 82, Application US/09972656

Publication No. US20030099647A1

GENERAL INFORMATION:

APPLICANT: Deshpande, Rajendra

APPLICANT: Tsai, Mei-Mei

TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

TITLE OF INVENTION: Neutralizing Activity

FILE REFERENCE: A-799

CURRENT APPLICATION NUMBER: US/09/972,656

CURRENT FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PatentIn version 3.0

SEQ ID NO 82

LENGTH: 229

TYPE: PRT

ORGANISM: Homo sapiens

US-09-972-656-82

Query Match 62.5%; Score 624; DB 10; Length 229;

Best Local Similarity 64.9%; Pred. No. 1.1e-39;

Matches 124; Conservative 19; Mismatches 38; Indels 10; Gaps 4;

QY 1 SETLSLTCAVYGGSFSGYVSWIRQPPGKGLWIGI- INHSGSTNPNPGLKSRVTISVDT 60

Db 15 SETLSLTCAVYGGSFSGYVSWIRQPPGKGLWIGI- INHSGSTNPNPGLKSRVTISVDT 74

QY 61 KNQFSLKLSVTAADTAVYVCARGGTTVTFDA-----FDWGGTMTVTVSSGSAASAPTL 114

Db 75 KNQFSLKLSVTAADTAVYVCARGGTTVTFWGSRPKGYFDWGGTMTVTVSSASTKGPSV 134

QY 115 FPLVSCNSPDTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGFPSPVL- GGYAA 173

Db 135 FPLAPSSKSTSG-GTAALGCLVKDYRPEPVTSM--NSGALTSGVHTFPAVLQSSGLYSL 191

QY 174 TSQVLLPSKDV 184

Db 192 SSVTVTPSSSL 202

RESULT 5

US-09-972-656-66

Sequence 66, Application US/09972656

Publication No. US20030099647A1

GENERAL INFORMATION:

APPLICANT: Deshpande, Rajendra

APPLICANT: Tsai, Mei-Mei

TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma

TITLE OF INVENTION: Neutralizing Activity

FILE REFERENCE: A-799

CURRENT APPLICATION NUMBER: US/09/972,656

CURRENT FILING DATE: 2001-10-05

NUMBER OF SEQ ID NOS: 135

SOFTWARE: PatentIn version 3.0

SEQ ID NO 66

LENGTH: 223


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; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-656-66

Query Match      62.4%; Score 623; DB 10; Length 223;
Best Local Similarity 66.5%; Pred. No. 1.3e-39;
Matches 123; Conservative 17; Mismatches 41; Indels 4; Gaps 3

Qy 1 SETLSLTCAYVGGSFSGYYWIRQPPCKGLEWIGEINHSGSTNYPNPKSRVTISVDTS 60
Db 15 SETLSLTCAYVGGSFSGYYWIRQPPCKGLEWIGEINHSGSTNYPNPKSRVTISVDTS 74
Qy 61 KNPQSLKLSSVTAADTAIVYVCARGGTTVTFADPWGQGTMTVTVSSGSASAPTLPLVSC 120
Db 75 KNPQSLKLSSVTAADTAIVYVCARGRARNRGRFDYWGQGTLLTVSSASTKGPSVFLAPS 134
Qy 121 ENSPDSSTSSVAVGCLAODFLPDSITFSWKYKNNSDISSTRGFPVSLR-CGKYAATSQVLL 179
Db 135 SKSTSG-GTAALGCLVKDYFFPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVTV 191
Qy 180 PSKDV 184
Db 192 PSSSL 196

RESULT 6
US-09-972-656-72
; Sequence 72, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 72
; LENGTH: 230
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-972-656-72

Query Match      61.8%; Score 616.5; DB 10; Length 230;
Best Local Similarity 64.6%; Pred. No. 4.2e-39;
Matches 124; Conservative 19; Mismatches 38; Indels 11; Gaps 5

Qy 1 SETLSLTCAYVGGSFSGYYWIRQPPCKGLEWIGEINHSGSTNYPNPKSRVTISVDTS 60
Db 15 SETLSLTCAYVGGSFSGYYWIRQPPCKGLEWIGEINHSGSTNYPNPKSRVTISVDTS 74
Qy 61 KNPQSLKLSSVTAADTAIVYVCARG-GTTVTF-----DAPDWGQGTMTVTVSSGSASAPT 113
Db 75 KNPQSLKLSSVTAADTAIVYVCARDKGRSITIFGVVGSAGFDYWGQGTLLTVSSASTKGPS 134
Qy 114 LFLVSCNSPDSSTSSVAVGCLAODFLPDSITFSWKYKNNSDISSTRGFPVSLR-CGKYA 172
Db 135 VFPLAPSKSTSG-GTAALGCLVKDYFFPEPTVSW--NSGALTSGVHTFPAVLQSSGLY 191
Qy 173 ATSOVLPLPSKDV 184
Db 192 LSSVTVFPSSSL 203

RESULT 7
US-10-292-088-86
; Sequence 86, Application US/10292088
; Publication No. US2003021100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.

```



```
RESULT 12
US-10-292-088-22
; Sequence 22, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-22

Query Match      56.6%; Score 564.5; DB 15; Length 464;
Best Local Similarity 61.4%; Pred. No. 7.5e-35;
Matches 113; Conservative 21; Mismatches 45; Indels 5; Gaps 4;

Qy 1 SETSLTCAVYGGSPGYWWSWIRQPPGKGLWIGENHSGSTNNPGLKSRVTISVDTS 60
Db 34 SETSLTCTVSGGSISSYWIWQIPACKGLWIGRVTSGSTNNPGLKSRVTISVDTS 93

Qy 61 KNQFSLKSSVTAADTAIVYCARGTTFDPAFDIWGGQTMVTVSSGSASAPTLFPLV 179
Db 94 KNQFSLKSSVTAADTAIVYCARGLYRGY-GMDVWGQGTTVTVSSASTKGPSVFPLAPC 152

Qy 121 ENSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGKYAATSOV 179
Db 153 SRSTSE--STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSVTV 209

Qy 180 PSKD 183
Db 210 PSSN 213

RESULT 13
US-09-972-656-80
; Sequence 80, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-80

Query Match      55.7%; Score 556; DB 10; Length 221;
Best Local Similarity 62.0%; Pred. No. 1.6e-34;
Matches 116; Conservative 18; Mismatches 43; Indels 10; Gaps 5;

Qy 1 SETSLTCAVYGGSPGS--GYWWSWIRQPPGKGLWIGENHSGSTNNPGLKSRVTISVD 58
Db 15 SETSLTCAVSGGSISSGYWWSWIRQPPGKGLWIGYIYHSGSTYNNPGLKSRVTISVD 74
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Qy 59 TSKNQFSLKSSVTAADTAIVYCARGTTFDPAFDIWGGQTMVTVSSGSASAPTLFPLV 118
Db 75 RSKNQFSLKSSVTAADTAIVYCARGTTFDPAFDIWGGQTMVTVSSASTKGPSVFPLA 130

Qy 119 SCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-GGKYAATSOV 177
Db 131 PSSKSTSG-GTAAAGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSV 187

Qy 178 LLPSKDV 184
Db 188 TVPSSSL 194

RESULT 14
US-10-309-762-171
; Sequence 171, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; TITLE OF INVENTION: (CA IX) TUMOR ANTIGEN
; FILE REFERENCE: ABGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 171
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-171

Query Match      55.7%; Score 555.5; DB 15; Length 179;
Best Local Similarity 63.7%; Pred. No. 1.4e-34;
Matches 109; Conservative 17; Mismatches 38; Indels 7; Gaps 3;

Qy 1 SETSLTCAVYGGSPGYWWSWIRQPPGKGLWIGENHSGSTNNPGLKSRVTISVDTS 60
Db 9 SETSLTCTVSGGSISSYWWSWIRQPPGKGLWIGYIYSGSTYNNPGLKSRVTISVDTS 68

Qy 61 KNQFSLKSSVTAADTAIVYCARGTTFDPAFDIWGGQTMVTVSSGSASAPTLFPL 116
Db 69 KNQFSLKSSVTAADTAIVYCARQHSVSSVYIYGGMDVWGQGTTVTVSSASTKGPSVFP 128

Qy 117 LVSCENSPDSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR 167
Db 129 LAPCSRSTSE--STAALGCLVKDYFPPEPTVSW--NSGALTSGVHTFPAVLQ 176

RESULT 15
US-10-684-109-106
; Sequence 106, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: Devries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 6989.US.02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 106
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-106

Query Match          55.2%; Score 551; DB 16; Length 241;
Best Local Similarity 60.8%; Pred. No. 4.1e-34;
Matches 113; Conservative 22; Mismatches 41; Indels 10; Gaps 5;

Qy 1 SETLSLTCAVYGGFSGYMSWIRQPPGKGLEWIGEINHSGSTNYPNPKSRVTISV-D 58
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
36 SETLSLACTVSGGSISRYSRWIRQPPGKGLEWIGYVSGSYNPNPKSRVTISVASP 95
Qy 59 TSKNQPSLKLSSVTAADTAVYCARGGTTVTFDAFDINGOGTMVTVSSGSASAPLFLV 118
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
96 TSKNQPSLKLSSVTAADTAVYCARDKLGIG- ---DYWGQGTLVTVSSASTKGPSVPFLA 151
Qy 119 SCENSPSDTSSVAVGCLAQDPLPDSITFSWKYKNNSDISSTRGPPSVLR-GGKYAATSQV 177
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
152 PCSRSTSE-STALGCLVKDYFPEPVTVSW--NSGALTSGVHTFPAVLQSSGLYSLSSV 208
Qy 178 LLPSKD 183
Db ||| :
209 TVPSSN 214
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Search completed: March 8, 2005, 07:05:54
Job time : 100.828 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 20.8917 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-33
Perfect score: 998
Sequence: 1 SETLSUTCAVYGGSFSGYYW.....YAATSQVLLPSKDVQMGTDE 190

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	599.5	60.1	472	3	US-08-793-450-8
2	553	55.4	473	3	US-09-049-672A-4
3	515.5	51.7	172	4	US-09-472-087-7
4	515.5	51.7	172	4	US-09-472-087-7
5	509	51.0	832	3	US-08-630-820-7
6	509	51.0	832	4	US-09-273-453-7
7	504.5	50.6	487	4	US-09-800-729-145
8	499.5	50.1	476	3	US-08-487-550-12
9	499.5	50.1	476	4	US-09-526-098-12
10	499.5	50.1	476	4	US-09-383-916-12
11	496.5	49.7	476	3	US-08-487-550-4
12	496.5	49.7	476	4	US-09-526-098-4
13	496.5	49.7	476	4	US-09-383-916-4
14	495	49.6	139	4	US-09-203-768A-2
15	492.5	49.3	467	3	US-08-523-894-8
16	492.5	49.3	467	3	US-08-523-894-10
17	492.5	49.3	467	3	US-08-523-894-12
18	490.5	49.1	219	3	US-09-460-384-37
19	480.5	48.1	123	3	US-08-793-450-4
20	474	47.5	429	4	US-09-372-425A-6
21	472	47.3	467	4	US-08-030-175-42
22	469	47.0	467	4	US-08-030-175-41
23	466	46.7	118	3	US-09-025-769B-25
24	466	46.7	118	4	US-09-490-070A-25
25	466	46.7	118	4	US-09-490-153-25
26	466	46.7	118	4	US-09-490-324-25
27	466	46.7	447	4	US-09-372-425A-2

28	460	46.1	120	4	US-09-424-840B-20	Sequence 20, Appl
29	456.5	45.7	229	2	US-08-887-352B-20	Sequence 20, Appl
30	456.5	45.7	229	3	US-09-109-207C-20	Sequence 20, Appl
31	456.5	45.7	229	3	US-09-296-005-20	Sequence 20, Appl
32	456.5	45.7	229	4	US-09-920-171-20	Sequence 20, Appl
33	456.5	45.7	229	4	US-09-716-028-20	Sequence 20, Appl
34	456.5	45.7	229	4	US-10-113-996-20	Sequence 20, Appl
35	456.5	45.7	233	2	US-08-887-352B-25	Sequence 25, Appl
36	456.5	45.7	233	3	US-09-109-207C-25	Sequence 25, Appl
37	456.5	45.7	233	3	US-09-296-005-25	Sequence 25, Appl
38	456.5	45.7	233	4	US-09-920-171-25	Sequence 25, Appl
39	456.5	45.7	233	4	US-09-716-028-25	Sequence 25, Appl
40	456.5	45.7	233	4	US-10-113-996-25	Sequence 25, Appl
41	456.5	45.7	451	2	US-08-887-352B-14	Sequence 14, Appl
42	456.5	45.7	451	2	US-08-887-352B-16	Sequence 16, Appl
43	456.5	45.7	451	3	US-08-466-151-65	Sequence 65, Appl
44	456.5	45.7	451	3	US-09-109-207C-14	Sequence 14, Appl
45	456.5	45.7	451	3	US-09-109-207C-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-793-450-8
; Sequence 8, Application US/08793450
; Patent No. 6312690
; GENERAL INFORMATION:
; APPLICANT: EDELMAN, LENA
; APPLICANT: MARGARITTE, CHRISTEL
; APPLICANT: KACZOREK, MICHEL
; APPLICANT: CHABBIH, HASSAN
; TITLE OF INVENTION: MONOCLONAL RECOMBINANT ANTI-RHESUS D
; TITLE OF INVENTION:
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.S.
; STREET: 1755 SOUTH JEFFERSON DAVIS HIGHWAY, SUITE 400
; CITY: ARLINGTON
; STATE: VA
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/793,450
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 94/10566
; FILING DATE: 02-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: OBLON, NORMAN F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 660-118-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-413-3000
; TELEFAX: 703-413-2220
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 472 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-793-450-8

Query Match 60.1%; Score 599.5; DB 3; Length 472;
Best Local Similarity 63.2%; Pred No. 5.7e-46;
Matches 122; Conservative 17; Mismatches 37; Indels 17; Gaps 5;

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Qy 1 SETLSLTCVYGGSFSGYWSWIRQPGKGLWIGIEINHSGSTNPNPSLKSRVTISVDTS 60
Db 34 SETLSLTCVYGGSFSGYWSWIRQPGKGLWIGIEINHSGSTNPNPSLKSRVTISVDTS 93
Qy 61 KNPQSLKLSVTAADTAIVYICAR-----GTTVTDFADPDWQGTMTVTVSSGSASAP 112
Db 94 KNPQSLKLSVTAADTAIVYICARPEYKWKYHG-----DWFDPWQGTMTVTVSSASTKGP 148
Qy 113 TLPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-CGKY 171
Db 149 SVFPLAESSKSTSG-GTAALGCLVKDYFPBPVTVSW--NSGALTSGVHTTFFAVLQSSGLY 205
Qy 172 AATSOVLLPSKDV 184
Db 206 SLSSVTVTPSSSL 218
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RESULT 2
US-09-049-672A-4
; Sequence 4, Application US/09049672A
; Patent No. 6135941
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Lal, Preeti
; APPLICANT: Tang, Y. Tom
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice
; APPLICANT: Corley, Neil C.
; APPLICANT: Guegler, Karl J.
; APPLICANT: Baughn, Mariah R.
; TITLE OF INVENTION: HUMAN IMMUNE SYSTEM ASSOCIATED PROTEINS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA: US/09/049,672A
; APPLICATION NUMBER: 536
; FILING DATE: HEREWITH
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Cerrone, Michael C
; REGISTRATION NUMBER: 39,132
; REFERENCE/DOCKET NUMBER: PF-0497 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 473 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: PANCYTUT01
; CLONE: 1513264
; US-09-049-672A-4
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Query Match 55.4%; Score 553; DB 3; Length 473;
Best Local Similarity 60.1%; Pred. No. 8.9e-42;

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Matches 116; Conservative 20; Mismatches 41; Indels 16; Gaps 6;
Qy 1 SETLSLTCVYGGSFSGYWSWIRQPGKGLWIGIEINHSGSTNPNPSLKSRVTISVD 58
Db 34 SETLSLTCVYGGSFSGYWSWIRQPGKGLWIGIEINHSGSTNPNPSLKSRVTISVD 93
Qy 59 TSKNQPSLKLSSVTAADTAIVYICAR-----RGGTTVTDFADPDWQGTMTVTVSSGSASAP 112
Db 94 TSKNQPSLKLSSVTAADTAIVYICARDDVGLRGNY-----GMDVMGQGTTLTVSSASTKGP 149
Qy 113 TLPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR-CGKY 171
Db 150 SVFPLAESSKSTSG-GTAALGCLVKDYFPBPVTVSW--NSGALTSGVHTTFFAVLQSSGLY 206
Qy 172 AATSOVLLPSKDV 184
Db 207 SLSSVTVTPSSSL 219
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RESULT 3
US-09-472-087-7
; Sequence 7, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 7
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-7
```

Query Match 51.7%; Score 515.5; DB 4; Length 172;
Best Local Similarity 61.5%; Pred. No. 5.9e-39;
Matches 104; Conservative 20; Mismatches 38; Indels 7; Gaps 4;

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Qy 1 SETLSLTCVYGGSFSGYWSWIRQPGKGLWIGIEINHSGSTNPNPSLKSRVTISVD 58
Db 9 SQILSLTCTVSGGSISGHHWSWIRQHPGKLEWIGIYIYIGNTYNPSLKSRVTISVD 68
Qy 59 TSKNQPSLKLSSVTAADTAIVYICARGGTTVTDFADPDWQGTMTVTVSSGSASAPTLPLV 118
Db 69 TSKNQPSLKLSSVTAADTAIVYICAR--DSGDYIGIDVMGQGTTLTVSSASTKGPSVFPLA 126
Qy 119 SCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNSDISSTRGPPSVLR 167
Db 127 PCSRSTSE-STAALGCLVKDYFPBPVTVSW--NSGALTSGVHTTFFAVLQ 172
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```
RESULT 4
US-09-472-087-86
; Sequence 86, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
```

APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PFI
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: Patent in Ver. 2.1
SEQ ID NO 86
LENGTH: 172
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-86

Query Match 51.7%; Score 515.5; DB 4; Length 172;
Best Local Similarity 61.5%; Pred. No. 5.9e-39;
Matches 104; Conservative 20; Mismatches 39; Indels 7; Gaps 4;
Qy 1 SETLSLTCVAVGGSF--GYTWSMIRQPPGKLEWIGEHNSGTYNPNPSLKSRVTISVD 58
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 68
Qy 59 TSKNQFSLKSSVTAADTAVYYCAR--DSGDYGYGIDVWGQGTITVTSSASTKGPSPFLA 118
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 126
Qy 119 SCENSPSTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR 167
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 172

RESULT 5
US-08-630-820-7
Sequence 7, Application US/08630820
Patent No. 6008023
GENERAL INFORMATION:
APPLICANT: Oppfer, Martin
APPLICANT: BOSSLET, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,820
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19513676.4
FILING DATE: 11-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-630-820-7
Query Match 51.0%; Score 509; DB 3; Length 832;
Best Local Similarity 55.5%; Pred. No. 1.7e-37;
Matches 106; Conservative 27; Mismatches 44; Indels 14; Gaps 7;
Qy 1 SETLSLTCVAVGGSF-SGYTWSMIRQPPGKLEWIGEHNSGTYNPNPSLKSRVTISVD 59
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 75
Qy 60 SKNQFSLKSSVTAADTAVYYCAR--AFDINQGTW--VTVSSGSASAPTL 114
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 131
Qy 115 FPLVSCNSPSTSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-GGKYAA 173
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 188
Qy 174 TSQVLLPSKDV 184
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||: 199
RESULT 6
US-09-273-453-7
Sequence 7, Application US/09273453
Patent No. 6602688
GENERAL INFORMATION:
APPLICANT: Oppfer, Martin
APPLICANT: BOSSLET, Klaus
APPLICANT: CZECH, Joerg
TITLE OF INVENTION: CYTOPLASMIC EXPRESSION OF ANTIBODIES,
TITLE OF INVENTION: ANTIBODY FRAGMENTS AND ANTIBODY FRAGMENT FUSION MOLECULES
TITLE OF INVENTION: IN E. COLI
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,453
FILING DATE: 22-Mar-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/630,820
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: GRANADOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/306
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-273-453-7

[illegible]

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RESULT 7
US-09-800-729-145
; Sequence 145, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: P2044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn ver. 2.0
; SEQ ID NO 145
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-145

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Query Match	50.68;	Score	504.5;	DB 4;	Length	487;	
Best Local Similarity	55.5%;	Pred. No.	2.2e-37;				
Matches 111; Conservative	23;	Mismatches	47;	Indels	19;	Gaps	7;
QY	1	SETLSLTCAYVGGFS--GYWWSWIRPPGKGLEWIGSEINHSGSTNYPNLSKSRVTISVD	58				
Db	34	SETLSLTCVTSGGSISSGGHWWSWIRQHPGKGLEWIGYISNGVTYNPLSKSRVTISVD	93				
QY	59	TSKNQFSLKLSVTAADTANYICA-----RGGTVTFDAFDINGOGTWTVTSSGSASAP	112				
Db	94	TSQNQFSLRLSSVTAADTANYICAADHRATRDGQLEYRGFDYWGQGIILVTVSSASPTSP	153				
QY	113	TLPLVSCENSPTSSVAVGCLAQDFLPD---SITFSWKYKNNSDISSTRGFP--SVLR	167				
Db	154	KVPFL-SLDTFPD-GNVVACLVOGFPPQEPPLSVTWSSEQN-----VTARNFPSPQAS	207				
QY	168	GGKYAATSOVLLPSKDVNQVQ	187				
Db	208	GDLYTTSQTLTPATQCPDG	227				

RESULT 8
US-08-487-550-12
; Sequence 12, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS

TITLE OF INVENTION: IMMUNOPRESENTANTS"
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
 STREET: 699 Prince Street
 CITY: Alexandria
 STATE: VA
 COUNTRY: USA
 ZIP: 22314
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,550
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Teskin, Robin L.
 REGISTRATION NUMBER: 35,030
 REFERENCE/DOCKET NUMBER: 012712-131
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 703-836-6620
 TELEFAX: 703-836-2021
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 476 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-487-550-12

Query Match	50.1%;	Score	499.5;	DB 3;	Length	476;
Best Local Similarity	55.4%;	Pred. No.	5.9e-37;			
Matches 106;	Conservative	24;	Mismatches	51;	Indels	11; Gaps 6

QY	1	SETLSLTCAVYGSGFS-GYYWSWIROP	PPGKGLEWIGEI-NHSGSTNPNPSLKSRVTISVD	58
DB	34	SETLSLTCAVSGGSI	SGYCGWIRPPGKGLEWIGSFYSSGNTYNPNPSLKSOVTISD	93
QY	59	TSKNQPSLKLSSVTAADTA	VTATVYTCARGGT-----TVTFDAFDIQCGTMTVTSSGSASAPT	113
DB	94	TSKNQPSLKLNSMTAADTA	VYTCVRDLFSVGMVYNNWFVDWPGVLVTVSSASTGKPS	153
QY	114	LFLPLVCENSPSPTSSVAVGCLAQD	FLPDSITTSWKYKNNSDISSTRGRFPSPVLR-GGKYA	172
DB	154	VFELAPSSKSTSG-GTAALGCLVKD	YFPEPTVYSW--NSGALTSGVHTFPAVLQSSGLYS	210
QY	173	ATSQVLLPSKDV	184	
DB	211	LSSVWTVPPSSL	222	

RESULT 9
US-09-526-098-12
; Sequence 12, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/526,098
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/383,916
;; FILING DATE:
;; APPLICATION NUMBER: US 08/487,550
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-131
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6620
;; TELEFAX: 703-836-2021
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 476 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-526-098-12

Query Match 50.1%; Score 499.5; DB 4; Length 476;
Best Local Similarity 55.2%; Pred. No. 5.9e-37;
Matches 106; Conservative 24; Mismatches 51; Indels 11; Gaps 6;

Qy 1 SETLSLTCVYGGGFS-GYYWSWIRQPPGKLEWIGEI-NHSGSTNYPNPSLKSRVTISVD 58
Db 34 SETLSLTCVAGSGISGGYGGWIRQPPGKLEWIGSFYSSGNTYNNPSLKSVQVTISTD 93
Qy 59 TSKNQPSLKLSVTAADTAVYVCARGGT-----TVTFDAFDIWGQGTMTVYSSGSASAPT 113
Db 94 TSKNQPSLKLSMTAADTAVYVCVRDLRFSVGVYNNWFDVWPGVLVTVYSSASTKGPS 153
Qy 114 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSVLR-GGKYA 172
Db 154 VFPLAPSKSTSG-GTAAIGCLVKDYFPEPTVSM--NSGALTSGVHTFFPAVLQSSGLYS 210
Qy 173 ATSOVLPLSKDV 184
Db 211 LSSVTVTPSSSL 222

RESULT 10
US-09-383-916-12
; Sequence 12, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/383,916
;; FILING DATE: 26-AUG-1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/487,550
;; FILING DATE: 07-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Teskin, Robin L.
;; REGISTRATION NUMBER: 35,030
;; REFERENCE/DOCKET NUMBER: 012712-131
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 703-836-6620
;; TELEFAX: 703-836-2021
;; INFORMATION FOR SEQ ID NO: 12:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 476 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-09-383-916-12

Query Match 50.1%; Score 499.5; DB 4; Length 476;
Best Local Similarity 55.2%; Pred. No. 5.9e-37;
Matches 106; Conservative 24; Mismatches 51; Indels 11; Gaps 6;

Qy 1 SETLSLTCVYGGGFS-GYYWSWIRQPPGKLEWIGEI-NHSGSTNYPNPSLKSRVTISVD 58
Db 34 SETLSLTCVAGSGISGGYGGWIRQPPGKLEWIGSFYSSGNTYNNPSLKSVQVTISTD 93
Qy 59 TSKNQPSLKLSVTAADTAVYVCARGGT-----TVTFDAFDIWGQGTMTVYSSGSASAPT 113
Db 94 TSKNQPSLKLSMTAADTAVYVCVRDLRFSVGVYNNWFDVWPGVLVTVYSSASTKGPS 153
Qy 114 LPPLVSCNSPDSSTSSVAVGCLAQDFLPDSITFSWKYKNNDSISSTRGFPSVLR-GGKYA 172
Db 154 VFPLAPSKSTSG-GTAAIGCLVKDYFPEPTVSM--NSGALTSGVHTFFPAVLQSSGLYS 210
Qy 173 ATSOVLPLSKDV 184
Db 211 LSSVTVTPSSSL 222

RESULT 11
US-08-487-550-4
; Sequence 4, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/487,550
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-4

Query Match 49.7%; Score 496.5; DB 3; Length 476;
Best Local Similarity 54.7%; Pred. No. 1.1e-36;
Matches 105; Conservative 26; Mismatches 50; Indels 11; Gaps 7;

QY 1 SETLSLTCVAVGGFSG-YVWSWIRQPPGKLEWIGBHNHSG-STNNPSLKSRVTISVD 58
Db 34 SETLSRTCVCVSGGSGISGYYWTWIRQTPGRGLEWIGHYGNAGATTNNPSLKSRVTISKD 93

QY 59 TSKNQFSLKSSVTAADTAVVYCARGG---TTVTDFAP-DINGOGTMVTVSSGSASAPT 113
Db 94 TSKNQFFNLNSVTDADTAVVYCARGPRPDCTTICYGWVDVWGPGLVTVSSASTKGPS 153

QY 114 LFPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-GGKYA 172
Db 154 VFPLAPSSKSTSG-GTAALGCLVKDYFPPEPTVTSW--NSGALTSGVHTFFPAVLQSSGLYS 210

QY 173 ATSOVLPLSKDV 184
Db 211 LSSVTVTPSSSL 222

RESULT 12

US-09-526-098-4
Sequence 4, Application US/09526098
Patent No. 6492134
GENERAL INFORMATION:
APPLICANT: Anderson, Dattell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
AND USE THEREOF AS
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/526,098
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/383,916
FILING DATE:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-4

LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-526-098-4

Query Match 49.7%; Score 496.5; DB 4; Length 476;
Best Local Similarity 54.7%; Pred. No. 1.1e-36;
Matches 105; Conservative 26; Mismatches 50; Indels 11; Gaps 7;

QY 1 SETLSLTCVAVGGFSG-YVWSWIRQPPGKLEWIGBHNHSG-STNNPSLKSRVTISVD 58
Db 34 SETLSRTCVCVSGGSGISGYYWTWIRQTPGRGLEWIGHYGNAGATTNNPSLKSRVTISKD 93

QY 59 TSKNQFSLKSSVTAADTAVVYCARGG---TTVTDFAP-DINGOGTMVTVSSGSASAPT 113
Db 94 TSKNQFFNLNSVTDADTAVVYCARGPRPDCTTICYGWVDVWGPGLVTVSSASTKGPS 153

QY 114 LFPLVSCNSPSTSSVAVGCLAQDFLPDSITFSWKYKNNSDISSTRGPPSVLR-GGKYA 172
Db 154 VFPLAPSSKSTSG-GTAALGCLVKDYFPPEPTVTSW--NSGALTSGVHTFFPAVLQSSGLYS 210

QY 173 ATSOVLPLSKDV 184
Db 211 LSSVTVTPSSSL 222

RESULT 13

US-09-383-916-4
Sequence 4, Application US/09383916
Patent No. 6709654
GENERAL INFORMATION:
APPLICANT: Anderson, Dattell R.
TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
AND USE THEREOF AS
PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
IMMUNOSUPPRESSANTS"
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
STREET: 699 Prince Street
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,916
FILING DATE: 26-AUG-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,550
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 476 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-916-4

Query Match 49.7%; Score 496.5; DB 4; Length 476;

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.4472 Seconds
(without alignments)
1353.842 Million cells updates/sec

Title: US-09-784-950-34

Perfect score: 771

Sequence: 1 LAVSLGERATINCKSSQSVL.....VCLLNFPYPREAKVQWKV 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: PIR1:*

2: PIR2:*

3: PIR3:*

4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	646	83.8	216	2 JEO241	Ig kappa chain Am3
2	611	79.2	240	2 S06084	Ig kappa chain pre
3	597.5	77.5	215	2 JEO242	Ig kappa chain NIG
4	582	75.5	214	2 S68212	Ig kappa chain (Ma
5	575.5	74.6	215	2 JEO244	Ig kappa chain NIG
6	575	74.6	220	2 A31790	Ig kappa chain V r
7	565.5	73.3	215	2 A23746	Ig kappa chain V-I
8	544.5	70.6	215	2 JEO243	Ig kappa chain NIG
9	527	68.4	120	2 S51147	antibody light cha
10	521	67.6	114	1 K4HULN	Ig kappa chain V-I
11	520	67.4	113	2 S34002	Ig kappa chain V r
12	515	66.8	134	2 S49531	anti-Sm antibody V
13	512	66.4	129	2 S40347	Ig kappa chain - h
14	508.5	66.0	219	2 PC4203	Ig kappa chain (mo
15	504	65.4	134	1 K4HU17	Ig kappa chain pre
16	502	65.1	113	2 S30520	Ig kappa chain V r
17	502	65.1	113	2 S34003	Ig kappa chain V r
18	501.5	65.0	225	2 S37484	Ig kappa chain - m
19	499.5	64.8	219	2 S52028	Ig kappa chain - m
20	498.5	64.7	133	1 K4HUJ1	Ig kappa chain pre
21	496.5	64.4	138	2 AS3261	Ig kappa chain pre
22	496.5	64.4	217	2 S42772	Ig kappa chain - m
23	496	64.3	113	2 S30523	Ig kappa chain V r
24	496	64.3	114	2 S44119	Ig kappa chain V-J
25	494	64.1	210	2 AS6169	Ig kappa chain V r
26	494	64.1	218	2 JCS810	monoclonal antibod
27	493.5	64.0	219	2 S38865	Ig kappa chain - m
28	493	63.9	114	2 S44116	Ig kappa chain V-J
29	491	63.7	218	2 S68241	Ig kappa chain V r

30 487.5 63.2 219 2 S16112 Ig kappa chain V r
31 480 62.3 124 2 S40364 Ig kappa chain - h
32 479 62.1 132 2 S46373 Ig kappa chain V-J
33 478 62.0 145 2 PL0014 Ig kappa chain pre
34 477.5 61.9 225 2 JL0029 Ig kappa chain pre
35 477 61.9 92 2 S37533 Ig kappa chain V r
36 477 61.9 230 2 S33161 Ig kappa chain - s
37 474 61.5 121 1 K4HU Ig kappa chain pre
38 472 61.2 92 2 S37532 Ig kappa chain V r
39 472 61.2 92 2 S37534 Ig kappa chain V r
40 471 61.1 92 2 S37535 Ig kappa chain V r
41 471 61.1 92 2 S37529 Ig kappa chain V r
42 470 61.0 101 2 PH0869 Ig kappa chain V r
43 469 60.8 92 2 S37530 Ig kappa chain V r
44 467.5 60.6 197 2 S29593 Ig kappa chain (WM
45 466.5 60.5 118 2 PT0356 Ig kappa chain V r

ALIGNMENTS

RESULT 1

JEO241

Ig kappa chain Am37 precursor - human

C:Species: Homo sapiens (man)

C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000

C:Accession: JEO241

R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.

submitted to JIPID, November 1998

A:Description: Structure relationship of kappatype light chains with AL amyloidosis: Mult

A:Reference number: JEO241

A:Accession: JEO241

A:Molecule type: protein

A:Residues: 1-216 <Alif>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:116-92/Domain: immunoglobulin homology <IMM>

Query Match 83.8%; Score 646; DB 2; Length 216;

Best Local Similarity 88.4%; Pred. No. 3.6e-45;

Matches 129; Conservative 7; Mismatches 6; Indels 4; Gaps 3;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNVLAHYQKQPPKLLIYWASTRESGVDRFRSG 60
Db 11 LAVSLGERATINCKSSQSVLY--NSKNFLAWYQKQPGO-PKLLI-WANVRSQVDRFRSG 66
Qy 61 SGSGTDFLTITSSLOAEDVAVVYCOQYVSTPRTFGQTKVEIKRTVAAPSVFIFPPSDEQ 120
Db 67 SGVGTDFLTITSNLOAELVAVVYCOQYVSTPYSFGQGRLEIKRTVAAPSVFIFPPSDEQ 126
Qy 121 LKSGTASVCLLNFPYPREAKVQWKV 146
Db 127 LKSGTASVCLLNFPYPREAKVQWKV 152

RESULT 2

S06084

Ig kappa chain precursor - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000

C:Accession: S06084

R:Crowe, J.S.; Smith, M.A.; Cooper, H.J.

Nucleic Acids Res. 17, 7992, 1989

A:Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA.

A:Reference number: S06084; MUID:90016888; PMID:2508067

A:Accession: S06084

A:Molecule type: mRNA

A:Residues: 1-240 <CRO>

A:Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-240/Product: Ig kappa chain #status predicted <MAT>

F:153-222/Domain: immunoglobulin homology <IMM>

```
Query Match 79.2%; Score 611; DB 2; Length 240;
Best Local Similarity 77.4%; Pred. No. 2.7e-42;
Matches 113; Conservative 13; Mismatches 20; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 60
DB 31 LAVSAGETVTITNCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRQSGVDPDRFG 90
QY 61 SGSGTDFTLTSSLOAEDVAVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
DB 91 SGSGTDFTLTSSVQAEADLAIYCLQYETPTFGAGTKLEKRAADAAPTIVSIFPPSTEQ 150
QY 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
DB 151 LATGASVVCVCLMNNFYPRDISVKWKI 176

RESULT 3
IG kappa chain NIG26 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0242
R;Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A;Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A;Reference number: JE0241
A;Accession: JE0242
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-91/Domain: immunoglobulin homology <IMM>

Query Match 77.5%; Score 597.5; DB 2; Length 215;
Best Local Similarity 79.5%; Pred. No. 2.9e-41;
Matches 116; Conservative 11; Mismatches 14; Indels 5; Gaps 1;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 60
DB 11 LSLSPGERATLSCRSQSV-----SNLYAWYQKPGQAPSLIYDASSRATGIPDRFG 65
QY 61 SGSGTDFTLTSSLOAEDVAVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
DB 66 SGSGTDFTLTISGLEPDEFAVYCCQYVDRPPTFGQTKVEIKRTVAAPSVFIPPPSDEQ 125
QY 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
DB 126 LKSGTASVVCVCLMNNFYPREAKVQWKV 151

RESULT 4
IG kappa chain (Mab03-1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C;Accession: S68212
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68212
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-214 <TAK>
A;Cross-references: EMBL:D29668
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 75.5%; Score 582; DB 2; Length 214;
Best Local Similarity 74.0%; Pred. No. 5.2e-40;
Matches 108; Conservative 20; Mismatches 18; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 60
```

```
DB 11 LAMSVGQKVTMSCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYFASVFIPPPSDEQ 70
QY 61 SGSGTDFTLTSSLOAEDVAVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
DB 71 SGSGTDFTLTISTVQAEADLADYFCQHYSTPTFGGGTKLEIKRAADAAPTIVSIFPPSSEQ 130
QY 121 LKSGTASVVCVCLMNNFYPREAKVQWKV 146
DB 131 LTSGASVVCVCLMNNFYPKDINVKWKI 156

RESULT 5
IG kappa chain NIG2 precursor - human
C;Species: Homo sapiens (man)
C;Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C;Accession: JE0244
R;Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; Te
submitted to JIPID, November 1998
A;Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A;Reference number: JE0243
A;Accession: JE0244
A;Molecule type: protein
A;Residues: 1-215 <ALI>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 575.5; DB 2; Length 215;
Best Local Similarity 78.2%; Pred. No. 1.7e-39;
Matches 115; Conservative 12; Mismatches 13; Indels 7; Gaps 2;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 60
DB 11 LSVSPGERATLSCRSQSV-----HSNLYAWYQKPGQAPALLIYRATGIPARFG 64
QY 61 SGSGTDFTLTSSLOAEDVAVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDE 119
DB 65 SGSGTDFTLTSSLOAEDFALYCCQYVTPPLTFFGGTKVEIKRTVAAPSVFIPPPSDE 124
QY 120 QLSGTASVVCVCLMNNFYPREAKVQWKV 146
DB 125 QLSGTASVVCVCLMNNFYPREAKVQWKV 151

RESULT 6
IG kappa chain V region (17/9) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C;Accession: A31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A;Title: Preliminary crystallographic data, primary sequence, and binding data for an ant
A;Reference number: A92686; MUID:89034213; PMID:3182835
A;Accession: A31790
A;Molecule type: mRNA
A;Residues: 1-220 <SCH>
A;Cross-references: GB:M23626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 74.6%; Score 575; DB 2; Length 220;
Best Local Similarity 72.6%; Pred. No. 2e-39;
Matches 106; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 60
DB 11 LTVAGEKVTMSCTSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 70
QY 61 SGSGTDFTLTSSLOAEDVAVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
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Db 71 SSGSTDFTLTISVQAEADVAVVYQNDYSNPLTFGGGTKLEKRAAPTVSIFPPRSEQ 130
Qy 121 LKSGTASVCLNNFYPREAKVQWKV 146
Db 131 LTSGGASVVCPLNNFYPRKDINVKWKI 156

RESULT 7
A:kappa chain V-III (KAV cold agglutinin) - human
C:Species: Homo sapiens (man)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAV, a monoclonal immunoglobulin
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 73.3%; Score 565.5; DB 2; Length 215;
Best Local Similarity 78.1%; Pred. No. 1.1e-38;
Matches 114; Conservative 12; Mismatches 15; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPFRSG 60
Db 11 LSLSPGERATISGASQSV-----SSNYLAWYQKPGQAPRLIYDASSRATGIPDRPSG 65

Qy 61 SSGSTDFTLTISLQAEADVAVVYQYQYSTPTRTFGQTKVEIKRTVAAPSFIIPPSDEQ 120
Db 66 SSGSTDFTLTISRLEPEDFAVYQYQYSGSPITFGGTKVEIKRTVAAPSFIIPPSDEQ 125

Qy 121 LKSGTASVCLNNFYPREAKVQWKV 146
Db 126 LKSGTASVCLNNFYPREAKVQWKV 151

RESULT 8
A:kappa chain NIG93 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JF0243
R:Alim, M.A.; Hara, Y.; Hossain, M.S.; Takeda, K.; Yamagata, P.; Yamaki, S.; Kazi, H.; T
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A:Reference number: JF0243
A:Accession: JF0243
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 70.6%; Score 544.5; DB 2; Length 215;
Best Local Similarity 74.8%; Pred. No. 5.5e-37;
Matches 110; Conservative 13; Mismatches 17; Indels 7; Gaps 2;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPFRSG 60
Db 11 LSVSPGERATISCRASQVATN-----VVMYMKLGQAPRLIYDASTRATGVPARFSG 64

Qy 61 SSGSTDFTLTISLQAEADVAVVYQYQYSTPTRTFGQTKVEIK-RTVAAPSFIIPPSDE 119
Db 65 SSGSTFTLTISLQSEDFAIYVCOHNNAPPTFGQTKVETKRTVAAPSFIIPPSDE 124

Qy 120 QLKSGTASVCLNNFYPREAKVQWKV 146
Db 125 QLKSGTASVCLNNFYPREAKVQWKV 151
```

```
RESULT 9
S51147
antibody light chain V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S51147
R:de Kruijf, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A:Description: Selection and application of human SCFV antibody fragments from a semi-syn
A:Reference number: S51147
A:Accession: S51147
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <DBK>
A:Cross-references: EMBL:X83714; NID:g633227; PIDN:CAAS8689.1; PID:g633228
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 68.4%; Score 527; DB 2; Length 120;
Best Local Similarity 94.4%; Pred. No. 8.1e-36;
Matches 102; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPFRSG 60
Db 11 LAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPFRSG 70

Qy 61 SSGSTDFTLTISLQAEADVAVVYQYQYSTPTRTFGQTKVEIKRTVA 108
Db 71 SSGSTDFTLTISLQAEADVAVVYQYQYSTLTWTFGQTKVEIKRAAS 118

RESULT 10
K4HULN
Ig kappa chain V-IV region (Len) - human
C:Species: Homo sapiens (man)
C>Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 01-Dec-2000
C:Accession: A01903; F61458
R:Schneider, M.; Hilschmann, N.
Hoppe-Sevler's Z. Physiol. Chem. 356, 507-557, 1975
A:Title: Die Primärstruktur einer monoklonalen Immunglobulin-L-Kette der Subgruppe IV v
A:Reference number: A01903; MUID:76004342; PMID:50995
A:Accession: A01903
A:Molecule type: protein
A:Residues: 1-114 <SCH>
A:Note: this is the first completely sequenced V region of a new kappa chain subgroup, de
A:Note: the C region of this chain has the Inv (3) marker
R:Brouet, J.C.; Deillegi, K.; Gendron, M.C.; Chevallier, A.; Schmitt, C.; Mihaesco, E.
J. Exp. Med. 170, 1551-1558, 1989
A:Title: Expression of a public idiotype by human monoclonal IgM directed to myelin-associ
A:Reference number: A61458; MUID:90039128; PMID:2478651
A:Accession: F61458
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-13 <BRO>
C:Comment: This is a Bence Jones protein.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)
chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into lai
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>
F:23-94/Disulfide bonds: #status predicted

Query Match 67.6%; Score 521; DB 1; Length 114;
Best Local Similarity 95.2%; Pred. No. 2.3e-35;
Matches 99; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPFRSG 60
Db 11 LAVSLGERATINCKSSQSVLYSSNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPFRSG 70

Qy 61 SSGSTDFTLTISLQAEADVAVVYQYQYSTPTRTFGQTKVEIKR 104
```

Db 71 SSGSGTDTLTISLQAEDVAVYCCQYVSTPSPGQGTKEIKR 114
|||||

RESULT 11

S34002
Ig kappa chain V region - human
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C/Accession: S34002; S30522
C/Mariette, X.; Tsapis, A.; Brouet, J.C.
Eur. J. Immunol. 23, 846-851, 1993
A/Title: Nucleotide sequence analysis of the variable domains of four human monoclonal
A/Reference number: S34001; MUID:93209281; PMID:7661398
A/Accession: S34002
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-113 <MAR>
A/Cross-references: EMBL:Z18328
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 67.4%; Score 520; DB 2; Length 113;
Best Local Similarity 96.1%; Pred. No. 2.8e-35;
Matches 99; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFSG 60
Db 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFSG 70
Qy 61 SSGSGTDTLTISLQAEDVAVYCCQYVSTPRTFGQGTKEIK 103
Db 71 SSGSGTDTLTISLQAEDVAVYCHQYIGPRTFGQGTKEIK 113

RESULT 12

S49531
anti-Sm antibody VL chain (V kappa 4/J kappa 3) - human
C/Species: Homo sapiens (man)
C/Date: 01-Feb-1995 #sequence_revision 12-May-1995 #text_change 21-Jan-2000
C/Accession: S49531
R/Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A/Description: Molecular characterization of natural human anti-Sm autoantibodies.
A/Reference number: S48797
A/Accession: S49531
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-134 <MAH>
A/Cross-references: EMBL:Z46347; NID:g560841; PIDN:CAA86466.1; PID:g560842
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;36-116/Domain: immunoglobulin homology <IMM>

Query Match 66.8%; Score 515; DB 2; Length 134;
Best Local Similarity 95.2%; Pred. No. 8.3e-35;
Matches 99; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFSG 60
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFSG 90
Qy 61 SSGSGTDTLTISLQAEDVAVYCCQYVSTPRTFGQGTKEIKR 104
Db 91 SSGSGTDTLTISLQAEDVAVYCCQYVSTPRTFGPGTKVDIKR 134

RESULT 13

S40347
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40347

R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40347
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-129 <KLE>
A/Cross-references: EMBL:X72457; NID:g441382; PIDN:CAA51125.1; PID:g441383
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;33-113/Domain: immunoglobulin homology <IMM>

Query Match 66.4%; Score 512; DB 2; Length 129;
Best Local Similarity 94.1%; Pred. No. 1.4e-34;
Matches 96; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFSG 60
Db 28 LTVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFSG 87
Qy 61 SSGSGTDTLTISLQAEDVAVYCCQYVSTPRTFGQGTKEI 102
Db 88 SSGSGTDTLTISLQAEDVAVYCCQYVSTPRTFGQGTKEI 129

RESULT 14

PC4203
Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C/Accession: PC4203
R/Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A/Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mor
A/Reference number: PC4202; MUID:97082978; PMID:8964510
A/Accession: PC4203
A/Molecule type: mRNA
A/Residues: 1-219 <KWA>
A/Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226
C/Comment: This protein is specific for human plasma apolipoprotein A-I of high-density J
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F;1-112/Domain: V region #status predicted <VRG>
F;113-219/Domain: C region #status predicted <CRG>

Query Match 66.0%; Score 508.5; DB 2; Length 219;
Best Local Similarity 67.1%; Pred. No. 4.5e-34;
Matches 98; Conservative 18; Mismatches 29; Indels 1; Gaps 1;
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGPKLLIYWASTRESGVDPDRFSG 60
Db 11 LPVSLGDAQISCRSSQSVIHT-NGNTYLEWYLOKQSPKLLIYKVSNRFSGVDPDRFSG 69
Qy 61 SSGSGTDTLTISLQAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPTPPSDEQ 120
Db 70 SSGSGTDTLTISLQAEDVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPTPPSDEQ 129
Qy 121 LKSGTASVCLNPFYPREAKVQKV 146
Db 130 LTSGGASWCVCLNPFYPREAKVQKV 155

RESULT 15

K4HUL7
Ig kappa chain precursor V-IV region (B17) - human
C/Species: Homo sapiens (man)
C/Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jan-2000
C/Accession: A01905
R/Marsh, P.; Mills, F.; Gould, H.
Nucleic Acids Res. 13, 6531-6544, 1985
A/Title: Detection of a unique human V kappa IV germline gene by a cloned cDNA probe.
A/Reference number: A01905; MUID:86041854; PMID:2997713
A/Accession: A01905

A:Molecule type: mRNA
A:Residues: 1-134 <MAR>
A>Note: the sequence was determined from the differentiated gene
A>Note: the authors translated the codon TGC for residue 76 as Trp
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-134/Product: Ig kappa chain V-IV region (B17) #status predicted <MAT>
F:21-43/Region: framework 1
F:36-116/Domain: immunoglobulin homology <IMW>
F:44-60/Region: complementarity-determining 1
F:61-75/Region: framework 2
F:76-82/Region: complementarity-determining 2
F:83-114/Region: framework 3
F:115-121/Region: complementarity-determining 3
F:122-134/Region: framework 4
F:43-114/Disulfide bonds: #status predicted

Query Match 65.4%; Score 504; DB 1; Length 134;
Best Local Similarity 93.3%; Pred. No. 6.4e-34;
Matches 97; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDRPFG 60
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDRPFG 90

Qy 61 SGSGTDFTLTISLQAEADVAVYCOQYVSTPRTFGQGTKEIKR 104
Db 91 SGSGTDFTLTISLQAEADVAVYCOQYVSTPRTFGQGTKEIKR 134

Search completed: March 8, 2005, 06:39:28
Job time : 11.4972 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 54.8971 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-34

Perfect score: 771

Sequence: 1 LAVSLGRATINCKSSQSVL.....VCLLNFFPREAKVQWKVI 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	587.5	76.2	235	2	Q6GMV9	Q6gm9v homo sapien
2	586	76.0	236	2	Q6PIT5	Q6pit5 homo sapien
3	586	76.0	240	2	Q6PIH6	Q6pih6 homo sapien
4	585.5	75.9	239	2	Q8NEK0	Q8nek0 homo sapien
5	582	75.5	234	2	Q72473	Q72473 homo sapien
6	581	75.4	236	2	Q6PIL8	Q6pil8 homo sapien
7	577	74.8	236	2	Q6PIH7	Q6pih7 homo sapien
8	574.5	74.5	239	2	Q6P491	Q6p491 homo sapien
9	573.5	74.4	235	2	Q6PJF2	Q6pjf2 homo sapien
10	573	74.3	236	2	Q6GMW1	Q6gmw1 homo sapien
11	571	74.1	236	2	Q6GMX8	Q6gmx8 homo sapien
12	569	73.8	236	2	Q723Y4	Q723y4 homo sapien
13	567	73.5	236	2	Q6P5S8	Q6p5s8 homo sapien
14	565.5	73.3	235	2	Q6GMW0	Q6gmw0 homo sapien
15	562.5	73.0	239	2	Q8TCD0	Q8tcd0 homo sapien
16	561	72.8	236	2	Q6GMX0	Q6gmx0 homo sapien
17	555	72.0	236	2	Q6GMX9	Q6gmx9 homo sapien
18	551	71.5	236	2	Q6PIH4	Q6pih4 homo sapien
19	521	67.6	114	1	KV4A_HUMAN	P01625 homo sapien
20	517	67.1	134	1	KV4C_HUMAN	P06314 homo sapien
21	501	65.0	238	2	Q6GJS7	Q6gjs7 mus musculus
22	498.5	64.7	133	1	KV4B_HUMAN	P06313 homo sapien
23	495	64.2	241	2	Q632X4	Q632x4 mus musculus
24	493.5	64.0	219	2	Q6SZC0	Q6szc0 mus musculus
25	475	61.6	236	2	Q7ITS9	Q7it98 mus musculus
26	474	61.5	121	1	KV4D_HUMAN	P06312 homo sapien
27	473.5	61.4	243	2	Q6NTU5	Q6ntu5 xenopus lae
28	471	61.1	237	2	Q7SZ36	Q7sz36 xenopus lae
29	457	59.3	109	1	KV4D_HUMAN	P83593 homo sapien
30	414	53.7	255	2	Q6KB05	Q6kb05 mus musculus
31	394.5	51.2	129	1	KV3L_HUMAN	P18135 homo sapien

32	386.5	50.1	109	1	KV3B_HUMAN	P01620 homo sapien
33	385.5	50.0	109	1	KV3D_HUMAN	P01622 homo sapien
34	383.5	49.7	109	2	Q9UL78	Q9ul78 homo sapien
35	381.5	49.5	109	1	KV3E_HUMAN	P01623 homo sapien
36	378	49.0	108	2	Q9UL70	Q9ul70 homo sapien
37	378	49.0	108	2	Q9UL79	Q9ul79 homo sapien
38	376	48.8	108	1	KV1M_HUMAN	P01605 homo sapien
39	374.5	48.6	109	1	KV3G_HUMAN	P04206 homo sapien
40	374.5	48.6	129	1	KV3H_HUMAN	P04207 homo sapien
41	374.5	48.6	129	1	KV3M_HUMAN	P18136 homo sapien
42	373.5	48.4	109	1	KV3F_HUMAN	P01624 homo sapien
43	371	48.1	99	2	Q9JL74	Q9jl74 mus musculus
44	369	47.9	149	1	KV5A_MOUSE	P01633 mus musculus
45	363.5	47.1	117	1	KV2E_HUMAN	P06309 homo sapien

ALIGNMENTS

RESULT 1

ID	Q6GMV9	PRELIMINARY;	PRT;	235 AA.
AC	Q6GMV9;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DB	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RX	MEDLINE=32388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Ueidi T.B., Tohiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fabey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnrerch A., Schein J.E.,			
RT	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RC	SEQUENCE FROM N.A.			
RC	TISSUE=Spleen;			
RA	Strausberg R.;			
RA	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC073793; AAH73793.1; -			
DR	InterPro; IPR003599; IG.			
DR	InterPro; IPR007110; IG-like.			
DR	InterPro; IPR003597; IG cl.			
DR	InterPro; IPR003006; IG MHC.			
DR	InterPro; IPR003596; IG v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	Pfam; PF00047; IG; 2.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PS50835; IG LIKE; 2.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.			

KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25646 MW; DF32B580BAD19E4B CRC64;

Query Match 76.2%; Score 587.5; DB 2; Length 235;
Best Local Similarity 76.7%; Pred. No. 4.8e-50;
Matches 112; Conservative 16; Mismatches 13; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LLSLFGGERALSQRSQSV-----NSKYLAWYQKQPGQAPRLNLYASIRATGIPDRFSG 85
Qy 61 SSGSTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 86 SSGSTDFTLTISLSESDFALYCCQYGTSTPLTEGGGTKEIKRTVAAPSVFIPPPSDEQ 145
Qy 121 LKSGTASVCLLNFFYPREAKVQWKV 146
Db 146 LKSGTASVCLLNFFYPREAKVQWKV 171

RESULT 2
Q6PIT5 ID Q6PITS PRELIMINARY; PRT; 236 AA.
AC Q6PITS;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.;
RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC029444; AAH29444.1; --
DR HSSP; P01607; 1AR2
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG ci.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003006; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGci; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FEE351 CRC64;

Query Match 76.0%; Score 586; DB 2; Length 236;
Best Local Similarity 78.1%; Pred. No. 6.8e-50;
Matches 114; Conservative 10; Mismatches 16; Indels 6; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 33 LLSASGERVITTCRASQGI-----SSALAWYQKQPGPKLLIYDASTWESGVPSRFSG 86
Qy 61 SSGSTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 87 SSGSTDFTLTISLQPEDFATFYCCQYKSYPRIFGGGTTLEIKRTVAAPSVFIPPPSDEQ 146
Qy 121 LKSGTASVCLLNFFYPREAKVQWKV 146
Db 147 LKSGTASVCLLNFFYPREAKVQWKV 172

RESULT 3
Q6PIH6 ID Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.;
RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC034142; AAH34142.1; --
DR HSSP; P01837; 1KB5.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG ci.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003006; IG v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGci; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.

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DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.  
KW Hypothetical protein.  
SQ SEQUENCE 240 AA; 26234 MW; 189D4DD8BB781EC4 CRC64;  
  
Query Match 76.0%; Score 586; DB 2; Length 240;  
Best Local Similarity 78.2%; Pred. No. 6,9e-50;  
Matches 115; Conservative 11; Mismatches 19; Indels 2; Gaps 2;  
  
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAQQKPGOPPKLLIYWASTRESGVDPDRFSG 60  
Db 31 LSVTPGEPASISCRSSQSLHLS-NGYNYFDWYLRKPGQSPOLLIIYWGNSRASGVDPDRFSG 89  
Qy 61 SGSCTDFTLTSSLOAEDVAVYYCOQYYST-PRTFGQGTKEIKRTVAAPSFIIPPSDE 119  
Db 90 SGSCTDFTLTISRVEADVGVYCMQALQTPPTFGQGTKEIKRTVAAPSFIIPPSDE 149  
Qy 120 QKSGTASVVCLLNNFYPREAKVQWKV 146  
Db 150 QKSGTASVVCLLNNFYPREAKVQWKV 176  
  
RESULT 4  
Q8NEKO PRELIMINARY; PRT; 239 AA.  
ID Q8NEKO  
AC Q8NEKO; 01-OCT-2002 (TReMBLrel. 22, Created)  
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshitaki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Prostate;  
RA Strausberg R.;  
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC030814; AAH30814.1; -.  
DR PIR; S23638; S23638.  
DR PIR; S34091; S34091.  
DR PIR; S40342; S40342.  
DR PIR; S40357; S40357.  
DR HSSP; P01834; I172.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG_c1.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_v.  
DR SMART; SM00406; IGv; 1.
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DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IGv; 1.  
DR PROSITE; PS50835; IG LIKE; 2.  
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.  
KW Hypothetical protein.  
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;  
  
Query Match 75.9%; Score 585.5; DB 2; Length 239;  
Best Local Similarity 78.1%; Pred. No. 7,7e-50;  
Matches 114; Conservative 12; Mismatches 19; Indels 1; Gaps 1;  
  
Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAQQKPGOPPKLLIYWASTRESGVDPDRFSG 60  
Db 31 LSVTPGEPASISCRSSQSLHLS-DCYNYLDWYLRKPGQSPOLLIIYWGNSRASGVDPDRFSG 89  
Qy 61 SGSCTDFTLTSSLOAEDVAVYYCOQYYST-PRTFGQGTKEIKRTVAAPSFIIPPSDEQ 120  
Db 90 SGSCTDFTLTISRVEADVGVYCMQGLQTPPTFGQGTKEIKRTVAAPSFIIPPSDEQ 149  
Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146  
Db 150 LKSGTASVVCLLNNFYPREAKVQWKV 175  
  
RESULT 5  
Q7Z473 PRELIMINARY; PRT; 234 AA.  
ID Q7Z473  
AC Q7Z473; 01-OCT-2003 (TReMBLrel. 25, Created)  
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)  
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshitaki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Lung;  
RA Strausberg R.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC056256; AAH56256.1; -.  
DR HSSP; P01834; I1HEZ.  
DR InterPro; IPR007110; IG-like.  
DR InterPro; IPR003597; IG_c1.  
DR InterPro; IPR003006; IG_MHC.  
DR InterPro; IPR003596; IG_v.  
DR Pfam; PF07654; Cl-set; 1.  
DR SMART; SM00406; IGv; 1.
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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_12.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 75.5%; Score 582; DB 2; Length 234;
Best Local Similarity 77.2%; Pred. No. 1.7e-49;
Matches 112; Conservative 12; Mismatches 15; Indels 6; Gaps 1;

QY 2 AVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRSGS 61
Db 32 SASTGSDRTVITCRASQSI-----GSLAWYQKPGKAPOLLIIYAASLTQSGVPSRSGS 85
QY 62 GSGTDFTLTISLQAEVAVVYCOQYVSTPTFGQTKVEIKRTVAAPSFIIPPSPDEQL 121
Db 86 ASGTDFTLTISLQAEVAVVYCOQYVSTPTFGQTKVEIKRTVAAPSFIIPPSPDEQL 145
QY 122 KSGTASVVCLLNPNFYPREAKVQWKV 146
Db 146 KSGTASVVCLLNPNFYPREAKVQWKV 170

RESULT 6
Q6PIL8 PRELIMINARY; PRT; 236 AA.
AC Q6PIL8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC032451; AAH32451.1; -.
DR HSSP; P01837; 1KC0.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG ci.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IG; 2.
DR SMART; SM00409; IG; 2.
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DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein_12.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match 75.4%; Score 581; DB 2; Length 236;
Best Local Similarity 76.2%; Pred. No. 2.1e-49;
Matches 112; Conservative 17; Mismatches 12; Indels 6; Gaps 2;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFG 60
Db 31 LSLSPGERATISCRASQSL-----SSSYLAWYQKPGQAPRLIIYGVSRRATGIPDRFG 85
QY 61 SSGTDFTLTISLQAEVAVVYCOQYVSTPTFGQTKVEIKRTVAAPSFIIPPSPDE 119
Db 86 SSGTDFTLTISLQAEVAVVYCOQYVSTPTFGQTKVEIKRTVAAPSFIIPPSPDE 145
QY 120 QLKSGTASVVCLLNPNFYPREAKVQWKV 146
Db 146 QLKSGTASVVCLLNPNFYPREAKVQWKV 172

RESULT 7
Q6PIH7 PRELIMINARY; PRT; 236 AA.
AC Q6PIH7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034141; AAH34141.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG ci.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
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DR   InterPro: IPR003596; Ig_v.
DR   Pfam: PF07654; Cl-set; 1.
DR   Pfam: PF00047; Ig; 2.
DR   SMART: SM00409; IG; 2.
DR   SMART: SM00407; IGc1; 1.
DR   SMART: SM00406; Igv; 1.
DR   PROSITE; PS50835; IG LIKE; 2.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE 236 AA; 25707 MW; 4FC8B14B6559EFC9 CRC64;

      Query Match      74.1%; Score 571; DB 2; Length 236;
      Best Local Similarity 75.3%; Pred. No. 2.1e-48;
      Matches 110; Conservative 14; Mismatches 16; Indels 6; Gaps 1;

Qy   1  LAVSLGERATINCKSSQVLYSFNNKYNVLAWYQOKPGQPKLLIYWASTRESGVDPDRFSG 60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   33  VSASVGDRVTITCRASOGI-----SSWLAWYQOKPGKAPKLLIYAASSLQSGVPSRFSG 86

Qy   61  SGSGTDTFTLTSSLQAEDVAVYVYCCQYVSTPRTFGQGTKVKEIKETVAAPSVFIIPPSDEQ 120
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   87  SGSGTDTFTLTSSLQPEDFATYVYCCQAHSPFTTGPGTKVDIKETVAAPSVFIIPPSDEQ 146

Qy   121  LKGTASVCLLNFPYPREAKVOMV 146

Db   147  LKGTASVCLLNFPYPREAKVOMV 172

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RESULT 12
Q723Y4 PRELIMINARY; PRT; 236 AA.
Q723Y4
AC Q723Y4; 25 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUS=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., Ketteran K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUS=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AA005332.1; -;
DR HESP; P01834; 1HEZ.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.

DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; C1-set; 1.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS00835; IG_LIKE; 2.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW	Hypothetical protein.
SW	SEQUENCE 236 AA; 25702 MW; 7FBFB4ED23084BC6 CRC64;
Query Match 73.8%; Score 569; DB 2; Length 236;	
Best Local Similarity 75.3%; Pred. No. 3.3e-48;	
Matches 110; Conservative 12; Mismatches 18; Indels 6; Gaps 1	
QY	1 LAVSLGERATINCKSSQVLYSFNNKNLAWYQQKPGOPPKLLIYWASTRESGVDPFRSG 60
Db	33 LSASVGDVTITCRASQDI-----SNVLAWFQKPGKAPKSLIYGASSLQSGVQSKFSG 86
QY	61 SSGSDTFTLISSLOAEDVAVYICQYYSIPRTFGQTKVIEIKRTVAAPSVFIPPSDEQ 120
Db	87 SSGSDTFTLISSLPQEDFATYYCQYKSPVTFGQTKLEIKRTVAAPSVFIPPSDEQ 146
QY	121 LKSGTASVVCLLANFYPREAKVQWKV 146
Db	147 LKSGTASVVCLLANFYPREAKVQWKV 172
RESULT 13	
Q6P5S8	PRELIMINARY; PRT; 236 AA.
ID	Q6P5S8
AC	Q6P5S8;
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	Hypothetical protein.
OS	Homo sapiens (Human)
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;	
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Glandular pool- thyroid;
RX	MEDLINE=42348257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Stalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.
RT	"Generation and initial analysis of more than 15,000 full-length human
RT	and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	
RN	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Glandular pool- thyroid;
RA	Strausberg R.
RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RL	EMBL; BC062704; AAH62704.1; -.
DR	HGSP; P01837; IKCU
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig_c1.
DR	InterPro; IPR003006; Ig_MHC.


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DR PIR; S40374; S40374.
DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSSP; P01834; 117Z.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FACEDC3A3B03871D CRC64;

Query Match 73.0%; Score 562.5; DB 2; Length 239;
Best Local Similarity 74.0%; Pred. No. 1.5e-47;
Matches 108; Conservative 17; Mismatches 20; Indels 1; Gaps 1;

QY 1 LAVSLGSRATINCKSSQSVLYSFNNKNYLAWYQQKPGQPPKLLIYWASTRESGVPDFRFSG 60
Db 31 LPVTLGQPAISCSRESTQSLVYSDGN-TYLNWFQQRPGQSPRLIYKYVNRDSGVPDFRFSG 89
QY 61 SGSGTDFTLTISSIQAEADVAVYVCOQYYSPTRTFGQGTKEIVKRTVAAPSVFIPPPSDEQ 120
Db 90 SGSGTDFTLKITRVEADVGVYFCMQGTHWSTFGQGTKEIVKRTVAAPSVFIPPPSDEQ 149
QY 121 LKSGTASVCLNNFYPREAKVQWKV 146
Db 150 LKSGTASVCLNNFYPREAKVQWKV 175

```

Search completed: March 8, 2005, 06:35:53
Job time : 55.8971 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 68.1532 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-34
Perfect score: 771
Sequence: 1 LAVSLGRATINCKSSQSVL.....VCLLNFFYPRAKQVKVI 147

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	771	100.0	147	2 AAY34314	Aay34314 Igm antib
2	747	96.9	211	5 ABP43134	Abp43134 Human ova
3	743	96.4	179	8 ADK52434	Adk52434 Human ant
4	737	95.6	240	4 AAU00815	Aau00815 Human Imm
5	736	95.5	163	8 ADK52394	Adk52394 Human ant
6	735	95.3	149	2 AAY34311	Aay34311 Igm antib
7	735	95.3	220	8 ADK52314	Adk52314 Human ant
8	734	95.2	159	8 ADK52406	Adk52406 Human ant
9	731	94.8	173	8 ADK52430	Adk52430 Human ant
10	731	94.8	220	8 ADK52386	Adk52386 Human ant
11	730	94.7	171	8 ADK52422	Adk52422 Human ant
12	730	94.7	220	8 ADK52334	Adk52334 Human ant
13	729	94.6	159	8 ADK52382	Adk52382 Human ant
14	729	94.6	163	8 ADK52310	Adk52310 Human ant
15	726	94.2	220	8 ADK52362	Adk52362 Human ant
16	724	93.9	163	8 ADK52346	Adk52346 Human ant
17	724	93.9	163	8 ADK52306	Adk52306 Human ant
18	724	93.9	163	8 ADK52326	Adk52326 Human ant
19	723	93.8	154	8 ADK52342	Adk52342 Human ant
20	722	93.6	159	8 ADK52302	Adk52302 Human ant
21	722	93.6	264	5 ABP43142	Abp43142 Human ova
22	721	93.5	158	8 ADK52378	Adk52378 Human ant
23	721	93.5	240	2 AAY50161	Aay50161 Human res
24	719	93.3	163	8 ADK52398	Adk52398 Human ant
25	717	93.0	220	2 AAY08601	Aay08601 JP1112785

26	716	92.9	159	8	ADK52410	Adk52410 Human ant
27	716	92.9	220	8	ADK52298	Adk52298 Human ant
28	715	92.7	178	8	ADK52418	Adk52418 Human ant
29	714	92.6	163	8	ADK52338	Adk52338 Human ant
30	714	92.6	244	3	AAY96305	Aay96305 Human IGF
31	711.5	92.3	241	2	AAR28809	Aar28809 Vector pm
32	709	92.0	163	8	ADK52374	Adk52374 Human ant
33	708	91.8	158	8	ADK52366	Adk52366 Human ant
34	706	91.6	166	7	ADD28248	Add28248 Human het
35	703.5	91.2	238	8	ADL23055	Adl23055 Humanised
36	703.5	91.2	238	8	ADK52305	Adk52305 Humanised
37	702	91.1	240	5	AAE27927	Aae27927 Human CC4
38	702	91.1	240	6	ABB82836	Abb82836 Antibody
39	696	90.3	173	8	ADK52438	Adk52438 Human ant
40	695	90.1	149	8	ADK52402	Adk52402 Human ant
41	688	89.2	240	4	ADJ65029	Adj65029 Plasmid p
42	674	87.4	242	4	AAU80338	Aau80338 Human mil
43	674	87.4	242	4	AAU97949	Aau97949 HMF61 Fab
44	674	87.4	242	4	AAU80039	Aau80039 HMF61 Fab
45	669	86.8	154	6	ABO04851	Abo04851 Human epi

ALIGNMENTS

RESULT 1

AAAY34314
ID AAY34314 standard; protein; 147 AA.
XX
AC AAY34314;
XX
DT 19-NOV-1999 (first entry)
XX
DE Igm antibody CEM 13.5 kappa chain sequence.
XX
KW Antibody; CD147; Igm; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
PN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
XX
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
XX
DR N-PSDB; AAZ20415.
XX
XX New monoclonal antibody, used for treating e.g. graft versus host
XX disease, cancer, autoimmune diseases and inflammatory diseases.
XX
XX Claim 61; Fig 29; 245pp; English.
XX
XX This sequence represents the kappa chain of an antibody of the invention.
XX The antibody is a monoclonal antibody (MAB) with an isotype that fixes
XX complement and a variable region that binds to the epitope on CD147 bound
XX by the Igm MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
XX can selectively kill activated T-cells, activated B-cells or resting or
XX activated monocytes. The products and methods can be used for treating
XX diseases involving activated T-cells or B-cells or monocytes, e.g. graft
XX versus host disease (GVHD), organ transplant rejection diseases (e.g.
XX renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
 XX
 SQ Sequence 147 AA;
 Query Match 100.0%; Score 771; DB 2; Length 147;
 Best Local Similarity 100.0%; Pred. No. 4e-53;
 Matches 147; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 60
 DB 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 60
 QY 61 SSGSGTDFTLTSSIQAEADVAVVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
 DB 61 SSGSGTDFTLTSSIQAEADVAVVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
 QY 121 LKSGTASVCLLNFFYPREAKVQWKVI 147
 DB 121 LKSGTASVCLLNFFYPREAKVQWKVI 147
 RESULT 2
 ABP43134
 ID ABP43134 standard; protein; 211 AA.
 AC ABP43134;
 XX
 XX 22-AUG-2002 (first entry)
 DT
 XX Human ovarian antigen HVVBK13, SEQ ID NO:4266.
 DE
 XX Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
 KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
 KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
 KW PCOS; ovarian cyst; dysmenorrhea; endocrine disorder; infection;
 KW inflammatory condition; immune disorder; blood disorder;
 KW cardiovascular disorder; respiratory disorder; neurological disorder;
 KW gastrointestinal disorder; urinary system disorder; drug screening;
 KW gene therapy; chromosome mapping; forensic analysis;
 KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
 KW antiinflammatory; gynaecological; reproductive.
 XX
 OS Homo sapiens.
 XX
 XX WO200200677-A1.
 PN
 XX 03-JAN-2002.
 PD
 XX 07-JUN-2001; 2001WO-US018569.
 PF
 XX 07-JUN-2000; 2000US-0209467P.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Birse CE, Rosen CA;
 PI
 XX WPI; 2002-147878/19.
 DR
 DR N-PSDB; ABQ56211.
 XX
 XX Isolated nucleic acid molecules encoding novel ovarian polypeptides,
 PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
 PT cancer), immune disorders, cardiovascular disorders and neurological
 PT diseases.
 XX
 XX Claim 11; SEQ ID NO 4266; 2922pp; English.
 PS
 XX The invention relates to 2175 novel human ovarian antigens (ABP41054-
 CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
 CC encompasses polypeptides 90% identical and polynucleotides 95% identical
 CC to the sequences of the invention. The invention additionally relates to
 CC recombinant vectors and host cells comprising human ovarian antigen
 CC polynucleotides, antibodies against human ovarian antigens, and the use

CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
 CC treating, prognosing or preventing various ovary and/or breast-related
 CC disorders. Such conditions include ovarian cancer and breast cancer, and
 CC metastatic tumours of ovarian or breast origin, reproductive system
 CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
 CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhea), endocrine
 CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
 CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
 CC vaginitis), immune disorders (e.g. congenital and acquired
 CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
 CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
 CC respiratory disorders, neurological disorders, gastrointestinal disorders
 CC and urinary system disorders. Ovarian antigen polypeptides and
 CC polynucleotides may also be used in screening for compounds which
 CC modulate ovarian antigen expression or activity. The polynucleotides may
 CC further be used for gene therapy, chromosome mapping, in the
 CC identification of individuals and in forensic analysis, and the
 CC polypeptides may be used as food additives or to prepare antibodies
 CC useful in disease diagnosis, drug targeting and phenotyping. The present
 CC sequence represents a human ovarian antigen of the invention. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 211 AA;
 Query Match 96.9%; Score 747; DB 5; Length 211;
 Best Local Similarity 96.8%; Pred. No. 4.5e-51;
 Matches 141; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 60
 DB 35 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRYGG 94
 QY 61 SSGSGTDFTLTSSIQAEADVAVVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
 DB 95 SSGSGTDFTLTSSIQAEADVAVVYCCQYVSTPRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 154
 QY 121 LKSGTASVCLLNFFYPREAKVQWKV 146
 DB 155 LKSGTASVCLLNFFYPREAKVQWKV 180
 RESULT 3
 ADK52434
 ID ADK52434 standard; protein; 179 AA.
 XX
 XX ADK52434;
 AC
 XX 20-MAY-2004 (first entry)
 DT
 XX Human anti-MCP-1 variable region light chain #35.
 DE
 XX monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
 KW Antiirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
 KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
 KW inflammatory condition; cancer; arthritis; multiple sclerosis;
 KW anti-MCP-1; heavy chain; light chain.
 XX
 OS Homo sapiens.
 XX
 XX WO2004016769-A2.
 PN
 XX 26-FEB-2004.
 PD
 XX 19-AUG-2003; 2003WO-US026232.
 PF
 XX 19-AUG-2002; 2002US-0404802P.
 PR
 XX (ABGE-) ABGENIX INC.
 PA
 XX Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
 PI Bhakta S;

XX WPI; 2004-203794/19.
DR N-PSDB; ADK52433.
XX
XX New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
XX Claim 2; SEQ ID NO 140; 154pp; English.
XX
XX The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX
XX Sequence 179 AA;
SQ
Query Match 96.4%; Score 743; DB 8; Length 179;
Best Local Similarity 96.6%; Pred. No. 7.8e-51;
Matches 141; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
Qy 1 LAVSLGERATINCKSSQVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDFSG 60
Db 27 LAVSLGERATINCKSSQVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDFSG 86
Qy 61 SGSGTDFTLTISSLAQEDVAVYQCYYSPTPTGGTKVEIKRTVAAPSVFIPPSDEQ 120
Db 87 SGSGTDFTLTISSLAQEDVAVYQCYYSPTPTGGTKVEIKRTVAAPSVFIPPSDEQ 146
Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 147 LKSGTASVVCLLNNFYPREAKVQWKV 172
RESULT 4
AAU00815
ID AAU00815 standard; protein; 240 AA.
AC AAU00815;
XX
XX 01-JUN-2001 (first entry)
XX Human Immunoglobulin superfamily, IgSF, protein #1.
XX Human; Immunoglobulin superfamily protein; IgSF; Immune response;
KW inflammatory response; cell-cell interaction; cell-surface recognition;
KW neural disorder; immune system disorder; muscular disorder;
KW reproductive disorder; gastrointestinal disorder; pulmonary disorder;
KW cardiovascular disorder; renal disorder; proliferative disorder; cancer;
KW common variable adhesion deficiency syndrome; AIDS; SCID;
KW acquired immunodeficiency syndrome; anaemia; rheumatoid arthritis;
KW Alzheimer's disease; Crohn's disease; liver cancer; leukaemia;
KW Hodgkin's lymphoma; Parkinson's disease; Huntington's disease; dementia;
KW arteriosclerosis; stroke; diabetes mellitus; Addison's disease;
KW urticaria; severe combined immunodeficiency; antibody.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FT Region 52..58
FT /label= Immunogenic_epitope
FT Region 63..70
FT /label= Immunogenic_epitope
FT

FT Region 79..90
FT /label= Immunogenic_epitope
FT Region 118..126
FT /label= Immunogenic_epitope
FT Region 146..154
FT /label= Immunogenic_epitope
FT Domain 160..240
FT /label= Immunoglobulin_like_domain
FT Region 183..199
FT /label= Immunogenic_epitope
FT Region 209..215
FT /label= Immunogenic_epitope
FT Region 233..240
FT /label= Immunogenic_epitope
WO200118176-A1.
15-MAR-2001.
29-AUG-2000; 2000WO-US023662.
03-SEP-1999; 99US-0152248P.
(HUMA-) HUMAN GENOME SCI INC.
(NIJ/) NI J.
Young PE, Ruben SM, Shi Y;
WPI; 2001-203084/20.
N-PSDB; AAS00145.
Isolated nucleic acid molecule encoding a human secreted protein is used
in preventing, treating or ameliorating a medical condition.
Claim 11; Page 237; 247pp; English.
The sequence is a Human Immunoglobulin superfamily, IgSF, protein, a
diverse family of proteins involved in cell-cell interactions, cell-
surface recognition, intercellular communication and immune and
inflammatory responses. Polypeptides and antibodies directed to
polypeptides of the present invention are useful to provide immunological
probes for differential identification of tissues. Antibodies can be used
to assay levels of polypeptides encoded by polynucleotides of the
invention. Polypeptides of the present invention can be used to treat or
prevent diseases or conditions such as neural disorders, immune system
disorders, muscular disorders, reproductive disorders, gastrointestinal
disorders, proliferative disorders, cardiovascular disorders, renal
conditions. Polynucleotides of the invention are also useful in treating
the above disorders. Examples of the disorders include common variable
adhesion deficiency syndrome, acquired immunodeficiency syndrome (AIDS),
anaemia, rheumatoid arthritis, Alzheimer's disease, Crohn's disease,
liver cancer, leukaemia, Hodgkin's lymphoma, Parkinson's disease,
Huntingdon's disease, dementia, arteriosclerosis, stroke, diabetes
mellitus, Addison's disease, urticaria, severe combined immunodeficiency
specification
Many more examples of diseases and disorders are given in the
specification
Sequence 240 AA;
Query Match 95.6%; Score 737; DB 4; Length 240;
Best Local Similarity 95.9%; Pred. No. 3.1e-50;
Matches 140; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
Qy 1 LAVSLGERATINCKSSQVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDFSG 60
Db 31 LAVSLGERATINCKSSQVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDFSG 90
Qy 61 SGSGTDFTLTISSLAQEDVAVYQCYYSPTPTGGTKVEIKRTVAAPSVFIPPSDEQ 120
Db 91 SGSGTDFTLTISSLAQEDVAVYQCYYSPTPTGGTKVEIKRTVAAPSVFIPPSDEQ 150
Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146

Db 151 LKSGTASVCLNNFYPREAKVQWK 176
|||||

RESULT 5
ADK52394
ID ADK52394 standard; protein; 163 AA.

XX AC ADK52394;

XX DT 20-MAY-2004 (first entry)

XX DE Human anti-MCP-1 variable region light chain #25.

XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.

XX OS Homo sapiens.

XX PN W02004016769-A2.

XX PD 26-FEB-2004.

XX PF 19-AUG-2003; 2003WO-US026232.

XX PR 19-AUG-2002; 2002US-0404802P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;

XX DR WPI; 2004-203794/19.

XX DR N-PSDB; ADK52393.

XX PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.

XX PS Claim 2; SEQ ID NO 100; 154pp; English.

XX CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.

XX SQ Sequence 163 AA;

Query Match 95.5%; Score 736; DB 8; Length 163;
Best Local Similarity 95.9%; Pred. No. 2.5e-50;
Matches 140; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDFRFSG 60

Db 11 LAVSLGERATINCKSSQSVLYSSNNFNLAWYQKPGPPKLLIYWASTRESGVDFRFSG 70

Qy 61 SSGSTDTFTLTSSLAQEDVAVYCCQYYSTPRTFGQTKVEIKRTVAAPSVFIIPPSDEQ 120

Db 71 SSGSTDTFTLTSSLAQEDVAVYCCQYYNSPWTFGQTKVEIKRTVAAPSVFIIPPSDEQ 130

Qy 121 LKSGTASVCLNNFYPREAKVQWK 146
Db 131 LKSGTASVCLNNFYPREAKVQWK 156
|||||

RESULT 6
AAV34311

ID AAV34311 standard; protein; 149 AA.

XX AC AAV34311;

XX DT 19-NOV-1999 (first entry)

XX DE IGM antibody CEM 10.12 F3 kappa chain sequence.

XX KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX PN W09945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;

XX DR WPI; 1999-540816/45.

XX DR N-PSDB; AAZ20412.

XX PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 61; Fig 26; 245pp; English.

XX CC This sequence represents the kappa chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

XX SQ Sequence 149 AA;

Query Match 95.3%; Score 735; DB 2; Length 149;
Best Local Similarity 97.2%; Pred. No. 2.8e-50;
Matches 141; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDFRFSG 60

Db 3 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGPPKLLIYWASTRESGVDFRFSG 62

Qy 61 SSGSTDTFTLTSSLAQEDVAVYCCQYYSTPRTFGQTKVEIKRTVAAPSVFIIPPSDEQ 120

Db 63 SSGSTDTFTLTSSLAQEDVAVYCCQYYSTPRTFGQTKVEIKRTVAAPSVFIIPPSDEQ 122

Qy 121 LKSGTASVCLNNFYPREAKVQWK 145

Db 123 LKSGTASVCLNNFYPREAKVQWK 147
|||||

RESULT 7
ADK52314
ID ADK52314 standard; protein; 220 AA.
XX AC ADK52314;
XX AC ADK52314;
XX DT 20-MAY-2004 (first entry)
XX DE Human anti-MCP-1 variable region light chain #5.
XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
XX KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoaritic;
XX KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;
XX KW inflammatory condition; cancer; arthritis; multiple sclerosis;
XX KW anti-MCP-1; heavy chain; light chain.
XX OS Homo sapiens.
XX PN WO2004016769-A2.
XX FN
XX PD 26-FEB-2004.
XX PF 19-AUG-2003; 2003WO-US026232.
XX PR 19-AUG-2002; 2002US-0404802P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX DR WPI; 2004-203794/19.
XX DR N-PSDB; ADK52313.
XX PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX PS Claim 2; SEQ ID NO 20; 154pp; English.
XX CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX SQ Sequence 220 AA;
Query Match 95.3%; Score 735; DB 8; Length 220;
Best Local Similarity 96.6%; Pred. No. 4.1e-50;
Matches 141; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 60
DB 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 70
QY 61 SGSCTDFTLTISSLQAEADVAVYCCQYVSTPRFTGQGTKEIKRTVAAPSVFIIPPSEDEQ 120
DB 71 SGSCTDFTLTISSLQAEADVAVYCCQYVSTPRFTGQGTKEIKRTVAAPSVFIIPPSEDEQ 130
QY 121 LKSGTASVCLLNFPYPREAKVQWKV 146
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Db 131 LKSGTASVCLLNFPYPREAKVQWKV 156
RESULT 8
ADK52406
ID ADK52406 standard; protein; 159 AA.
XX AC ADK52406;
XX AC ADK52406;
XX DT 20-MAY-2004 (first entry)
XX DE Human anti-MCP-1 variable region light chain #28.
XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
XX KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoaritic;
XX KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;
XX KW inflammatory condition; cancer; arthritis; multiple sclerosis;
XX KW anti-MCP-1; heavy chain; light chain.
XX OS Homo sapiens.
XX PN WO2004016769-A2.
XX FN
XX PD 26-FEB-2004.
XX PF 19-AUG-2003; 2003WO-US026232.
XX PR 19-AUG-2002; 2002US-0404802P.
XX PA (ABGE-) ABGENIX INC.
XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX DR WPI; 2004-203794/19.
XX DR N-PSDB; ADK52405.
XX PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX PS Claim 2; SEQ ID NO 112; 154pp; English.
XX CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX SQ Sequence 159 AA;
Query Match 95.2%; Score 734; DB 8; Length 159;
Best Local Similarity 96.6%; Pred. No. 3.5e-50;
Matches 141; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 60
DB 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLLIYWASTRESGVDPDRFSG 70
QY 61 SGSCTDFTLTISSLQAEADVAVYCCQYVSTPRFTGQGTKEIKRTVAAPSVFIIPPSEDEQ 120
DB 71 SGSCTDFTLTISSLQAEADVAVYCCQYVSTPRFTGQGTKEIKRTVAAPSVFIIPPSEDEQ 130
QY 121 LKSGTASVCLLNFPYPREAKVQWKV 146
|||||

Db 131 LKSGTASVVCLLNNFYPREAKVQWKV 156
|||||

RESULT 9
ADK52430
ID ADK52430 standard; protein; 173 AA.

XX AC ADK52430;

XX DT 20-MAY-2004 (first entry)

XX DE Human anti-MCP-1 variable region light chain #34.

XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.

XX OS Homo sapiens.

XX PN WO2004016769-A2.

XX PD 26-FEB-2004.

XX PF 19-AUG-2003; 2003WO-US026232.

XX PR 19-AUG-2002; 2002US-0404802P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;

XX DR WPI; 2004-203794/19.

XX DR N-PSDB; ADK52429.

XX PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.

XX PS Claim 2; SEQ ID NO 136; 154pp; English.

XX CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.

XX SQ Sequence 173 AA;

Query Match 94.8%; Score 731; DB 8; Length 173;
Best Local Similarity 95.2%; Pred. No. 6.6e-50;
Matches 139; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 26 LAVSLGERAAINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 85

Qy 61 SGSCTDFTLTSSLOAEDVAVYCOQYVSTPRTGQGTKEIKETVAAPSVFIIPPDSDEQ 120

Db 86 SGSCTDFTLTSSLOAEDVAVYCOQYVSTPRTGQGTKEIKETVAAPSVFIIPPDSDEQ 145

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 146 LKSGTASVVCLLNNFYPREAKVQWKV 171

RESULT 10
ADK52386

ID ADK52386 standard; protein; 220 AA.

XX AC ADK52386;

XX DT 20-MAY-2004 (first entry)

XX DE Human anti-MCP-1 variable region light chain #23.

XX KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antipsoriatic;
KW Vasotrophic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.

XX OS Homo sapiens.

XX PN WO2004016769-A2.

XX PD 26-FEB-2004.

XX PF 19-AUG-2003; 2003WO-US026232.

XX PR 19-AUG-2002; 2002US-0404802P.

XX PA (ABGE-) ABGENIX INC.

XX PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;

XX DR WPI; 2004-203794/19.

XX DR N-PSDB; ADK52385.

XX PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.

XX PS Claim 2; SEQ ID NO 92; 154pp; English.

XX CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.

XX SQ Sequence 220 AA;

Query Match 94.8%; Score 731; DB 8; Length 220;
Best Local Similarity 95.2%; Pred. No. 8.4e-50;
Matches 139; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 70

Qy 61 SGSCTDFTLTSSLOAEDVAVYCOQYVSTPRTGQGTKEIKETVAAPSVFIIPPDSDEQ 120

Db 71 SGSCTDFTLTSSLOAEDVAVYCOQYVSTPRTGQGTKEIKETVAAPSVFIIPPDSDEQ 130


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Db 71 SSGSDFTLTISLQAEADVAVYCCQYFSPWTFGQTKVEIKRTVAAPSVFIPPSDEQ 130
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Qy 121 LKSGTASVCLNNFYPREAKVQKV 146
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 131 LKSGTASVCLNNFYPREAKVQKV 156
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
ADK52382
ID ADK52382 standard; protein; 159 AA.
XX
AC ADK52382;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #22.
XX
KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52381.
XX
PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 88; 154pp; English.
XX
CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX
SQ Sequence 159 AA;
Query Match 94.6%; Score 729; DB 8; Length 159;
Best Local Similarity 95.9%; Pred. No. 8.8e-50;
Matches 140; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFSG 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFSG 70
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Qy 61 SSGSDFTLTISLQAEADVAVYCCQYFSPWTFGQTKVEIKRTVAAPSVFIPPSDEQ 120
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Db 71 SSGSDFTLTISLQAEADVAVYCCQYFSPWTFGQTKVEIKRTVAAPSVFIPPSDEQ 130
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 LKSGTASVCLNNFYPREAKVQKV 146
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 131 LKSGTASVCLNNFYPREAKVQKV 156
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
ADK52310
ID ADK52310 standard; protein; 163 AA.
XX
AC ADK52310;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #4.
XX
KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiartherosclerotic; Antipsoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN WO2004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52309.
XX
PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix, useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 16; 154pp; English.
XX
CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also
CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX
SQ Sequence 163 AA;
Query Match 94.6%; Score 729; DB 8; Length 163;
Best Local Similarity 95.2%; Pred. No. 9e-50;
Matches 139; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFSG 60
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Db 11 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFSG 70
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 78.009 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-34

Perfect score: 771

Sequence: 1 LAVSLGRATINCKSSQSVL.....VCLLNFPYREAKVQWKVI 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
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 - 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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 - 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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 - 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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 - 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
 - 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
 - 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
 - 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	747	96.9	211	15	US-10-264-049-4266
2	737	95.6	240	9	US-09-799-514-8
3	722	93.6	264	15	US-10-264-049-4274
4	721	93.5	240	9	US-09-301-593-36
5	721	93.5	240	14	US-10-159-006-36
6	696.5	90.3	165	15	US-10-384-743-26
7	688	89.2	240	16	US-10-630-406-8
8	677.5	87.9	239	9	US-09-249-011A-22
9	674	87.4	239	9	US-09-825-012-9
10	674	87.4	242	10	US-09-819-266-26
11	667	86.5	220	9	US-09-995-693-1
12	667	86.5	220	14	US-10-232-408-1
13	662	85.9	153	9	US-09-187-693-62

14	656	85.1	220	9	US-09-301-593-17
15	656	85.1	220	14	US-10-159-006-17
16	656	85.1	240	9	US-09-301-593-28
17	656	85.1	240	14	US-10-159-006-28
18	653	84.7	220	9	US-09-917-410-5
19	645	83.7	218	15	US-10-449-566-102
20	641	83.1	218	15	US-10-449-566-119
21	638	82.7	218	14	US-10-171-452A-39
22	638	82.7	218	14	US-10-171-452A-57
23	638	82.7	218	15	US-10-353-708-39
24	638	82.7	218	15	US-10-353-708-57
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29	638	82.7	238	15	US-10-353-708-38
30	638	82.7	238	15	US-10-353-708-56
31	638	82.7	238	16	US-10-731-984-3
32	638	82.7	238	16	US-10-731-984-27
33	637	82.6	218	15	US-10-449-566-98
34	628	81.5	218	14	US-10-171-452A-45
35	628	81.5	218	14	US-10-171-452A-51
36	628	81.5	218	15	US-10-353-708-45
37	628	81.5	218	15	US-10-353-708-51
38	628	81.5	218	16	US-10-731-984-12
39	628	81.5	218	16	US-10-731-984-20
40	628	81.5	238	14	US-10-171-452A-44
41	628	81.5	238	14	US-10-171-452A-50
42	628	81.5	238	15	US-10-353-708-44
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44	628	81.5	238	16	US-10-731-984-11
45	628	81.5	238	16	US-10-731-984-19

ALIGNMENTS

RESULT 1
US-10-264-049-4266
; Sequence 4266, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264.049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4266
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-049-4266

Query Match	96.9%	Score 747;	DB 15;	Length 211;
Best Local Similarity	96.6%	Pred. No. 1.3e-49;		
Matches 141;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	1	LAVSLGRATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDFRSG	60	
Db	35	LAVSLGRATINCKSSQSVLYSFNNKNYLAWYQKPGHPKLLIYWASTRESGVDFRSG	94	
Qy	61	SGSGTDFLTLSLQAEADVAVYCCQYYSPTRTGQGTKEIKRTVAAPSFIFPPSDEQ	120	

Db 95 SSGSTDFTLTSSQAEDVAVYVCOQYNTPTREGQGTKEIKRTVAAPSVFIPPPSDEQ 154
Qy 121 LKSGTASVCLNNFYPREAKVQWKV 146
Db 155 LKSGTASVCLNNFYPREAKVQWKV 180

RESULT 2
US-09-799-514-8
; Sequence 8, Application US/09799514
; Patent No. US20020065220A1
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: Immunoglobulin Superfamily Polynucleotides, Polypeptides, and Ant
; CURRENT APPLICATION NUMBER: US/09/799,514
; CURRENT FILING DATE: 2001-03-07
; PRIOR APPLICATION NUMBER: PCT/US00/23662
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 60/152,248
; PRIOR FILING DATE: 1999-09-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-799-514-8

Query Match 95.6%; Score 737; DB 9; Length 240;
Best Local Similarity 95.9%; Pred. No. 8.3e-49;
Matches 140; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 90
Qy 61 SSGSTDFTLTSSQAEDVAVYVCOQYNTPTREGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 91 SSGSTDFTLTSSQAEDVAVYVCOQYNTPTREGQGTKEIKRTVAAPSVFIPPPSDEQ 150
Qy 121 LKSGTASVCLNNFYPREAKVQWKV 146
Db 151 LKSGTASVCLNNFYPREAKVQWKV 176

RESULT 3
US-10-264-049-4274
; Sequence 4274, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 4274
; LENGTH: 264
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (163)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (201)

; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (212)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (215)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (226)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (230)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (236)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (249)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (258)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (263)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
; US-10-264-049-4274

Query Match 93.6%; Score 722; DB 15; Length 264;
Best Local Similarity 94.5%; Pred. No. 1.3e-47;
Matches 138; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 35 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 94
Qy 61 SSGSTDFTLTSSQAEDVAVYVCOQYNTPTREGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 95 SSGSTDFTLTSSQAEDVAVYVCOQYNTPTREGQGTKEIKRTVAAPSVFIPPPSDEQ 154
Qy 121 LKSGTASVCLNNFYPREAKVQWKV 146
Db 155 LKSGTASVCLNNFYPREAKVQWKV 180

RESULT 4
US-09-301-593-36
; Sequence 36, Application US/09301593A
; Publication No. US20020052480A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301,593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0


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; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match      93.5%; Score 721; DB 9; Length 240;
Best Local Similarity 94.5%; Pred. No. 1.4e-47;
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGOPPKLLIYWASTRESGVDPDRFSG 90

Qy 61 SGSGTDFTLTSSLAQEDVAVYQCOYVSTPRTGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 91 SGFGTDFTLTSSLAQEDVAVYQCOYVSTPRTGQGTKEIKRTVAAPSVFIPPPSDEQ 150

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 151 LKSGTASVVCLLNNFYPREAKVQWKV 176

RESULT 5
US-10-159-006-36
; Sequence 36, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saidanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-36

Query Match      93.5%; Score 721; DB 14; Length 240;
Best Local Similarity 94.5%; Pred. No. 1.4e-47;
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGOPPKLLIYWASTRESGVDPDRFSG 90

Qy 61 SGSGTDFTLTSSLAQEDVAVYQCOYVSTPRTGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 91 SGFGTDFTLTSSLAQEDVAVYQCOYVSTPRTGQGTKEIKRTVAAPSVFIPPPSDEQ 150

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 151 LKSGTASVVCLLNNFYPREAKVQWKV 176

RESULT 6
US-10-364-743-26
; Sequence 26, Application US/10364743
; Publication No. US20040009178A1
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; GENERAL INFORMATION:
; APPLICANT: Bowdich, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178A1an, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 165
; TYPE: PRT
; ORGANISM: human
US-10-364-743-26

Query Match      90.3%; Score 696.5; DB 15; Length 165;
Best Local Similarity 91.1%; Pred. No. 7.3e-46;
Matches 133; Conservative 7; Mismatches 5; Indels 1; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 13 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGOPPKLLIYWASTRESGVDPDRFSG 71

Qy 61 SGSGTDFTLTSSLAQEDVAVYQCOYVSTPRTGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 72 SGSGTDFTLTSSLAQEDVAVYQCOYVSTPRTGQGTKEIKRTVAAPSVFIPPPSDEQ 131

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 132 LKSGTASVVCLLNNFYPREAKVQWKV 157

RESULT 7
US-10-630-406-8
; Sequence 8, Application US/10630406
; Publication No. US20040105855A1
; GENERAL INFORMATION:
; APPLICANT: Jure-Kunkel, Maria
; APPLICANT: Ganguly, Subinay
; APPLICANT: Abraham, Ralph
; APPLICANT: Hollenbaugh, Diane L.
; APPLICANT: Rillema, Jill
; APPLICANT: Thorne, Barbara
; APPLICANT: Shuford, Walter W.
; APPLICANT: Mittler, Robert S.
; TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN 4-1BB
; FILE REFERENCE: D0288 NP
; CURRENT APPLICATION NUMBER: US/10/630,406
; CURRENT FILING DATE: 2003-07-30
; PRIOR APPLICATION NUMBER: US 60/399,646
; PRIOR FILING DATE: 2002-07-30
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-630-406-8

Query Match      89.2%; Score 688; DB 16; Length 240;
Best Local Similarity 91.8%; Pred. No. 4.6e-45;
Matches 134; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LAVSLGERATINCKSSQSVLYSFNNKNYLAHYQKPGOPPKLLIYWASTRESGVDPDRFSG 90
```



```

;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/995,693
; FILING DATE: 29-No. US20020136721A1-2001
; CLASSIFICATION DATA: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/952,235
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Marschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P0938P1
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-5416
; TELEFAX: 650/952-9881
;
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-995-693-1

Query Match 86.5%; Score 667; DB 9; Lend
Best Local Similarity 84.2%; Pred. No. 1.7e-43;
Matches 123; Conservative 15; Mismatches 8;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPPKLL
Ddb 11 LVTVSGEKTIVSCKSSQSLITSSQKNYLAWYQKPGQSPKLL
QY 61 SSGSGTDFTLTISLQAEADVAVVYCCQYYSPTPTFGGTGKVEIH
Ddb 71 SSGSGTDFTLTITSVKADDLAVVYCCQYVYVPTFGGTGKLEIH
QY 121 LKSGTASVCLLNFPYREAKVQWKV 146
Ddb 131 LKSGTASVCLLNFPYREAKVQWKV 156

RESULT 12
US-10-232-408-1
; Sequence 1, Application US/10232408
; Publication No. US20030118587A1
; GENERAL INFORMATION:
; APPLICANT: Schwall, Ralph H.
; TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
; Antagonists and Uses Thereof
;
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)

```

Query Match 85.1%; Score 662; DB 9; Length 153;
Best Local Similarity 90.3%; Pred. No. 2.9e-43;
Matches 130; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLA WYQKPGQPPKLLIYWASTRESGVDRFSG 60
Db 7 LAVSLGERATINCKSSQSVLYSGKNQNYLA WYQKPGQPPKLLIYWASTRESGVDRFRG 66

Qy 61 SGSGTDFTLTSSQLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 67 SGSGTDFTLTSSQLQAEADVAVFCHQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 126

Qy 121 LKSGTASVVCLLNNFY--PREAKV 142
Db 127 LKSGTASVVCLLNNLYRKPRTKV 150

RESULT 14
US-09-301-593-17
Sequence 17, Application US/09301593A
Publication No. US20020052480A1
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301.593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 220
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-17

Query Match 85.1%; Score 656; DB 9; Length 220;
Best Local Similarity 84.2%; Pred. No. 1.2e-42;
Matches 123; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLA WYQKPGQPPKLLIYWASTRESGVDRFSG 60
Db 11 LAVSVGEKVTMSCKSSQSVLYSRNQNYLA WYQKPGQPPKLLIYWASTRESGVDRFTG 70

Qy 61 SGSGTDFTLTSSQLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 71 SGFGTDFTLTSSVQAEADVAVDCQYVSYPLTFGAGTKLEKRTVAAPSVFIPPPSDEQ 130

Qy 121 LKSGTASVVCLLNNFYPREAKVQMKV 146
Db 131 LKSGTASVVCLLNNFYPREAKVQMKV 156

RESULT 15
US-10-159-006-17
Sequence 17, Application US/10159006
Publication No. US20030143229A1
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility

FILE REFERENCE: 0652.1890002
CURRENT APPLICATION NUMBER: US/10/159,006
CURRENT FILING DATE: 2002-06-03
PRIOR APPLICATION NUMBER: US 09/301,593
PRIOR FILING DATE: 1999-04-29 98107925.4
PRIOR APPLICATION NUMBER: EP 98107925.4
PRIOR FILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: US 60/086,049
PRIOR FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 220
TYPE: PRT
ORGANISM: Homo sapiens
US-10-159-006-17

Query Match 85.1%; Score 656; DB 14; Length 220;
Best Local Similarity 84.2%; Pred. No. 1.2e-42;
Matches 123; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLA WYQKPGQPPKLLIYWASTRESGVDRFSG 60
Db 11 LAVSVGEKVTMSCKSSQSVLYSRNQNYLA WYQKPGQPPKLLIYWASTRESGVDRFTG 70

Qy 61 SGSGTDFTLTSSQLQAEADVAVYCCQYVSTPRTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 71 SGFGTDFTLTSSVQAEADVAVDCQYVSYPLTFGAGTKLEKRTVAAPSVFIPPPSDEQ 130

Qy 121 LKSGTASVVCLLNNFYPREAKVQMKV 146
Db 131 LKSGTASVVCLLNNFYPREAKVQMKV 156

Search completed: March 8, 2005, 07:05:55
Job time : 79.009 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.1636 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-34

Perfect score: 771

Sequence: 1 LAVSLGERATINCKSSQSVL.....VVCLLNNFYPREAKVQWKVI 147

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pap.*
- 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pap.*
- 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pap.*
- 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pap.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pap.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles.pap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	721	93.5	240	4	US-09-301-593-36
2	711.5	92.3	241	2	US-07-916-098A-56
3	677.5	87.9	239	4	US-09-627-896B-22
4	667	86.5	220	3	US-08-952-235-1
5	667	86.5	220	4	US-09-669-971-1
6	656	85.1	220	4	US-09-301-593-17
7	656	85.1	240	4	US-09-301-593-28
8	635	82.4	239	3	US-08-812-586-29
9	635	82.4	239	4	US-09-535-832A-30
10	601	78.0	214	4	US-09-472-087-71
11	598.5	77.6	235	4	US-09-472-087-14
12	598.5	77.6	235	4	US-09-472-087-65
13	597	77.4	226	4	US-09-456-090A-74
14	597	77.4	226	4	US-09-453-234-74
15	596	77.3	226	4	US-09-456-090A-86
16	596	77.3	226	4	US-09-453-234-86
17	595	77.2	224	4	US-09-456-090A-82
18	595	77.2	224	4	US-09-456-090A-88
19	595	77.2	224	4	US-09-456-090A-90
20	595	77.2	224	4	US-09-453-234-82
21	595	77.2	224	4	US-09-453-234-88
22	595	77.2	224	4	US-09-453-234-90
23	595	77.2	226	4	US-09-456-090A-80
24	595	77.2	226	4	US-09-453-234-80
25	593	76.9	226	4	US-09-456-090A-50
26	593	76.9	226	4	US-09-453-234-50
27	591	76.7	224	4	US-09-456-090A-36

28	591	76.7	224	4	US-09-453-234-36	Sequence 36, Appl
29	590	76.5	226	4	US-09-456-090A-38	Sequence 38, Appl
30	590	76.5	226	4	US-09-453-234-38	Sequence 38, Appl
31	589	76.4	146	4	US-09-472-087-21	Sequence 21, Appl
32	589	76.4	146	4	US-09-472-087-93	Sequence 93, Appl
33	589	76.4	226	4	US-09-456-090A-42	Sequence 42, Appl
34	589	76.4	226	4	US-09-453-234-42	Sequence 42, Appl
35	588	76.3	218	2	US-08-887-352B-13	Sequence 13, Appl
36	588	76.3	218	3	US-08-466-151-9	Sequence 9, Appl
37	588	76.3	218	3	US-09-109-207C-13	Sequence 13, Appl
38	588	76.3	218	3	US-09-296-005-13	Sequence 13, Appl
39	588	76.3	218	3	US-08-466-163B-9	Sequence 9, Appl
40	588	76.3	218	4	US-09-920-171-13	Sequence 13, Appl
41	588	76.3	218	4	US-09-802-096-9	Sequence 9, Appl
42	588	76.3	218	4	US-09-802-077-9	Sequence 9, Appl
43	588	76.3	218	4	US-09-716-028-13	Sequence 13, Appl
44	588	76.3	218	4	US-10-113-996-13	Sequence 13, Appl
45	587	76.1	218	5	PCT-US96-13152-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-09-301-593-36
; Sequence 36, Application US/09301593A
; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saidanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890001
; CURRENT APPLICATION NUMBER: US/09/301.593A
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 36
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-301-593-36

Query Match 93.5%; Score 721; DB 4; Length 240;
Best Local Similarity 94.5%; Pred. No. 3.3e-62;
Matches 138; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy	1	LAVSLGERATINCKSSQSVLYSFNNKYLAWYQKPGOPPKLLIYWASTRESGVDPDRFG	60
Db	31	LAVSLGERATINCKSSQSLLYSRNQKYLAWYQKPGOPPKLLIFWASTRESGVDPDRFG	90
Qy	61	SGSGTDTLTISLQAEADVYVYCOQYVSTPRTGQGTKEIKETVAAPSVEIFPPSDEQ	120
Db	91	SGFTDTLTISLQAEADVYVYCOQYVSTPRTGQGTKEIKETVAAPSVEIFPPSDEQ	150
Qy	121	LKSGTASVVCLLNNFYPREAKVQWKV	146
Db	151	LKSGTASVVCLLNNFYPREAKVQWKV	176

RESULT 2
US-07-916-098A-56
; Sequence 56, Application US/07916098A
; Patent No. 5871732
; GENERAL INFORMATION:
; APPLICANT: BURKLY, LINDA C.

APPLICANT: CHISHOLM, PATRICIA L.
APPLICANT: THOMAS, DAVID W.
APPLICANT: ROSA, MARGARET D.
APPLICANT: ROSA, JOSEPH J.
TITLE OF INVENTION: ANTI-CD4 ANTIBODY HOMOLOGS USEFUL IN
TITLE OF INVENTION: PROPHYLAXIS AND TREATMENT OF AIDS, ARC AND HIV INFECTION
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: ALLEGRETTI & WITCOFF, LTD.
STREET: 10 SOUTH WACKER DRIVE
CITY: CHICAGO
STATE: ILLINOIS
COUNTRY: U.S.A.
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILING DATE: July 24, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/08843
FILING DATE: No. 5871732ember 27, 1991
CLASSIFICATION: 424
APPLICATION NUMBER: 07/618,542
FILING DATE: No. 5871732ember 27, 1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: JOHN J. MC DONNELL
REGISTRATION NUMBER: 26,949
REFERENCE/DOCKET NUMBER: 92,310-G
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 715-1000
TELEFAX: (312) 715-1234
TELEX: 910/221-5317
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 241 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-916-098A-56

Query Match 92.3%; Score 711.5; DB 2; Length 241;
Best Local Similarity 94.5%; Pred. No. 2.8e-61;
Matches 138; Conservative 3; Mismatches 4; Indels 1; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDRFSG 60
Db 33 LAVSLGERATINCKSSGSLYSTQKNYLAWYQKQPPKLLIYWASTRESGVDRFSG 92

Qy 61 SSGSTDFTLTSSLAEDVAVYCCQYVSTRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
Db 93 SSGSTDFTLTSSLAEDVAVYCCQYVSY-RTEGRGTGKLEIKRTVAAPSVFIPPPSDEQ 151

Qy 121 LKSGTASVVCLLNNFYPREAKVQKV 146
Db 152 LKSGTASVVCLLNNFYPREAKVQKV 177

RESULT 3
US-09-627-896B-22
Sequence 22, Application US/09627896B
Patent No. 6827934
GENERAL INFORMATION:
APPLICANT: CO, MAN SUNG
APPLICANT: VASQUEZ, MAXIMILIANO
APPLICANT: CARRENO, BEATRIZ
APPLICANT: CELNIKER, ABBIE CHERYL
APPLICANT: COLLINS, MARY

APPLICANT: GOLDMAN, SAMUEL
APPLICANT: GRAY, GARY S.
APPLICANT: KNIGHT, ANDREA
APPLICANT: O'HARA, DENISE
APPLICANT: RUP, BONITA
APPLICANT: VELDMAN, GEBTRUIDA M.
TITLE OF INVENTION: HUMANIZED IMMUNOGLOBULIN REACTIVE WITH B7-2 AND METHODS
TITLE OF INVENTION: OF TREATMENT THEREWITH
FILE REFERENCE: 08702.0081-01000
CURRENT APPLICATION NUMBER: US/09/627,896B
CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 22
LENGTH: 239
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: 3D1 light chain
US-09-627-896B-22

Query Match 87.9%; Score 677.5; DB 4; Length 239;
Best Local Similarity 91.1%; Pred. No. 5.4e-58;
Matches 133; Conservative 4; Mismatches 8; Indels 1; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKQPPKLLIYWASTRESGVDRFSG 60
Db 31 LAVSLGERATINCKSSQSLNSRTRENYLAWYQKQPPKLLIYWASTRESGVDRFSG 90

Qy 61 SSGSTDFTLTSSLAEDVAVYCCQYVSTRTFGQTKVEIKRTVAAPSVFIPPPSDEQ 120
Db 91 SSGSTDFTLTSSLAEDVAVYCCSQSYNL-YTFGQGTKEIKRTVAAPSVFIPPPSDEQ 149

Qy 121 LKSGTASVVCLLNNFYPREAKVQKV 146
Db 150 LKSGTASVVCLLNNFYPREAKVQKV 175

RESULT 4
US-08-952-235-1
Sequence 1, Application US/08952235
Patent No. 6207152
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
APPLICANT: Tabor, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
TITLE OF INVENTION: Antagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/460368
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416

TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-952-235-1

Query Match 86.5%; Score 667; DB 3; Length 220;
Best Local Similarity 84.2%; Pred. No. 5.1e-57;
Matches 123; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 60
DB 11 LTVSVGEKVTVCSSQSLLYTSQKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFTG 70

QY 61 SGSGTDFLTITSSLOAEDVAVYQYVSTPRTFGQTKVEIKRTVAAPSFIPPPSDEQ 120
DB 71 SGSGTDFLTITSVKADDLAVYQYVAYPTWTEGGGKLEIKRTVAAPSFIPPPSDEQ 130

QY 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
DB 131 LKSGTASVVCLLNNFYPREAKVQWKV 156

RESULT 5
US-09-669-971-1
Sequence 1, Application US/09669971
Patent No. 6468529
GENERAL INFORMATION:
APPLICANT: Schwall, Ralph H.
TABOR, Kelly H.
TITLE OF INVENTION: Hepatocyte Growth Factor Receptor
Antagonists and Uses Thereof
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/669,971
FILING DATE: 05-Jul-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/952,235
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/460368
FILING DATE: 02-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P0938P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 220 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-669-971-1

Query Match 86.5%; Score 667; DB 4; Length 220;
Best Local Similarity 84.2%; Pred. No. 5.1e-57;

Matches 123; Conservative 15; Mismatches 8; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 60
DB 11 LTVSVGEKVTVCSSQSLLYTSQKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFTG 70

QY 61 SGSGTDFLTITSSLOAEDVAVYQYVSTPRTFGQTKVEIKRTVAAPSFIPPPSDEQ 120
DB 71 SGSGTDFLTITSVKADDLAVYQYVAYPTWTEGGGKLEIKRTVAAPSFIPPPSDEQ 130

QY 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
DB 131 LKSGTASVVCLLNNFYPREAKVQWKV 156

RESULT 6
US-09-301-593-17
Sequence 17, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 17
LENGTH: 220
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-17

Query Match 85.1%; Score 656; DB 4; Length 220;
Best Local Similarity 84.2%; Pred. No. 5.9e-56;
Matches 123; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFG 60
DB 11 LTVSVGEKVTVCSSQSLLYTSQKNYLAWYQKPGQPKLLIYWASTRESGVDPDRFTG 70

QY 61 SGSGTDFLTITSSLOAEDVAVYQYVSTPRTFGQTKVEIKRTVAAPSFIPPPSDEQ 120
DB 71 SGSGTDFLTITSVKADDLAVYQYVAYPTWTEGGGKLEIKRTVAAPSFIPPPSDEQ 130

QY 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
DB 131 LKSGTASVVCLLNNFYPREAKVQWKV 156

RESULT 7
US-09-301-593-28
Sequence 28, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Producibility
FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301,593A

; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 98107925.4
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/086,049
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 28
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-301-593-28

Query Match 85.1%; Score 656; DB 4; Length 240;
Best Local Similarity 84.2%; Pred. No. 6.6e-56;
Matches 123; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWSQKPGPKLLIYWASTRESGVDPDRFSG 60
Db 31 LAVSVGEKVTMSCKSSQSVLYSRNKNYLAWSQKPGPKLLIYWASTRESGVDPDRFTG 90

Qy 61 SSGSDTFTLTSSLOAEDVAVYCCQVYSTPRTFGQTKVEIKRTVAAPSVFIFPPPSDEQ 120
Db 91 SSGTDFNLTISSQVADLAVIDCQVYFSLPTFGAGTKLEKRTVAAPSVFIFPPPSDEQ 150

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 151 LKSGTASVVCLLNNFYPREAKVQWKV 176

RESULT 8
US-08-812-586-29
; Sequence 29, Application US/08812586
; Patent No. 6048704
; GENERAL INFORMATION:
; APPLICANT: Martin David Tilson
; TITLE OF INVENTION: PURIFIED AND RECOMBINANT ANTIGENIC
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH ABDOMINAL AORTIC ANEURYSM (AAA)
; TITLE OF INVENTION: DISEASE, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/812,586
; FILING DATE: 07-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0575/53862-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-812-586-29

Query Match 82.4%; Score 635; DB 3; Length 239;

Best Local Similarity 86.3%; Pred. No. 7.1e-54;
Matches 126; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWSQKPGPKLLIYWASTRESGVDPDRFSG 60
Db 30 LAVSLGERATINCKSSQSVLYSFNNKNYLAWSQKPGPKLLIYWASTRESGVDPDRFSG 89

Qy 61 SSGSDTFTLTSSLOAEDVAVYCCQVYSTPRTFGQTKVEIKRTVAAPSVFIFPPPSDEQ 120
Db 90 SSGSDTFTLTISRLEPEDFAVYCCQVYGGSSPLTFGGTKVEIKRTVAAPSVFIFPPPSDEQ 149

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 150 LKBITASVVGLLNNFYPREAKVQWKV 175

RESULT 9
US-09-535-832A-30
; Sequence 30, Application US/09535832A
; Patent No. 6537769
; GENERAL INFORMATION:
; APPLICANT: Tilson, Martin David
; TITLE OF INVENTION: Purified and Recombinant Antigenic Proteins Associated
; TITLE OF INVENTION: with Abdominal Aortic Aneurysm (AAA) Disease, and
; TITLE OF INVENTION: Diagnostic and Therapeutic use Thereof
; FILE REFERENCE: 53862-AZ
; CURRENT APPLICATION NUMBER: US/09/535,832A
; CURRENT FILING DATE: 2000-03-28
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 30
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-535-832A-30

Query Match 82.4%; Score 635; DB 4; Length 239;
Best Local Similarity 86.3%; Pred. No. 7.1e-54;
Matches 126; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWSQKPGPKLLIYWASTRESGVDPDRFSG 60
Db 30 LAVSLGERATINCKSSQSVLYSFNNKNYLAWSQKPGPKLLIYWASTRESGVDPDRFSG 89

Qy 61 SSGSDTFTLTSSLOAEDVAVYCCQVYSTPRTFGQTKVEIKRTVAAPSVFIFPPPSDEQ 120
Db 90 SSGSDTFTLTISRLEPEDFAVYCCQVYGGSSPLTFGGTKVEIKRTVAAPSVFIFPPPSDEQ 149

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 150 LKBITASVVGLLNNFYPREAKVQWKV 175

RESULT 10
US-09-472-087-71
; Sequence 71, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEORFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1


```
; SEQ ID NO 71
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-71

Query Match      78.0%; Score 601; DB 4; Length 214;
Best Local Similarity 79.5%; Pred. No. 1.2e-50;
Matches 116; Conservative 10; Mismatches 14; Indels 6; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 11 LSAVSGRVTTICRASQSI-----NSYLDWYQKPGKAPKLLIYAASSLQSGVPSRFSG 64

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 65 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 124

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 125 LKSGTASVVCLLNNFYPREAKVQWKV 150

RESULT 11
US-09-472-087-14
; Sequence 14, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14

Query Match      77.6%; Score 598.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.4e-50;
Matches 115; Conservative 15; Mismatches 11; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LSLSPGERATLSCRASQSISSSF-----LAWYQRPQAPRLLIYGASSRATGIPDRFSG 85

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 86 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 145

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 146 LKSGTASVVCLLNNFYPREAKVQWKV 171

RESULT 12
US-09-472-087-65
; Sequence 65, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-14

Query Match      77.6%; Score 598.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.4e-50;
Matches 115; Conservative 15; Mismatches 11; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LSLSPGERATLSCRASQSISSSF-----LAWYQRPQAPRLLIYGASSRATGIPDRFSG 85

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 86 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 145

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 146 LKSGTASVVCLLNNFYPREAKVQWKV 171

RESULT 13
US-09-456-090A-74
; Sequence 74, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-456-090A-74

Query Match      77.4%; Score 597; DB 4; Length 226;
Best Local Similarity 78.9%; Pred. No. 3.2e-50;
Matches 116; Conservative 15; Mismatches 10; Indels 6; Gaps 2;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 11 LSLSPGERATLSCRASQSV-----SSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSG 65

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 119
Db 66 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 125

Qy 120 QLKSGTASVVCLLNNFYPREAKVQWKV 146
Db 126 QLKSGTASVVCLLNNFYPREAKVQWKV 152
```

```
; APPLICANT: MUELLER, ELLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-65

Query Match      77.6%; Score 598.5; DB 4; Length 235;
Best Local Similarity 78.8%; Pred. No. 2.4e-50;
Matches 115; Conservative 15; Mismatches 11; Indels 5; Gaps 1;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 31 LSLSPGERATLSCRASQSISSSF-----LAWYQRPQAPRLLIYGASSRATGIPDRFSG 85

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 120
Db 86 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDEQ 145

Qy 121 LKSGTASVVCLLNNFYPREAKVQWKV 146
Db 146 LKSGTASVVCLLNNFYPREAKVQWKV 171

RESULT 13
US-09-456-090A-74
; Sequence 74, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 74
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-456-090A-74

Query Match      77.4%; Score 597; DB 4; Length 226;
Best Local Similarity 78.9%; Pred. No. 3.2e-50;
Matches 116; Conservative 15; Mismatches 10; Indels 6; Gaps 2;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNYLAWYQKPGOPPKLLIYWASTRESGVDPDRFSG 60
Db 11 LSLSPGERATLSCRASQSV-----SSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSG 65

Qy 61 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 119
Db 66 SGSGTDFTLTISLQAEADVAVYCCQYYSPTPTFGQGTKEIKRTVAAPSVFIPPPSDE 125

Qy 120 QLKSGTASVVCLLNNFYPREAKVQWKV 146
Db 126 QLKSGTASVVCLLNNFYPREAKVQWKV 152
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11 LSLSPGERATLSCRASQSV-----SSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSG 65
61 SGSGTDFTLTISSIQAEADVAVYYCQYYST-PRTFGOGTKVEIKRTVAAPSVFIFFPSDE 119
66 SGSGTDFTLTISSIRLEPEDFAVYYCQYYGSSPPYTFGGTKLEIKRTVAAPSVFIFFPSDE 125
120 QLKSGGTASVVCLLNFPYREAKVQWKV 146
126 QLKSGGTASVVCLLNFPYREAKVQWKV 152

Search completed: March 8, 2005, 05:54:11
Job time : 17.1636 secs

11 LSLSPGERATLSCRASQSV-----SSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSG 65
61 SGSGTDFTLTISSIQAEADVAVYYCQYYST-PRTFGOGTKVEIKRTVAAPSVFIFFPSDE 119
66 SGSGTDFTLTISSIRLEPEDFAVYYCQYYGSSPPYTFGGTKLEIKRTVAAPSVFIFFPSDE 125
120 QLKSGGTASVVCLLNFPYREAKVQWKV 146
126 QLKSGGTASVVCLLNFPYREAKVQWKV 152

Search completed: March 8, 2005, 05:54:11
Job time : 17.1636 secs

Query Match 77.4%; Score 597; DB 4; Length 226;
Best Local Similarity 78.9%; Pred. No. 3.2e-50;
Matches 116; Conservative 15; Mismatches 10; Indels 6; Gaps 2;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNVLAWSYQKPGQAPRLLIYWASTRESGVDPDRFSG 60
Db 11 LSLSPGERATLSCRASQSV-----SSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSG 65
Qy 61 SGSGTDFTLTISSIQAEADVAVYYCQYYST-PRTFGOGTKVEIKRTVAAPSVFIFFPSDE 119
Db 66 SGSGTDFTLTISSIRLEPEDFAVYYCQYYGSSPPYTFGGTKLEIKRTVAAPSVFIFFPSDE 125
Qy 120 QLKSGGTASVVCLLNFPYREAKVQWKV 146
Db 126 QLKSGGTASVVCLLNFPYREAKVQWKV 152

RESULT 15
US-09-456-090A-86
; Sequence 86, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Loberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456.090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-33L
US-09-456-090A-86

Query Match 77.3%; Score 596; DB 4; Length 226;
Best Local Similarity 78.9%; Pred. No. 4e-50;
Matches 116; Conservative 15; Mismatches 10; Indels 6; Gaps 2;

Qy 1 LAVSLGERATINCKSSQSVLYSFNNKNVLAWSYQKPGQAPRLLIYWASTRESGVDPDRFSG 60
Db 11 LSLSPGERATLSCRASQSV-----SSSYLAWYQKPGQAPRLLIYGASSRATGIPDRFSG 65
Qy 61 SGSGTDFTLTISSIQAEADVAVYYCQYYST-PRTFGOGTKVEIKRTVAAPSVFIFFPSDE 119
Db 66 SGSGTDFTLTISSIRLEPEDFAVYYCQYYGSSPPYTFGGTKLEIKRTVAAPSVFIFFPSDE 125
Qy 120 QLKSGGTASVVCLLNFPYREAKVQWKV 146
Db 126 QLKSGGTASVVCLLNFPYREAKVQWKV 152

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.5893 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-35

Perfect score: 803

Sequence: 1 NPQTLTLTCTFSGFSLTR.....SESTALGLCLVKDYFPEPVT 149

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: Pir1.*
- 2: Pir2.*
- 3: Pir3.*
- 4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	507.5	63.2	124	A49002	Ig heavy chain V r
2	461.5	57.5	374	S69339	Ig heavy chain V r
3	452	56.3	138	S31513	Ig heavy chain - h
4	430	53.5	119	S18555	Ig heavy chain V r
5	412.5	51.4	472	S21459	Ig gamma-1 chain -
6	412	51.3	121	GIHURH	Ig heavy chain V-I
7	411	51.2	121	A36005	Ig heavy chain V r
8	409	50.9	220	A49444	Ig gamma-1 heavy c
9	407	50.7	125	1 MHUUMC	Ig heavy chain V-I
10	391.5	48.8	470	S22080	Ig heavy chain pre
11	390.5	48.6	118	S18556	Ig heavy chain V r
12	389	48.4	231	PC4155	Ig gamma-2b chain
13	375.5	46.8	241	S69131	Ig heavy chain (DO
14	373.5	46.5	122	S11740	Ig heavy chain pre
15	364.5	45.4	143	PT0174	Ig heavy chain V r
16	363.5	45.3	113	S26465	Ig heavy chain V r
17	361	45.0	96	S26923	Ig heavy chain pre
18	359.5	44.8	147	G2HUCS	Ig heavy chain V r
19	355	44.2	96	S26924	Ig heavy chain V r
20	353	44.0	107	A49442	Ig heavy chain V r
21	351.5	43.8	120	1 GIHUCO	Ig heavy chain V-I
22	348.5	43.4	220	S68211	Ig heavy chain (Ma
23	348.5	43.4	444	2 PC4436	monoclonal antibod
24	347	43.2	231	2 B23746	Ig Fab region IV-J
25	345	43.0	143	S23624	Ig heavy chain V r
26	339.5	42.3	116	2 S26328	Ig heavy chain V r
27	337	42.0	119	1 GIHUDW	Ig heavy chain V-I
28	335	41.7	96	S26922	Ig heavy chain V r
29	330	41.1	121	2 S09959	Ig heavy chain V r

30	330	41.1	592	2	S25705	Ig mu chain - shee
31	328.5	40.9	254	2	B31790	Ig heavy chain V r
32	325.5	40.5	568	2	A34891	Ig heavy chain pre
33	325	40.5	149	2	S30752	Ig heavy chain pre
34	325	40.5	213	2	S68213	Ig heavy chain (Ma
35	321.5	40.0	126	1	MHHUOU	Ig heavy chain V-I
36	319.5	39.8	548	2	S38864	Ig epsilon chain C
37	312.5	38.9	129	2	S44114	Ig heavy chain V r
38	309	38.5	144	1	G2MS14	Ig heavy chain pre
39	309	38.5	246	2	S38950	Ig gamma chain - m
40	309	38.5	446	2	S40295	Ig gamma-2a chain
41	307	38.2	221	2	S49220	Ig gamma-1 chain -
42	306.5	38.2	144	2	S11244	Ig gamma-2a chain
43	306.5	38.2	171	2	S23623	Ig heavy chain V r
44	304.5	37.9	474	1	G2MS11	Ig gamma-2b chain
45	304	37.9	103	2	B25913	Ig heavy chain pre

ALIGNMENTS

RESULT 1

A49002
Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C;Accession: A49002
R;Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.;
Arthritis Rheum. 35, 900-904, 1992
A;Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene
A;Reference number: A49002; MUID:92352481; PMID:1322670
A;Accession: A49002
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-124 <STU>
A;Cross-references: GB:M90808; NID:G185515; PIDN:AA52989.1; PID:G567176
A;Experimental source: EBV-transformed lymphoblastoid cell line SSH23
C;Note: sequence extracted from NCBI backbone (NCBIN:10261, NCBI:P:110262)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;15-99/Domain: immunoglobulin homology <IMM>

Query Match	63.2%	Score	507.5;	DB 2;	Length	124;			
Best Local Similarity	87.4%	Pred. No.	1.4e-38;						
Matches	97;	Conservative	3;	Mismatches	10;	Indels	1;	Gaps	1;
Qy	2 PQTTLTCTFSGFSLITRGVGVGWIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITK 61								
	: :								

RESULT 2

S69339
Ig heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamlichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664

A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140, 'C', 142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 57.5%; Score 461.5; DB 2; Length 374;
Best Local Similarity 58.9%; Pred. No. 6.2e-34;
Matches 96; Conservative 12; Mismatches 30; Indels 25; Gaps 4;

Qy 2 PQTTLTCTCFSGSLITRGVGVDMIRPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 33 PTQTLLTCTCFSGSLSTSGVGVGIRPPGKALEWLALYWNDDKRYSPSLKSLRLTITK 92

Qy 62 DTSKNQVLTMTNMDPVDATYYCAHFFDSSG---YPSDSWQGGTLVSVSSASTK--- 115
Db 93 DTSKNQVLTMTNMDPVDATYYCG---YSVEGYGOGYRFHSGQGGTLVTSSEPKSCDK 149

Qy 116 -----GPSVPEPLACSRST--SESTAALGCLVKD 142
Db 150 THTCPCPAPELGGPSVFLPPPKDKTLMISRPETVCVVVD 192

RESULT 3
S31513
Ig heavy chain - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S31513
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-138 <CHA>
A;Cross-references: EMBL:X69861; NID:G33084; PIDN:CAA9495.1; PID:G33085
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-114/Domain: immunoglobulin homology <IMM>

Query Match 56.3%; Score 452; DB 2; Length 138;
Best Local Similarity 79.8%; Pred. No. 1.5e-33;
Matches 87; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

Qy 2 PQTTLTCTCFSGSLITRGVGVDMIRPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 29 PTQTLLTCTCFSGSLSTSGVGVGIRPPGKTLLEWLALYWNDDKRYSPSLKSLRLTITK 88

Qy 62 DTSKNQVLTMTNMDPVDATYYCAHFFDSSG---YPSDSWQGGTLVSVSSASTK--- 110
Db 89 DTSKNQVLTMTNMDPVDATYYCAHFRPGIAVTCGNFDYWGQGLTVTS 137

RESULT 4
S18555
Ig heavy chain V region precursor (VII-5) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 21-Jul-2000
C;Accession: S18555
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18555
A;Molecule type: DNA
A;Residues: 1-119 <SHI>
A;Gene: GDB:IGHV@
C;Genetics:
A;Cross-references: EMBL:X62111; NID:G37839; PIDN:CAA44021.1; PID:G3980125
A;Introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-119/Product: Ig heavy chain V region (VII-5) #status predicted <MAT>
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 53.5%; Score 430; DB 2; Length 119;
Best Local Similarity 93.0%; Pred. No. 1.2e-31;
Matches 80; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 2 PQTTLTCTCFSGSLITRGVGVDMIRPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 33 PTQTLLTCTCFSGSLSTSGVGVGIRPPGKALEWLALYWNDDKRYSPSLKSLRLTITK 92

Qy 62 DTSKNQVLTMTNMDPVDATYYCAH 87
Db 93 DTSKNQVLTMTNMDPVDATYYCAH 118

RESULT 5
S31459
Ig gamma-1 chain - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C;Accession: S31459
R;Patri, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A;Reference number: S31459
A;Accession: S31459
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-472 <PAT>
A;Cross-references: EMBL:X69797
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;277-346/Domain: immunoglobulin homology <IMM>

Query Match 51.4%; Score 412.5; DB 2; Length 472;
Best Local Similarity 56.1%; Pred. No. 2e-29;
Matches 83; Conservative 17; Mismatches 43; Indels 5; Gaps 2;

Qy 5 TLTTLTCTCFSGSLITRGVGVDMIRPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 64
Db 34 TLSVTCITISGSL--NNYGVDMVRQAPGKALEWLGSGYDEIDINPVLKSLRLTITK 91

Qy 65 KNOVLTMTNMDPVDATYYCAHFFDSS--GYPPDSWQGGTLVSVSSASTKPSVFP 121
Db 92 KSOVSLTSLTSTTTEDTAVYYCARVDYDSHAFAYASYDFWGPGLISVLSTSTTPPKYIP 151

Qy 122 LAPCSRSTSESTAALGCLVKDYPPEPVT 149
Db 152 LTS CGDTSSSIIVTLGCLVSYMPPEVT 179

RESULT 6
GIHUHE
Ig heavy chain V-II region (He) - human
C;Species: Homo sapiens (man)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C;Accession: A02093
R;Cunningham, B.A.; Pflumm, M.N.; Rutishauser, U.; Edelman, G.M.
Proc. Natl. Acad. Sci. U.S.A. 64, 997-1003, 1969
A;Title: Subgroups of amino acid sequences in the variable regions of immunoglobulin hea
A;Reference number: A02093; MUID:70114712; PMID:5264153
A;Accession: A02093
A;Molecule type: protein
A;Residues: 1-121 <CUN>
A;Cross-references: UNIPROT:P01818
C;Comment: This gamma-1 chain was isolated from a myeloma protein.
C;Genetics:
A;Gene: GDB:IGHV@
A;Cross-references: GDB:128528; OMIM:147070
A;Map position: 14q32.33-14q32.33
C;Superfamily: immunoglobulin V region; immunoglobulin homology

Search completed: March 8, 2005, 06:39:28
Job time : 10.6393 secs

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Result No.	Query				DB	ID	Description
	Score	Match	Length				
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3	448.5	55.9	465	2	Q6GMX6	Q6GMX6 homo sapien	
4	442.5	55.4	476	2	Q6GMZX7	Q6GMZX7 homo sapien	
5	442.5	55.1	473	2	Q8TC63	Q8TC63 homo sapien	
6	426.5	53.1	473	2	Q6P055	Q6P055 homo sapien	
7	422.5	52.6	544	2	Q6PJ95	Q6PJ95 homo sapien	
8	420	52.3	493	2	Q68CN4	Q68CN4 homo sapien	
9	416	51.8	472	2	Q6N089	Q6N089 homo sapien	
10	412	51.3	121	1	HV2E HUMAN	P01818 homo sapien	
11	412	51.3	417	2	Q6N093	Q6N093 homo sapien	
12	410	51.1	470	2	Q6PJ44	Q6PJ44 homo sapien	
13	408	50.8	464	2	Q6MZU6	Q6MZU6 homo sapien	
14	407	50.7	125	1	HV2D HUMAN	P01817 homo sapien	
15	403	50.2	466	2	Q6IN78	Q6IN78 homo sapien	
16	403	50.2	482	2	Q7Z351	Q7Z351 homo sapien	
17	401	49.9	480	2	Q6N094	Q6N094 homo sapien	
18	397.5	49.5	465	2	Q6P6C4	Q6P6C4 homo sapien	
19	396	49.3	478	2	Q6P181	Q6P181 homo sapien	
20	392	48.8	521	2	Q8N4Y9	Q8N4Y9 homo sapien	
21	391.5	48.8	473	2	Q6MZV7	Q6MZV7 homo sapien	
22	389.5	48.5	475	2	Q6MZQ6	Q6MZQ6 homo sapien	
23	385.5	48.0	475	2	Q6N095	Q6N095 homo sapien	
24	383.5	47.8	518	2	Q6N030	Q6N030 homo sapien	
25	378	47.1	466	2	Q6N096	Q6N096 homo sapien	
26	378	47.1	470	2	Q7Z5W1	Q7Z5W1 homo sapien	
27	375	46.7	492	2	Q7Z374	Q7Z374 homo sapien	
28	373.5	46.5	481	2	Q6N097	Q6N097 homo sapien	
29	365.5	45.5	469	2	Q7Z7P5	Q7Z7P5 homo sapien	
30	364	45.3	208	2	Q6ZP87	Q6ZP87 homo sapien	
31	359.5	44.8	147	1	HV2B HUMAN	P04438 homo sapien	

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 476 AA; 52286 MW; 622AABAS62DDE9D CRC64;

Query Match 56.4%; Score 453; DB 2; Length 476;
Best Local Similarity 59.9%; Pred. No. 1.1e-36;
Matches 91; Conservative 17; Mismatches 40; Indels 4; Gaps 1;

Qy 2 PQTTLTCTFSGFLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRITK 61
Db 33 PSQTLSTCTVSGGSISSGDIYVWIRQPPGKLEWIGYIYSGTNTYNPSLKSRTISL 92
Qy 62 DTSKNQVLTMTNPDVDTATYCAH----HFFDSSGYYPFDSWGQGLVSVSSASTKGP 117
Db 93 DTSKNQSLKNSVTAADTAVYFCARAGWGSFSSWALDGNFNGQGTMTVSSASTKGP 152
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RESULT 3
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073766; AAH73766.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDBL386E CRC64;

Query Match 55.9%; Score 448.5; DB 2; Length 465;
Best Local Similarity 61.5%; Pred. No. 3.1e-36;
Matches 91; Conservative 15; Mismatches 35; Indels 7; Gaps 2;

Qy 2 PQTTLTCTFSGFLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRITK 61
Db 33 PSETLSLTCTVSGGSI--SGYVSWIRQPPAGKLEWIGRIYTGSTNTYNPSLKSRTVMSV 90
Qy 62 DTSKNQVLTMTNPDVDTATYCAHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 91 DTSKNQSLKLSVTAADTAVYFCARGRFY-----FDYWGQGLTVSVSSASTKGPSVFP 145
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPTV 149
Db 146 LAPSSKSTSGTAAALGCLVKDYFPEPTV 173

RESULT 4
Q6GMX7 PRELIMINARY; PRT; 476 AA.
AC Q6GMX7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686M24218.
OS Homo sapiens (Human).
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RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary Nervous System;
RA Strausberg R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC065820; AAH65820.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51344 MW; 9816D56A77129B57 CRC64;

Query Match 53.1%; Score 426.5; DB 2; Length 473;
Best Local Similarity 55.3%; Pred. No. 5e-34;
Matches 85; Conservative 22; Mismatches 39; Indels 5; Gaps 2;

QY 2 PQTTLTCTCFGSLITRGVGVDMIRQPPGKALQWLALIYWNDD---KRYSPSLKSLRT 58
DB 33 PGSLTSLCTSGSGFTF--SGANLSWVRQAPGKLEWAVRQTEDDGGTTHYIAVKGRT 90

QY 59 ITKDTSKNQVLTMTNMPDVTATYCAHFFDSSGYYPFDSMGQGLTVSVSSASTKGPS 118
DB 91 VSRDSSRLTYLQMSDLRTDTAFYFCATGSMNTVGLTGFDSMGQGLTVTVSSASTKGPS 150

QY 119 VFPLAPCSRSTSESTAALGCLVKDYFPEPVT 149
DB 151 VFPLAPSKSTSGGTAALGCLVKDYFPEPVT 181

RESULT 7
Q6PJ95 ID Q6PJ95 PRELIMINARY; PRT; 544 AA.
AC Q6PJ95;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Colling P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datschenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;

Query Match 52.8%; Score 422.5; DB 2; Length 544;
Best Local Similarity 55.8%; Pred. No. 1.5e-33;
Matches 87; Conservative 19; Mismatches 37; Indels 13; Gaps 4;

QY 2 PQTTLTCTCFGSLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRTIT 60
DB 33 PGSLTSLCTSGSGFTF--SNYGHMWVRQAPGKLEWAVFSYDESCKRYAASVKGRTIS 90

QY 61 KDTSKNQVLTMTNMPDVTATYCAHFFDSSGYYP-----FDSMGQGLTVSVSSAS 113
DB 91 RDNSKNTLSLQMSLRLVADTVVYCAK---DQKPWYSNSWFLTNFDSMGRTLTVTSSAS 147

QY 114 TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT 149
DB 148 TKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVT 183

RESULT 8
Q68CN4 ID Q68CN4 PRELIMINARY; PRT; 493 AA.
AC Q68CN4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKF2p686E23209 (Fragment).
GN Name=DKF2p686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749861; CAH18705.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
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Db 91 RDNGKNSLYIQMNSLRADFTALYYCAKEIGHNPFY-----YGMVDMVGQGTTVTVSSASTK 14

Qy 116 GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVT 149

Db 147 GPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVT 180

RESULT 10

HV2E HUMAN

ID	HV2E HUMAN	STANDARD;	PRT;	121 AA.
AC	P01818;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Ig heavy chain V-II region HE.			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RN	SEQUENCE.			
RP	MEDLINE=70114712; PubMed=5264153;			
RX	Cunningham B.A., Pflumm M.N., Rutishauser U., Edelman G.M.;			
RA	"Subgroups of amino acid sequences in the variable regions of			
RT	immunoglobulin heavy chains."			
RL	Proc. Natl. Acad. Sci. U.S.A. 64:997-1003 (1969).			
CC	-I- MISCCELLANEOUS: This gamma-1 chain was isolated from a myeloma			
CC	protein.			
CC	-I- SIMILARITY: Contains 1 immunoglobulin-like domain.			
DR	PIR; A02093; GIHUHE.			
DR	HSSP; P01820; IA7N.			
DR	GO; GO:0005576; C:extracellular; NAS.			
DR	GO; GO:0003823; F:antigen binding; NAS.			
DR	GO; GO:0006955; P:immune response; NAS.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003596; Ig_v.			
DR	Pfam; PF00047; Ig_1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG LIKE; 1.			
KW	Direct protein sequencing; Immunoglobulin V region;			
KW	Pyrrolidone carboxylic acid.			
FT	DOMAIN 1 120 Ig-like.			
FT	MOD RES 1 1 Pyrrolidone carboxylic acid.			
FT	NON TER 121 121			
SEQ	SEQUENCE 121 AA; 13483 MW; 88A5082C273753B4 CRC64;			
Query Match 51.3%; Score 412; DB 1; Length 121;				
Best Local Similarity 70.4%; Pred. No. 2.8e-33;				
Matches 81; Conservative 9; Mismatches 13; Indels 12; Gaps 3				
ID	Q6N093	PRELIMINARY;	PRT;	417 AA.
AC	Q6N093;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DE	Hypothetical protein DKF2p686I04196 (Fragment).			
OS	Homo sapiens (Human)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			

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RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wamburt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640623; CAE45777.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 3.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;

Query Match 51.3%; Score 412; DB 2; Length 417;
Best Local Similarity 64.0%; Pred. No. 1.2e-32;
Matches 80; Conservative 15; Mismatches 26; Indels 4; Gaps 2;

Qy 26 WIRPQKALQWALI-YWDDKEYSPSLKSLRLITKDTKNQVLTWNTWMDPVDATYY 84
Db 8 WVRQAPGKLEWAVIAYDGTQYADSVRGFRFTVSRDNSANTLFLFNMLRPEDTAVY 67
Qy 85 CAHFFDSSGYYPPDSWGQGLVSVSSASTKGPVFPFLAPCSRSTSESTALGCLVKDYF 144
Db 68 CAK---AHSGTSKEDPWGQGLTVTVSSASTKGPVFPFLAPCSRSTSESTALGCLVKDYF 124
Qy 145 PEPVT 149
Db 125 PEPVT 129

RESULT 12
Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marushina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
```

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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 51.1%; Score 410; DB 2; Length 470;
Best Local Similarity 56.3%; Pred. No. 2.2e-32;
Matches 85; Conservative 19; Mismatches 39; Indels 8; Gaps 4;

Qy 2 PQTTLTCTFSFSLITRGVGDWIRQPGKALQWALIYN-DDKRYSPSLKSLRJTIT 60
Db 33 FGSLSRLSCVSVSGTF--SSYMSWVRQAPGKGLIEWYANIKQDSEKYYVYDVKGRFTIS 90
Qy 61 KDTSKNQVLTWNTWMDPVDATYYCAHFFDSSGYYP--FDSWGQGLVSVSSASTKGPS 118
Db 91 RDNKNSLYQMSLRAEDTAVYICAR---DGSWYRDWDFPQCGGLTVTVSSASTKGPS 147
Qy 119 VFPLAPCSRSTSESTALGCLVKDYFPEPVT 149
Db 148 VFPLAPSKSTSGTALGCLVKDYFPEPVT 178

RESULT 13
Q6MZU6 PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloecher H., Boecker M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAB45931.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
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DR PROSITE: PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match          50.8%; Score 408; DB 2; Length 464;
Best Local Similarity 54.0%; Pred. No. 3.4e-32;
Matches 81; Conservative 22; Mismatches 39; Indels 8; Gaps 3;

Qy 2 PQTTLTCTSGSLITRGVGVWIRPPGKALQWLALI--YWNDDKRYSPSLKSLRTITK 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 PGSLRLSCAASGFTF--SSYSMMVVRQAPGKLEWVSFSSRGSGSYEYADSVKGRFTI 90
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 60 TKDTSKNQVLTWNTMDPVDVTATYCAHHFFDSSGYYPFDSWGQGTLVSVSSASTKGPSV 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 SRDNKNSLYLQMSLRARNTAVYICARDL---GWFLDYGQGTTLVTVSSASTKGPSV 146
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 120 FPLAPCSRSTSESTAALGCLVKDYFPEPTV 149
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 147 FPLAPCSRSTSESTVALGCLVKDYFPEPTV 176
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 14
ID HV2D HUMAN STANDARD; PRT; 125 AA.
AC P01817;
DT 21-JUL-1986 (Rel. 01, Created)
DR 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE IG heavy chain V-II region MCE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=81118242; PubMed=6780622;
RA Gerber-Jenson B., Kazin A., Kehoe J.M., Scheffel C., Erickson B.W.,
RA Litman G.W.;
RT "Molecular basis for the temperature-dependent insolubility of
RT cryoglobulins. X. The amino acid sequence of the heavy chain variable
RT region of McE.";
RL J. Immunol. 126:1212-1216(1981).
CC -!- MISCELLANEOUS: This chain was derived from a monoclonal IgM
CC -!- SMILARITY: Contains 1 immunoglobulin-like domain.
CC PIR; A02092; MHUUMC.
DR HSSP; P01820; 1A7N.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
FT Pyrolysine carboxylic acid.
FT DOMAIN 1 113 Ig-like.
FT MOD RES 1 125 Pyrolysine carboxylic acid.
FT NONTER 125 125
SQ SEQUENCE 125 AA; 13783 MW; 7A1ADF4C40F47BB5 CRC64;

Query Match          50.7%; Score 407; DB 1; Length 125;
Best Local Similarity 71.9%; Pred. No. 9.1e-33;
Matches 82; Conservative 9; Mismatches 17; Indels 6; Gaps 2;

Qy 2 PQTTLTCTSGSLITRGVGVWIRPPGKALQWLALIYWNDDKRYSPSLKSLRTITK 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 14 PTETLTCTSGSLTSGVGVWIRPPGKALEWLAFINWDDNRYSPSLRSLRTITK 73
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 DTSKNQVLTWNTMDPVDVTATYCAH---HFFDSSGYYPFDSWGQGTLVSVSS 111
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 74 DTSRNVVLTITNMDPVDVDSGYFCAHRPPWRFTGNLG--GFDXWGQGTTLTVSS 125
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

```
RESULT 15
Q6IN78 PRELIMINARY; PRT; 466 AA.
ID Q6IN78
AC Q6IN78;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Berge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uebin T.B., Toshikiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blackley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDE81076E CRC64;

Query Match          50.2%; Score 403; DB 2; Length 466;
Best Local Similarity 54.7%; Pred. No. 1.1e-31;
Matches 82; Conservative 21; Mismatches 37; Indels 10; Gaps 3;

Qy 2 PQTTLTCTSGSLITRGVGVWIRPPGKALQWLALIYWNDDKRYSPSLKSLRTITK 61
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 33 PGSLTILSCAASGLITVSN--YMHVVRQAPGKLEWVSIVIGATYVADSVKGRFTISR 90
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 62 DTSKNQVLTWNTMDPVDVTATYCAHHFFDSSGY--PFDSWGQGTLVSVSSASTKGPSV 119
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 91 DNSKNTLYLQMSLRARNTAVYCAR-----GNVVPAPAPGQGTTLTVSSASTKGPSV 144
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 120 FPLAPCSRSTSESTAALGCLVKDYFPEPTV 149
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
```

Db 145 FPLAPSSKSTGGTAALGCLVKDYFPEPVT 174

Search completed: March 8, 2005, 06:35:54
Job time : 56.644 secs

GenCore version 5.1.6
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QM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 69.0805 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-35

Perfect score: 803

Sequence: 1 NPQTLTLCTFGFSILTR.....SESTALGCLVVDYFPEPVT 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A_Geneseq_16Dec04:*
- 2: Geneseqpl9808:*
- 3: Geneseqpl9908:*
- 4: Geneseqpl2000s:*
- 5: Geneseqpl2001s:*
- 6: Geneseqpl2002s:*
- 7: Geneseqpl2003as:*
- 8: Geneseqpl2003bs:*
- 9: Geneseqpl2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	803	100.0	149	2 AAY34305	Aay34305 IGG antib
2	766	95.4	159	2 AAY34307	Aay34307 IGG antib
3	638.5	79.5	517	6 ABU08019	Abu08019 Monoclonal
4	638.5	79.5	518	7 ADF65782	Adf65782 Human ant
5	638.5	79.5	518	8 ADJ92518	Adj92518 Human SOJ
6	616.5	76.8	448	8 ADF71916	Adf71916 Hu3G8VH-2
7	608	75.7	453	6 ABP58287	Abp58287 Humanised
8	608	75.7	472	6 ABP58289	Abp58289 Humanised
9	602.5	75.0	448	8 ADF71908	Adf71908 Hu3G8VH-1
10	602.5	75.0	448	8 ADF71912	Adf71912 Hu3G8VH-5
11	602	75.0	228	7 ADJ32130	Adj32130 Human int
12	582.5	72.5	450	5 ABP66596	Abp66596 Human RSV
13	582.5	72.5	450	5 ABP66594	Abp66594 Human RSV
14	582.5	72.5	450	5 ABP66598	Abp66598 Human RSV
15	582.5	72.5	450	5 ABP66564	Abp66564 Human RSV
16	582.5	72.5	450	5 ABP66592	Abp66592 Human RSV
17	582.5	72.5	450	5 ABP66600	Abp66600 Human RSV
18	582.5	72.5	450	6 ABU69427	Abu69427 Respirato
19	582.5	72.5	450	6 ABU69455	Abu69455 Respirato
20	582.5	72.5	450	6 ABU69459	Abu69459 Respirato
21	582.5	72.5	450	6 ABU69457	Abu69457 Respirato
22	582.5	72.5	450	6 ABU69463	Abu69463 Respirato
23	582.5	72.5	450	6 ABU69461	Abu69461 Respirato
24	582.5	72.5	450	7 ADE35952	Ade35952 SYNAGIS a
25	582.5	72.5	450	7 ADE35956	Ade35956 SYNAGIS a

26	582.5	72.5	450	7 ADE35958	Ade35958 SYNAGIS a
27	582.5	72.5	450	7 ADE35954	Ade35954 SYNAGIS a
28	582.5	72.5	450	7 ADE35922	Ade35922 SYNAGIS a
29	582.5	72.5	450	7 ADE35950	Ade35950 SYNAGIS a
30	581.5	72.4	450	5 ABP66562	Abp66562 Human RSV
31	581.5	72.4	450	6 ABU69425	Abu69425 Respirato
32	581.5	72.2	450	7 ADE35920	Ade35920 SYNAGIS a
33	579.5	72.2	450	5 ABP66590	Abp66590 Human RSV
34	579.5	72.2	450	5 ABP66588	Abp66588 Human RSV
35	579.5	72.2	450	5 ABP66602	Abp66602 Human RSV
36	579.5	72.2	450	5 ABP66586	Abp66586 Human RSV
37	579.5	72.2	450	6 ABU69451	Abu69451 Respirato
38	579.5	72.2	450	6 ABU69453	Abu69453 Respirato
39	579.5	72.2	450	6 ABU69465	Abu69465 Respirato
40	579.5	72.2	450	6 ABU69448	Abu69448 Respirato
41	579.5	72.2	450	7 ADE35948	Ade35948 SYNAGIS a
42	579.5	72.2	450	7 ADE35946	Ade35946 SYNAGIS a
43	579.5	72.2	450	7 ADE35944	Ade35944 SYNAGIS a
44	578.5	72.0	450	4 AAE10517	Aae10517 Humanised
45	578.5	72.0	450	5 ABP66608	Abp66608 Human RSV

ALIGNMENTS

RESULT 1

AAY34305

ID AAY34305 standard; protein; 149 AA.

XX AC AAY34305;

XX AC AAY34305;

DT 19-NOV-1999 (first entry)

XX XX

DE IGG antibody 2.4.4 heavy chain sequence.

XX XX

KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX PN W09945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PR 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX DR WPI; 1999-540816/45.

XX DR N-PSDB; AAZ20406.

XX XX

PT New monoclonal antibody, used for treating e.g. graft versus host

PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 60; Fig 30; 245pp; English.

XX CC This sequence represents the heavy chain of an antibody of the invention.

CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes

CC complement and a variable region that binds to the epitope on CD147 bound

CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB

CC can selectively kill activated T-cells, activated B-cells or resting or

CC activated monocytes. The products and methods can be used for treating

CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft

CC versus host disease (GVHD), organ transplant rejection diseases (e.g.

CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
SQ Sequence 149 AA;
Query Match 100.0%; Score 803; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 2.7e-65;
Matches 149; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 NPQTTLTCTFSGFSLITRGVGVDMIRQPGKALQWLALIYWNDDKRYSPSLKSLRTIIT 60
Db 1 NPQTTLTCTFSGFSLITRGVGVDMIRQPGKALQWLALIYWNDDKRYSPSLKSLRTIIT 60
Qy 61 KDTSKNQVLTMTNMDPVDATYTCAHHFFDSSGYYPFDSWGQTLVSVSSASTKGPSVF 120
Db 61 KDTSKNQVLTMTNMDPVDATYTCAHHFFDSSGYYPFDSWGQTLVSVSSASTKGPSVF 120
Qy 121 PLAPCSRSTSESTAALGCLVKDYFPEPT 149
Db 121 PLAPCSRSTSESTAALGCLVKDYFPEPT 149
RESULT 2
AA34307
ID AAY34307 standard; protein; 159 AA.
AC AAY34307;
XX
XX
DT 19-NOV-1999 (first entry)
XX
DE IgG antibody 2.3.2 heavy chain sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
XX WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
XX 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
XX WPI; 1999-540816/45.
DR N-PSDB; AAZ20408.
XX
XX New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
XX Claim 60; Fig 32; 245pp; English.
XX
XX This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX

SQ Sequence 159 AA;
Query Match 95.4%; Score 766; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 6.8e-62;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 LTCFSGFSLITRGVGVDMIRQPGKALQWLALIYWNDDKRYSPSLKSLRTIITKDTSKNQ 67
Db 1 LTCFSGFSLITRGVGVDMIRQPGKALQWLALIYWNDDKRYSPSLKSLRTIITKDTSKNQ 60
Qy 68 VLTMTNMDPVDATYTCAHHFFDSSGYYPFDSWGQTLVSVSSASTKGPSVPLAPCSR 127
Db 61 VLTMTNMDPVDATYTCAHHFFDSSGYYPFDSWGQTLVSVSSASTKGPSVPLAPCSR 120
Qy 128 STSESTAALGCLVKDYFPEPT 149
Db 121 STSESTAALGCLVKDYFPEPT 142
RESULT 3
ABU08019
ID ABU08019 standard; protein; 517 AA.
AC ABU08019;
XX
XX 10-MAY-2003 (first entry)
DT
XX
DE Monoclonal rabies virus antibody heavy chain, clone JB.1.
XX
XX Human; antibody; constant region; monoclonal antibody 57; Mab 57;
KW variable region; Rabies; neurological disease; infection;
KW central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
KW pathogen; vaccine; virucide; heavy chain.
XX
XX Homo sapiens.
XX
XX WO2003016501-A2.
XX
XX 27-FEB-2003.
XX
XX 21-AUG-2002; 2002WO-US026584.
PF
XX
XX 21-AUG-2001; 2001US-0314023P.
PR
XX
XX (UYJB-) UNIV JEFFERSON THOMAS.
PA
XX
XX Hooper DC, Dietzschold B;
PI
XX
XX WPI; 2003-278566/27.
DR N-PSDB; ABX12861.
XX
XX New recombinant antibody comprising a constant region of Mab 57 linked to
PT a non-Mab 57 variable region, useful for treating an individual exposed
PT to a pathogen, e.g. rabies infection.
XX
XX Claim 1; Page 35; 38pp; English.
XX
XX The invention discloses a recombinant antibody comprising a constant
CC region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
CC region. Rabies is an acute, neurological disease caused by infection of
CC the central nervous system with the rabies virus, a member of the
CC Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods
CC for producing an isolated recombinant antibody by culturing a host cell,
CC containing a recombinant expression vector comprising the nucleic acid
CC molecule encoding the antibody, and isolating the recombinant antibody
CC expressed and treating an individual exposed to a pathogen by
CC administering to the individual the recombinant antibody. The recombinant
CC antibodies are useful for preventing (vaccine) and treating an individual
CC exposed to a pathogen, e.g. rabies infection. They are also useful for
CC the qualitative and quantitative determination of the rabies virus. The
CC sequences presented are the antibody protein fragments, the nucleic acids
CC encoding them or the PCR primers used to construct the recombinant
CC expression vector

XX SQ Sequence 517 AA;
Query Match 79.5%; Score 638.5; DB 6; Length 517;
Best Local Similarity 81.9%; Pred. No. 1e-49;
Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;
QY 2 PQTLLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKRLITTK 61
DB 33 PQTLLTCTCFSGSLSTSGVGVWIRQPPGKALEWTLIYWDKRYSPSLNRVTIRK 92
QY 62 DTSKNQVLTWNMDPVDATYCAHFFDSSGYYP-FDSMGQGLTVSVSSASTKGPSVF 120
DB 93 DTSKNQVLTWNMDPDLTGTYCAHRQHIS--FPWFDSMGQGLTVSVSSASTKGPSVF 150
QY 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149
DB 151 PLAPCSRSTSGGTAALGCLVKDYFPEPVT 179
RESULT 4
ADF65782
ID ADF65782 standard; protein; 518 AA.
XX AC ADF65782;
XX DT 12-FEB-2004 (first entry)
XX DE Human anti-rabies MAb JB.1 antibody heavy chain.
XX KW Immunoglobulin; Ig; heavy chain; light chain; human;
KW monoclonal rabies virus neutralising antibody; rabies virus protein;
KW neuronal tissue; antirabies; MAB JB.1.
XX OS Homo sapiens.
XX PN US2003157112-A1.
XX PD 21-AUG-2003.
XX PF 21-AUG-2002; 2002US-00225108.
XX PR 16-MAY-2000; 2000US-0204518P.
PR 04-MAY-2001; 2001US-00848832.
PR 21-AUG-2001; 2001US-0314023P.
XX PA (HOOP/) HOOPER D C.
PA (DIET/) DIETZSCHOLD B.
XX PI Hooper DC, Dietzschold B;
XX WPI; 2003-777974/73.
DR N-PSDB; ADF65781.
XX PT New isolated nucleic acid molecule encoding a sequence that neutralizes
PT an antibody that binds to rabies virus protein, useful for diagnosing,
PT preventing or treating infection of pathogens that target neuronal
PT tissues, e.g. rabies.
XX PS Claim 2; SEQ ID NO 10; 22pp; English.
XX CC The present invention relates to the isolation of immunoglobulin (Ig)
CC heavy and light chains of human monoclonal rabies virus neutralising
CC antibody, and the polynucleotide sequences encoding them. The antibody
CC specifically binds to a rabies virus protein. Also disclosed is a fused
CC gene encoding a chimeric immunoglobulin light or heavy chain comprising a
CC first DNA sequence encoding an immunoglobulin light or heavy chain
CC variable region of a monoclonal rabies virus neutralising antibody
CC produced by a heterohybridoma cell line and a second DNA sequence
CC encoding a human light or heavy chain constant region, and methods of
CC producing a recombinant antibody. The polynucleotide sequences, and
CC antibodies and methods are useful for diagnosing, preventing or treating
CC an infection of pathogens that target neuronal tissues, particularly

CC rabies. The present sequence represents human anti-rabies MAB JB.1
CC antibody heavy chain.
XX SQ Sequence 518 AA;
Query Match 79.5%; Score 638.5; DB 7; Length 518;
Best Local Similarity 81.9%; Pred. No. 1.1e-49;
Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;
QY 2 PQTLLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKRLITTK 61
DB 33 PQTLLTCTCFSGSLSTSGVGVWIRQPPGKALEWTLIYWDKRYSPSLNRVTIRK 92
QY 62 DTSKNQVLTWNMDPVDATYCAHFFDSSGYYP-FDSMGQGLTVSVSSASTKGPSVF 120
DB 93 DTSKNQVLTWNMDPDLTGTYCAHRQHIS--FPWFDSMGQGLTVSVSSASTKGPSVF 150
QY 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149
DB 151 PLAPCSRSTSGGTAALGCLVKDYFPEPVT 179
RESULT 5
ADJ92518
ID ADJ92518 standard; protein; 518 AA.
XX AC ADJ92518;
XX DT 06-MAY-2004 (first entry)
XX DE Human SOJB monoclonal antibody heavy chain protein.
XX KW Rabies virus infection; pharmaceutical; vaccine; gene therapy; virucide;
KW human; SOJB monoclonal antibody.
XX OS Homo sapiens.
XX PN US2004013672-A1.
XX PD 22-JAN-2004.
XX PF 13-JUN-2003; 2003US-00461148.
XX PR 16-MAY-2000; 2000US-0204518P.
PR 04-MAY-2001; 2001US-00848832.
PR 21-AUG-2001; 2001US-0314023P.
PR 21-AUG-2002; 2002US-00225108.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX PI Hooper DC, Dietzschold B;
XX WPI; 2004-108190/11.
DR N-PSDB; ADJ92517.
XX PT New pharmaceutical composition comprising at least two recombinant rabies
PT virus-neutralizing human antibodies, useful for treating or preventing
PT rabies virus infection.
XX PS Claim 1; SEQ ID NO 4; 28pp; English.
XX CC The present invention relates to a method of treating or preventing a
CC rabies virus infection in a subject. The invention also relates to novel
CC pharmaceutical composition comprising a carrier and at least two
CC recombinant rabies virus-neutralising human antibodies, where the
CC antibody comprises an antibody comprising an antibody light chain or its
CC homologue and an antibody heavy chain or its homologue. The
CC pharmaceutical composition is useful for treating or preventing rabies
CC virus infection. The invention is also useful as vaccine and in gene
CC therapy. The pharmaceutical composition is useful for treating or
CC preventing rabies virus infection. The present sequence is rabies virus-
CC neutralising human SOJB monoclonal antibody heavy chain protein used in
CC the invention.

XX SQ Sequence 518 AA;
 Query Match 79.5%; Score 638.5; DB 8; Length 518;
 Best Local Similarity 81.9%; Pred. No. 1.1e-49;
 Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;

QY 2 PQTLLTCTFSGFSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
 DB 33 PTQTLTCTFSGFSLTSGVGVWIRQPPGKALEWTLIYWNDDKRYSPSLNRTVIRK 92

QY 62 DTSKNQVLTWNTMNDPVDATYTCYCAHHFDPSSGGYYP-FDSWGQGLTVSVSSASTKGPSVF 120
 DB 93 DTSKNQVLTWNTMNDPDLDTGYTCYCAHHQHISS--FPWFDSWGQGLTVSVSSASTKGPSVF 150

QY 121 PLAPCSRSTSESTAALGCLVKDYPEPVT 149
 DB 151 PLAPCSRSTSGGTAALGCLVKDYPEPVT 179

RESULT 6
 ID ADF71916 standard; protein; 448 AA.
 XX ADF71916;
 XX XX
 DT 26-FEB-2004 (first entry)
 XX XX
 DE Hu3G8VH-22G1Ag amino acid sequence SEQ ID NO:115.
 XX anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
 KW immune response; haemostatic; antirheumatic; antiarthritic;
 KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
 KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
 KW opthalmological; antiasthmatic; inflammatory response;
 KW autoimmune disease; idiopathic thrombocytopenic purpura;
 KW rheumatoid arthritis; systemic lupus erythematosus;
 KW autoantibody triggered anaemia; scleroderma;
 KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
 KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
 KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
 KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
 KW allergic asthma.
 XX XX
 OS Synthetic.
 OS Mus sp.
 OS Homo sapiens.
 XX XX
 PN WO2003101485-A1.
 XX
 PD 11-DEC-2003.
 XX
 XX 29-MAY-2003; 2003WO-US017111.
 XX
 XX 30-MAY-2002; 2002US-0384689P.
 PR 10-JAN-2003; 2003US-0439320P.
 XX
 XX (MACR-) MACROGENICS INC.
 PA
 XX Johnson LS, Huang L, Li H, Tuallion N;
 PI
 XX WPI; 2004-042985/04.
 DR
 XX Novel anti-CD16A antibody comprising complementarity determining regions
 PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
 FT lacks effector function, useful for treating deleterious immune response.
 FT
 XX
 PS Disclosure; SEQ ID NO 115; 103pp; English.
 XX
 CC The present invention describes an anti-CD16A antibody (I) comprising a
 CC VH domain comprising complementarity determining regions (CDRs) derived
 CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
 CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A

CC antibody (II) that lacks effector function and comprises all six CDRs of
 CC mouse antibody 3G8. Also described is a method (M1) for reducing a
 CC deleterious immune response in a mammal in need of such reduction, which
 CC involves administering to the mammal a CD16A binding protein comprising
 CC an Fc region derived from a human IgG heavy chain, where the Fc region
 CC lacks effector function or is modified to reduce binding to an Fc
 CC effector ligand. (I) and (II) have haemostatic, antiinflammatory,
 CC antiarthritic, dermatological, immunosuppressive, antirheumatic,
 CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
 CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
 CC useful for reducing a deleterious immune response in a mammal which
 CC involves administering to the mammal (I) or (II). The deleterious immune
 CC response is an inflammatory response caused by autoimmune disease such as
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
 CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
 CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
 CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
 CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
 CC and also for treating diseases susceptible to treatment with intravenous
 CC immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence
 CC is used in the exemplification of the present invention.
 XX SQ Sequence 448 AA;
 Query Match 76.8%; Score 616.5; DB 8; Length 448;
 Best Local Similarity 81.1%; Pred. No. 9.1e-48;
 Matches 120; Conservative 9; Mismatches 14; Indels 5; Gaps 2;

QY 2 PQTLLTCTFSGFSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
 DB 14 PTQTLTCTFSGFSLTSGVGVWIRQPPGKALEWTLIYWNDDKRYSPSLKSLRLTISK 73

QY 62 DTSKNQVLTWNTMNDPVDATYTCYCAHHFDPSSGGYYPFDSWGQGLTVSVSSASTKGPSVFP 121
 DB 74 DTSKNQVLTWNTMNDPVDATYTCYCAR---INPAYFAY--WGQGLTVTVSSASTKGPSVFP 128

QY 122 LAPCSRSTSESTAALGCLVKDYPEPVT 149
 DB 129 LAPCSRSTSGGTAALGCLVKDYPEPVT 156

RESULT 7
 ABP58287
 ID ABP58287 standard; protein; 453 AA.
 XX ABP58287;
 AC ABP58287;
 XX
 DT 23-OCT-2003 (revised)
 DT 31-MAR-2003 (first entry)
 XX
 DE Humanised 10D5 antibody heavy chain.
 XX
 KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
 KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Region 1..123
 FT /note= "light chain variable region"
 FT Region 31..35
 FT /note= "CDR1"
 FT Region 52..67
 FT /note= "CDR2"
 FT Region 100..112
 FT /note= "CDR3"
 XX
 PN WO200288307-A2.
 XX

PD 07-NOV-2002.

XX 26-APR-2002; 2002WO-US011854.

PF 30-APR-2001; 2001US-0287653P.

PR (ELIL) LILLY & CO ELI.

XX Hinton PR, Vasquez M;

XX WPI; 2003-183836/18.

DR New humanized 10D5 antibody, useful for the manufacture of a medicament

PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's

PT disease or cerebral amyloid angiopathy.

XX Claim 5; Page 10-12; 52pp; English.

XX The present sequence is the protein sequence of the heavy chain of a

CC humanised antibody of the present invention. In the variable portion, the

CC complementarity determining regions (CDRs) originate from murine

CC monoclonal antibody 10D5 and the framework region originates from human

CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies

CC of the invention have CDRs from 10D5 and human framework sequences. These

CC humanised antibodies have binding affinities (affinity and epitope

CC location) approximately the same as those of the mouse 10D5 antibody. The

CC invention includes antibodies, single chain antibodies, and their

CC fragments, as well as nucleotide sequences, vectors, transformed host

CC cells, and methods of using the humanised antibody to treat, prevent,

CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology

CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or

CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or

CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise

CC OS field)

XX SQ Sequence 453 AA;

Query Match 75.7%; Score 608; DB 6; Length 453;

Best Local Similarity 79.1%; Pred. No. 5.5e-47;

Matches 117; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

Qy 2 PQTTLTCTFSGSLITRGVGVDMIRPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61

Db 14 PTEFLTCTFSGSLTSGMGVSWIRPPGKALEWLAHIYWDKRYNPSLKSRLITSK 73

Qy 62 DTSKNQVVLTMNDPVDVTATYYCAHHFFDSSGGYYPFDSWGQGLTVSVSSASTKGPSVFP 121

Db 74 DTSKSQVVLTMNDPVDVTATYYCVRRTPTPVLVDAMDYWGQGLTVTVSSASTKGPSVFP 133

Qy 122 LAPCSRSTSESTALGCLVKDYFPEPVT 149

Db 134 LAPSSKSTSGGTAALGCLVKDYFPEPVT 161

RESULT 8

ABP58289

ID ABP58289 standard; protein; 472 AA.

XX AC ABP58289;

XX 23-OCT-2003 (revised)

DT 31-MAR-2003 (first entry)

XX Humanised 10D5 antibody heavy chain.

XX Monoclonal antibody; 10D5; complementarity determining region; CDR;

KW mouse; human; humanised antibody; antibody; Alzheimer's disease;

KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.

XX Mus sp.

OS Homo sapiens.

OS Chimeric.

EH Key Location/Qualifiers

FT Peptide 1..19

FT Peptide /label= Signal_peptide

FT Peptide 20..472

FT /label= Mature protein

FT /note= "the mature light chain is claimed in Claim 5"

FT Region 20..142

FT /note= "light chain variable region, claimed in Claim 4"

FT Region 50..56

FT /note= "CDR1"

FT Region 71..86

FT /note= "CDR2"

FT Region 119..131

FT /note= "CDR3"

XX WO200288307-A2.

XX 07-NOV-2002.

XX 26-APR-2002; 2002WO-US011854.

XX 30-APR-2001; 2001US-0287653P.

XX (ELIL) LILLY & CO ELI.

XX Hinton PR, Vasquez M;

XX WPI; 2003-183836/18.

XX N-PSDB; ABZ24639, ABZ24641.

DR New humanized 10D5 antibody, useful for the manufacture of a medicament

DR for treating Down's syndrome, clinical or pre-clinical Alzheimer's

PT disease or cerebral amyloid angiopathy.

XX Disclosure; Page 13-15; 52pp; English.

XX The present sequence is the protein sequence of the heavy chain of a

CC humanised antibody of the present invention. In the variable portion, the

CC complementarity determining regions (CDRs) originate from murine

CC monoclonal antibody 10D5 and the framework region originates from human

CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies

CC of the invention have CDRs from 10D5 and human framework sequences. These

CC humanised antibodies have binding affinities (affinity and epitope

CC location) approximately the same as those of the mouse 10D5 antibody. The

CC invention includes antibodies, single chain antibodies, and their

CC fragments, as well as nucleotide sequences, vectors, transformed host

CC cells, and methods of using the humanised antibody to treat, prevent,

CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology

CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or

CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or

CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise

CC OS field)

XX SQ Sequence 472 AA;

Query Match 75.7%; Score 608; DB 6; Length 472;

Best Local Similarity 79.1%; Pred. No. 5.7e-47;

Matches 117; Conservative 8; Mismatches 23; Indels 0; Gaps 0;

Qy 2 PQTTLTCTFSGSLITRGVGVDMIRPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61

Db 33 PTEFLTCTFSGSLTSGMGVSWIRPPGKALEWLAHIYWDKRYNPSLKSRLITSK 92

Qy 62 DTSKNQVVLTMNDPVDVTATYYCAHHFFDSSGGYYPFDSWGQGLTVSVSSASTKGPSVFP 121

Db 93 DTSKSQVVLTMNDPVDVTATYYCVRRTPTPVLVDAMDYWGQGLTVTVSSASTKGPSVFP 152

Qy 122 LAPCSRSTSESTALGCLVKDYFPEPVT 149

Db 153 LAPSSKSTSGGTAALGCLVKDYFPEPVT 180

RESULT 9

AD71908
ID ADF71908 standard; protein; 448 AA.
AC ADF71908;
XX
XX
DT 26-FEB-2004 (first entry)
XX
XX Hu3G8VH-1G1 amino acid sequence SEQ ID NO:107.
DE
XX anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
XX WO2003101485-A1.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US017111.
XX
XX 30-MAY-2002; 2002US-0384689P.
PR
PR 10-JAN-2003; 2003US-0439320P.
XX
XX (MACR-) MACROGENICS INC.
XX
XX Johnson LS, Huang L, Li H, Tuailon N;
PI
XX WPI; 2004-042985/04.
DR
XX
XX Novel anti-CD16A antibody comprising complementarity determining regions
PT derived from mouse 3G8 antibody and humanised anti-CD16A antibody that
PT lacks effector function, useful for treating deleterious immune response.
XX
XX Disclosure; SEQ ID NO 107; 103pp; English.
XX
XX The present invention describes an anti-CD16A antibody (I) comprising a
CC VH domain comprising complementarity determining regions (CDRs) derived
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an Fc region derived from a human IgG heavy chain, where the Fc region
CC lacks effector function or is modified to reduce binding to an Fc
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence

CC is used in the exemplification of the present invention.
XX
SQ Sequence 448 AA;
Query Match 75.0%; Score 602.5; DB 8; Length 448;
Best Local Similarity 78.7%; Pred. No. 1.7e-46;
Matches 118; Conservative 9; Mismatches 14; Indels 9; Gaps 2;
QY 2 PQTTLTCTCFSGSLITRGVWDIROPFGKALQWLALYWNDDKRYSPSLKSLRLITIK 61
DB 14 PTQTLTCTCFSGSLSTSGMGVGNIRQPPGKALEWLHLWDDDKRYNPAKSLRLTISK 73
QY 62 DTSKNQVLLTMTNMDPVDATYTCYCAHHFFDSSGYYP--FDSWGQGTLLSVSSASTKGPSV 119
DB 74 DTSKNQVLLTMTNMDPVDATYTCYCAR-----INPAWFAYWGQGTLLTVSSASTKGPSV 126
QY 120 FPLAPCSRSTSESTAAALGCLVKDYFPEPVT 149
DB 127 FPLAPSKSTSGGTAALGCLVKDYFPEPVT 156
RESULT 10
ADF71912
ID ADF71912 standard; protein; 448 AA.
XX
XX ADF71912;
XX
XX 26-FEB-2004 (first entry)
XX
XX Hu3G8VH-5G1ag amino acid sequence SEQ ID NO:111.
XX
XX anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
XX WO2003101485-A1.
XX
XX 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US017111.
XX
XX 30-MAY-2002; 2002US-0384689P.
PR
PR 10-JAN-2003; 2003US-0439320P.
XX
XX (MACR-) MACROGENICS INC.
XX
XX Johnson LS, Huang L, Li H, Tuailon N;
PI
XX WPI; 2004-042985/04.
DR
XX
XX Novel anti-CD16A antibody comprising complementarity determining regions
PT derived from mouse 3G8 antibody and humanised anti-CD16A antibody that
PT lacks effector function, useful for treating deleterious immune response.
XX
XX Disclosure; SEQ ID NO 107; 103pp; English.
XX
XX The present invention describes an anti-CD16A antibody (I) comprising a
CC VH domain comprising complementarity determining regions (CDRs) derived
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an Fc region derived from a human IgG heavy chain, where the Fc region
CC lacks effector function or is modified to reduce binding to an Fc
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence

CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
 CC antibody (II) that lacks effector function and comprises all six CDRs of
 CC mouse antibody 3G8. Also described is a method (M1) for reducing a
 CC deleterious immune response in a mammal in need of such reduction, which
 CC involves administering to the mammal a CD16A binding protein comprising
 CC an Fc region derived from a human Igg heavy chain, where the Fc region
 CC lacks effector function or is modified to reduce binding to an Fc
 CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
 CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
 CC antianemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
 CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
 CC useful for reducing a deleterious immune response in a mammal which
 CC involves administering to the mammal (I) or (II). The deleterious immune
 CC response is an inflammatory response caused by autoimmune disease such as
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
 CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
 CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
 CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
 CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
 CC and also for treating diseases susceptible to treatment with intravenous
 CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence
 CC is used in the exemplification of the present invention.

XX Sequence 448 AA;

Query Match 75.0%; Score 602.5; DB 8; Length 448;
 Best Local Similarity 78.7%; Pred. No. 1.7e-46;
 Matches 118; Conservative 9; Mismatches 14; Indels 9; Gaps 2;

Qy 2 PQTTLTCTFSGLTRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
 Db 14 PTQTLTCTFSGLTRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITK 73
 Qy 62 DTSKNQVLLTNTNDPVDATYTCARHFFDSSGYVP--FDSWGQGLTVSVSSASTKGPSV 119
 Db 74 DTSKNQVLLTNTNDPVDATYTCARHFFDSSGYVP--FDSWGQGLTVSVSSASTKGPSV 126

Qy 120 FPLAPCSRSTSESTAALGCLVKDYFPEPT 149
 Db 127 FPLAPSKSTSGGTAALGCLVKDYFPEPT 156

RESULT 11
 ADJ32130
 ID ADJ32130 standard; protein; 228 AA.

AC ADJ32130;
 XX 22-APR-2004 (first entry)
 DT Human interferon-gamma antibody heavy chain amino acid sequence SeqID84.
 DE antibody; antigen binding domain; interferon-gamma; INF-gamma;
 KW antagonist antibody; antiinflammatory; immunosuppressive;
 KW autoimmune disease; inflammatory condition; human; heavy chain.
 XX Homo sapiens.

XX US2003099647-A1.
 XX 29-MAY-2003.
 XX 05-OCT-2001; 2001US-00972656.
 XX 05-OCT-2001; 2001US-00972656.

XX (DESH/) DESHPANDE R V.
 XX (TSAI/) TSAI M.

XX Deshpande RV, Tsai M;

XX WPI; 2003-696068/66.

DR N-PSDB; ADJ32129.

XX New antibody or antigen binding domain, or its fragment, variant or
 PT derivative, which binds to an interferon-gamma protein, useful for
 PT preparing a composition for preventing or treating inflammatory or
 PT autoimmune disorders.

XX Claim 10; SEQ ID NO 84; 113pp; English.

XX This invention relates to a novel antibody or antigen binding domain, or
 CC its fragment, variant or derivative, which binds to an interferon-gamma
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be
 CC useful for the development of compounds with an antiinflammatory or
 CC immunosuppressive activity through action as interferon-gamma agonists. A
 CC composition containing the antibody is useful for preventing or treating
 CC an autoimmune disease and an inflammatory condition. The present sequence
 CC is that of an antibody heavy chain of a human IFN-gamma antibody which
 CC may be part of the invention.

XX Sequence 228 AA;

Query Match 75.0%; Score 602; DB 7; Length 228;
 Best Local Similarity 76.0%; Pred. No. 9e-47;
 Matches 114; Conservative 11; Mismatches 23; Indels 2; Gaps 1;

Qy 2 PQTTLTCTFSGLTRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
 Db 14 PTQTLTCTFSGLTRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITK 73

Qy 62 DTSKNQVLLTNTNDPVDATYTCARHFFDSSGYVP--FDSWGQGLTVSVSSASTKGPSV 119
 Db 74 DTSKNQVLLTNTNDPVDATYTCARHFFDSSGYVP--FDSWGQGLTVSVSSASTKGPSV 133

Qy 120 FPLAPCSRSTSESTAALGCLVKDYFPEPT 149
 Db 134 FPLAPSKSTSGGTAALGCLVKDYFPEPT 163

RESULT 12
 ABP66596
 ID ABP66596 standard; protein; 450 AA.

XX ABP66596;
 XX 04-DEC-2002 (first entry)
 DT Human RSV antibody variable heavy chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.

XX Homo sapiens.
 XX WO200243660-A2.
 XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.

XX 28-NOV-2000; 2000US-00724396.

XX 28-NOV-2000; 2000US-00724531.

XX (MEDI-) MEDIUMMUNE INC.

XX Young JF, Koenig S, Johnson LS;

XX WPI; 2002-706803/76.

XX Antibody for treating respiratory syncytial virus (RSV) infection,

XX Young JF, Koenig S, Johnson LS;
XX WPI; 2002-706803/76.
XX Antibody for treating respiratory syncytial virus (RSV) infection,
XX comprises a variable heavy/light domain or complementarity determining
XX regions 1 - 3 of variable light/heavy chains, that immunospecifically
XX binds to RSV antigen.
XX Disclosure; Page 282-283; 298pp; English.
XX The invention relates to a novel antibody comprising a variable heavy
XX (VH) domain, variable light (VL) domain, VH complementarity determining
XX region (CDR)-1, VH CDR2, VL CDR1, VL CDR2 or VL CDR3, where the
XX antibody immunospecifically binds to a respiratory syncytial virus (RSV)
XX antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
XX invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
XX and immunostimulant activity. The polynucleotides of the invention may
XX have a use in a vaccine, and in gene therapy. The antibody is useful for
XX treating or ameliorating a RSV infection in a human. The antibody is also
XX useful for preventing, treating or ameliorating one or more symptoms
XX associated with RSV infection in a mammal, e.g. cystic fibrosis,
XX bronchopulmonary dysplasia, congenital heart disease, congenital
XX immunodeficiency or acquired immunodeficiency, or after a bone marrow
XX transplant. The sequence represents a variable domain of a human RSV
XX antibody of the invention
XX Sequence 450 AA;
Query Match 72.5%; Score 582.5; DB 5; Length 450;
Best Local Similarity 76.4%; Pred. No. 1.1e-44;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;
Qy 2 PQTTLTCTSGFSLITRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61
Db 14 PTQTLTCTSGFSLITRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITSK 73
Qy 62 DTSKNQVVLVTNNMDPVDATYTCYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLVTNNMDPVDATYTCYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTALGCLVVDYFPEPVT 149
Db 131 LAPSSKSTSGGTAALGCLVVDYFPEPVT 158
RESULT 15
ABP66564
ID ABP66564 standard; protein; 450 AA.
XX AC ABP66564;
XX DT 04-DEC-2002 (first entry)
XX DE Human RSV antibody variable heavy chain.
XX KW Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
XX complementarity determining region; respiratory syncytial virus;
XX virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
XX immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
XX bronchopulmonary dysplasia; congenital heart disease;
XX congenital immunodeficiency; acquired immunodeficiency.
XX Homo sapiens.
XX WO200243660-A2.
XX 06-JUN-2002.
XX 28-NOV-2001; 2001WO-US044807.
XX 28-NOV-2000; 2000US-00724396.

PR 28-NOV-2000; 2000US-00724531.
XX (MEDI-) MEDIUMMUNE INC.
XX Young JF, Koenig S, Johnson LS;
XX WPI; 2002-706803/76.
XX Antibody for treating respiratory syncytial virus (RSV) infection,
XX comprises a variable heavy/light domain or complementarity determining
XX regions 1 - 3 of variable light/heavy chains, that immunospecifically
XX binds to RSV antigen.
XX Disclosure; Page 243-245; 298pp; English.
XX The invention relates to a novel antibody comprising a variable heavy
XX (VH) domain, variable light (VL) domain, VH complementarity determining
XX region (CDR)-1, VH CDR2, VL CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
XX antibody immunospecifically binds to a respiratory syncytial virus (RSV)
XX antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
XX invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
XX and immunostimulant activity. The polynucleotides of the invention may
XX have a use in a vaccine, and in gene therapy. The antibody is useful for
XX treating or ameliorating a RSV infection in a human. The antibody is also
XX useful for preventing, treating or ameliorating one or more symptoms
XX associated with RSV infection in a mammal, e.g. cystic fibrosis,
XX bronchopulmonary dysplasia, congenital heart disease, congenital
XX immunodeficiency or acquired immunodeficiency, or after a bone marrow
XX transplant. The sequence represents a variable domain of a human RSV
XX antibody of the invention
XX Sequence 450 AA;
Query Match 72.5%; Score 582.5; DB 5; Length 450;
Best Local Similarity 76.4%; Pred. No. 1.1e-44;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;
Qy 2 PQTTLTCTSGFSLITRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITTK 61
Db 14 PTQTLTCTSGFSLITRGVGVWIRPPGKALQWLALYWNDDKRYSPSLKSLRLITSK 73
Qy 62 DTSKNQVVLVTNNMDPVDATYTCYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLVTNNMDPVDATYTCYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTALGCLVVDYFPEPVT 149
Db 131 LAPSSKSTSGGTAALGCLVVDYFPEPVT 158
Search completed: March 8, 2005, 06:17:17
Job time : 70.0805 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 79.0704 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-35

Perfect score: 803

Sequence: 1 NPQTLTLTCTFGSFLITR.....SESTALGCLVKDYFPPVPT 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	638.5	79.5	518	14	US-10-225-108A-10
2	638.5	79.5	518	15	US-10-461-148-4
3	616.5	76.8	448	15	US-10-449-566-115
4	602.5	75.0	448	15	US-10-449-566-107
5	602.5	75.0	448	15	US-10-449-566-111
6	602	75.0	228	10	US-09-972-656-84
7	582.5	72.5	450	9	US-09-996-288-210
8	582.5	72.5	450	9	US-09-996-288-238
9	582.5	72.5	450	9	US-09-996-288-240
10	582.5	72.5	450	9	US-09-996-288-242
11	582.5	72.5	450	9	US-09-996-288-244
12	582.5	72.5	450	9	US-09-996-288-246
13	582.5	72.5	450	10	US-09-996-265-210

14	582.5	72.5	450	10	US-09-996-265-238
15	582.5	72.5	450	10	US-09-996-265-240
16	582.5	72.5	450	10	US-09-996-265-242
17	582.5	72.5	450	10	US-09-996-265-244
18	582.5	72.5	450	10	US-09-996-265-246
19	582.5	72.5	450	16	US-10-900-230-210
20	582.5	72.5	450	16	US-10-900-230-238
21	582.5	72.5	450	16	US-10-900-230-240
22	582.5	72.5	450	16	US-10-900-230-242
23	582.5	72.5	450	16	US-10-900-230-244
24	582.5	72.5	450	16	US-10-900-230-246
25	581.5	72.4	450	9	US-09-996-288-208
26	581.5	72.4	450	10	US-09-996-265-208
27	581.5	72.4	450	16	US-10-900-230-208
28	579.5	72.2	450	9	US-09-996-288-232
29	579.5	72.2	450	9	US-09-996-288-234
30	579.5	72.2	450	9	US-09-996-288-236
31	579.5	72.2	450	9	US-09-996-288-248
32	579.5	72.2	450	10	US-09-996-265-232
33	579.5	72.2	450	10	US-09-996-265-234
34	579.5	72.2	450	10	US-09-996-265-236
35	579.5	72.2	450	10	US-09-996-265-238
36	579.5	72.2	450	16	US-10-900-230-232
37	579.5	72.2	450	16	US-10-900-230-234
38	579.5	72.2	450	16	US-10-900-230-236
39	579.5	72.2	450	16	US-10-900-230-248
40	578.5	72.0	450	9	US-09-996-288-45
41	578.5	72.0	450	9	US-09-996-288-252
42	578.5	72.0	450	9	US-09-996-288-256
43	578.5	72.0	450	9	US-09-996-288-254
44	578.5	72.0	450	9	US-09-996-288-256
45	578.5	72.0	450	10	US-09-996-265-226

ALIGNMENTS

RESULT 1
US-10-225-108A-10
; Sequence 10, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225.108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-10

Query Match 79.5%; Score 638.5; DB 14; Length 518;
Best Local Similarity 81.9%; Pred. No. 7.6e-46;
Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;
Qy 2 PQTTLTCTFGSFLITRGGVDWIRQPPGKALQWLAIYWNDDKRYSPSLKRLTITK 61
Db 33 PQTTLTCTFGSFLITRGGVDWIRQPPGKALEWTVLIYWDKRYSPSLNRVTIRK 92
Qy 62 DTSKNQVLTWNTMDPDVTATYICAHFFDSSGGYYP-FDSWGQCTLYSVSSASTKGRPVF 120

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Db 93 DTSKNQVLTWNTNDPLDTGTYCAHRQHISS--FPWFDSWGQGLTVTVSSASTKGPSVF 150
Qy 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 151 PLAPCSRSTSGGTAALGCLVKDYFPEPVT 179

RESULT 2
US-10-461-148-4
; Sequence 4, Application US/10461148
; Publication No. US20040013672A1
; GENERAL INFORMATION:
; APPLICANT: Dietzschold, Bernhard
; TITLE OF INVENTION: RECOMBINANT ANTIBODIES AND COMPOSITIONS
; TITLE OF INVENTION: AND METHODS FOR MAKING AND USING THE SAME
; FILE REFERENCE: 8321-110C11-185685
; CURRENT FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: US 10/225,108
; PRIOR FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Human
US-10-461-148-4

Query Match 79.5%; Score 638.5; DB 15; Length 518;
Best Local Similarity 81.9%; Pred. No. 7.6e-46;
Matches 122; Conservative 9; Mismatches 15; Indels 3; Gaps 2;

Qy 2 PQTTLTCTCFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db 33 PTQTLTCTCFSGFSLSTSGVGWIRQPPGKALEWVTLIYWNDDKRYSPSLNRRVTIRK 92
Qy 62 DTSKNQVLTWNTNDPVDYATYYCAHHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSVF 120
Db 93 DTSKNQVLTWNTNDPLDTGTYCAHRQHISS--FPWFDSWGQGLTVTVSSASTKGPSVF 150
Qy 121 PLAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 151 PLAPCSRSTSGGTAALGCLVKDYFPEPVT 179

RESULT 3
US-10-449-566-115
; Sequence 115, Application US/10449566
; Publication No. US20040010124A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: LI, Hua
; APPLICANT: HUANG, Ling
; APPLICANT: TUAILLON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529392000100
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
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; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-449-566-115

Query Match 76.8%; Score 616.5; DB 15; Length 448;
Best Local Similarity 81.1%; Pred. No. 4.8e-44;
Matches 120; Conservative 9; Mismatches 14; Indels 5; Gaps 2;

Qy 2 PQTTLTCTCFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db 14 PTQTLTCTCFSGFSLSTSGVGWIRQPPGKALEWLAHIWDDDKRYSPSLKSLRLITK 73
Qy 62 DTSKNQVLTWNTNDPVDYATYYCAHHFFDSSGYYPFDSWGQGLTVSVSSASTKGPSVF 121
Db 74 DTSKNQVLTWNTNDPVDYATYYCAR---INPAYFAY--WGQGLTVTVSSASTKGPSVF 128
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 129 LAPSSKSTSGGTAALGCLVKDYFPEPVT 156

RESULT 4
US-10-449-566-107
; Sequence 107, Application US/10449566
; Publication No. US20040010124A1
; GENERAL INFORMATION:
; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: HUANG, Ling
; APPLICANT: LI, Hua
; APPLICANT: TUAILLON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529392000100
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 107
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-449-566-107

Query Match 75.0%; Score 602.5; DB 15; Length 448;
Best Local Similarity 78.7%; Pred. No. 7.3e-43;
Matches 118; Conservative 9; Mismatches 14; Indels 9; Gaps 2;

Qy 2 PQTTLTCTCFSGFSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db 14 PTQTLTCTCFSGFSLSTSGVGWIRQPPGKALEWLAHIWDDDKRYSPSLKSLRLITK 73
Qy 62 DTSKNQVLTWNTNDPVDYATYYCAHHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSV 119
Db 74 DTSKNQVLTWNTNDPVDYATYYCAR-----INPAWFAWVGQGLTVTVSSASTKGPSV 126
Qy 120 FPLAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 127 FPLAPSKSTSGGTAALGCLVKDYFPEPVT 156

RESULT 5
US-10-449-566-111
; Sequence 111, Application US/10449566
; Publication No. US20040010124A1
```

; GENERAL INFORMATION:

; APPLICANT: JOHNSON, Leslie S.
; APPLICANT: HUANG, Ling
; APPLICANT: Li, Hua
; APPLICANT: TUAILON, Nadine
; TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
; TITLE OF INVENTION: TREATMENT OF IMMUNE DISORDERS
; FILE REFERENCE: 529332000100
; CURRENT APPLICATION NUMBER: US/10/449,566
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/384,689
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/439,320
; PRIOR FILING DATE: 2003-01-10
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 111
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-449-566-111

Query Match 75.0%; Score 602.5; DB 15; Length 448;
Best Local Similarity 78.7%; Pred. No. 7.3e-43;
Matches 118; Conservative 9; Mismatches 14; Indels 9; Gaps 2;

QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 14 PTQTLLTCTCFSGSLTSGMGVWIRQPPGKALEWLALHWWDDKKRYNPAKLSRLTISK 73

QY 62 DTSKNQVLTMTNMDPVDATYYCAHHFFDSSGYYP--FDSWGQGTLLVSSASTKGPSV 119
Db 74 DTSKNQVLTMTNMDPVDATYYCAQ-----INPAWFAWYGQGLTVTVSSASTKGPSV 126

QY 120 FPLAPCSRSTSESTAALGCLVKDYFPEPV 149
Db 127 FPLAPSKSTSGGTAALGCLVKDYFPEPV 156

RESULT 6

US-09-972-656-84
; Sequence 84, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 84
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-84

Query Match 75.0%; Score 602; DB 10; Length 228;
Best Local Similarity 76.0%; Pred. No. 4e-43;
Matches 114; Conservative 11; Mismatches 23; Indels 2; Gaps 1;

QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 14 PTQTLLTCTSYSGFSLTSGNEAGVWIRQPPGKAPLWLLYWNDDKKRYSPSLRLIVNK 73

QY 62 DTSKNQVLTMTNMDPVDATYYCAHHFFDSSGYYP--FDSWGQGTLLVSSASTKGPSV 119
Db 74 DTSKNQVLTMTNMDPVDATYYCAHRLVRYGGYSTGDFWVGQGTTVTVSSASTKGPSV 133

QY 120 FPLAPCSRSTSESTAALGCLVKDYFPEPV 149
Db 134 FPLAPSKSTSGGTAALGCLVKDYFPEPV 163

RESULT 7

US-09-996-288-210
; Sequence 210, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 210
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-210

Query Match 72.5%; Score 582.5; DB 9; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.6e-41;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 14 PTQTLLTCTCFSGSLTSGMGVWIRQPPGKALEWLALHWWDDKKDYNPSLKSRLTISK 73

QY 62 DTSKNQVLTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGTLLVSSASTKGPSVFP 121
Db 74 DTSKNQVLTMTNMDPVDATYYCARSMI--TNFY-FDWVGQGTTVTVSSASTKGPSVFP 130

QY 122 LAPCSRSTSESTAALGCLVKDYFPEPV 149
Db 131 LAPSKSTSGGTAALGCLVKDYFPEPV 158

RESULT 8

US-09-996-288-238
; Sequence 238, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-238

Query Match 72.5%; Score 582.5; DB 9; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.6e-41;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 2 PQTTLTCTCFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 14 PTQTLLTCTCFSGSLTSGMGVWIRQPPGKALEWLALHWWDDKKDYNPSLKSRLTISK 73

QY 62 DTSKNQVLTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGTLLVSSASTKGPSVFP 121

Db 74 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 9

US-09-996-288-240
; Sequence 240, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-240

Query Match 72.5%; Score 582.5; DB 9; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.6e-41;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 2 PQTTLTCTCFSGSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITK 61
Db 14 PTQTLTCTCFSGSLITRGVGDWIRQPPGKALEWLADIWDDKKDYNFSLKSLRTISK 73
QY 62 DTAKNQVVLKVTNMDPADTATYYCAHHFFDSSGYPFDSWGQGTFLVSSASTKGPSVFP 121
Db 74 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130

QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 10

US-09-996-288-242
; Sequence 242, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 242
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-242

Query Match 72.5%; Score 582.5; DB 9; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.6e-41;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 2 PQTTLTCTCFSGSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITK 61

Db 14 PTQTLTCTCFSGSLITRGVGDWIRQPPGKALEWLADIWDDKKDYNFSLKSLRTISK 73
QY 62 DTAKNQVVLKVTNMDPADTATYYCAHHFFDSSGYPFDSWGQGTFLVSSASTKGPSVFP 121
Db 74 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130
QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 11

US-09-996-288-244
; Sequence 244, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 244
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-244

Query Match 72.5%; Score 582.5; DB 9; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.6e-41;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

QY 2 PQTTLTCTCFSGSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITK 61
Db 14 PTQTLTCTCFSGSLITRGVGDWIRQPPGKALEWLADIWDDKKDYNFSLKSLRTISK 73
QY 62 DTAKNQVVLKVTNMDPADTATYYCAHHFFDSSGYPFDSWGQGTFLVSSASTKGPSVFP 121
Db 74 DTAKNQVVLKVTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130

QY 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 12

US-09-996-288-246
; Sequence 246, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 246
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-246

Query Match 72.5%; Score 582.5; DB 9; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.6e-41;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy 2 PQTTLTCTGSGSLTRGVGVDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 14 PTQTLTTLTCTGSGSLTAGMSVGMIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLTISK 73
Qy 62 DTSKNQVVLWTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADATYYCARDMI--TNPY-FDVWGQGTVTVTSSASTKGPSVFP 130

Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 13

US-09-996-265-210
; Sequence 210, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 210
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-210

Query Match 72.5%; Score 582.5; DB 10; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.6e-41;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;
Qy 2 PQTTLTCTGSGSLTRGVGVDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 14 PTQTLTTLTCTGSGSLTAGMSVGMIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLTISK 73
Qy 62 DTSKNQVVLWTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADATYYCARDMI--TNPY-FDVWGQGTVTVTSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 14

US-09-996-265-238
; Sequence 238, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-238

Query Match 72.5%; Score 582.5; DB 10; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.6e-41;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;
Qy 2 PQTTLTCTGSGSLTRGVGVDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 14 PTQTLTTLTCTGSGSLTAGMSVGMIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLTISK 73
Qy 62 DTSKNQVVLWTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADATYYCARDMI--TNPY-FDVWGQGTVTVTSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 15

US-09-996-265-240
; Sequence 240, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-240

Query Match 72.5%; Score 582.5; DB 10; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.6e-41;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;
Qy 2 PQTTLTCTGSGSLTRGVGVDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITK 61
Db 14 PTQTLTTLTCTGSGSLTAGMSVGMIRQPPGKALEWLADIWDDKDYNPSPSLKSLRLTISK 73
Qy 62 DTSKNQVVLWTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADATYYCARDMI--TNPY-FDVWGQGTVTVTSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

Search completed: March 8, 2005, 07:05:56
Job time : 80.0704 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 16.3835 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-35

Perfect score: 803

Sequence: 1 NPQTLTLTCTFSGFSLITR.....SESTAALGCLVKDYFPEPVT 149

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	582.5	72.5	450	4	US-09-996-288-210
2	582.5	72.5	450	4	US-09-996-288-238
3	582.5	72.5	450	4	US-09-996-288-240
4	582.5	72.5	450	4	US-09-996-288-242
5	582.5	72.5	450	4	US-09-996-288-244
6	582.5	72.5	450	4	US-09-996-288-246
7	581.5	72.4	450	4	US-09-996-288-208
8	579.5	72.2	450	4	US-09-996-288-232
9	579.5	72.2	450	4	US-09-996-288-234
10	579.5	72.2	450	4	US-09-996-288-236
11	579.5	72.2	450	4	US-09-996-288-248
12	578.5	72.0	450	4	US-09-996-288-226
13	578.5	72.0	450	4	US-09-996-288-252
14	578.5	72.0	450	4	US-09-996-288-254
15	578.5	72.0	450	4	US-09-996-288-256
16	578.5	72.0	475	4	US-09-740-002-27
17	577.5	71.9	450	4	US-09-996-288-212
18	577.5	71.9	450	4	US-09-996-288-214
19	576.5	71.8	450	4	US-09-996-288-218
20	571	71.1	451	4	US-09-996-288-230
21	570.5	71.0	450	4	US-09-996-288-218
22	570.5	71.0	450	4	US-09-996-288-222
23	570.5	71.0	450	4	US-09-996-288-224
24	570.5	71.0	450	4	US-09-996-288-250
25	569.5	70.9	450	4	US-09-996-288-216
26	569.5	70.9	450	4	US-09-996-288-220
27	561.5	69.9	462	4	US-09-289-942A-7

28	549.5	68.4	475	4	US-09-740-002-25	Sequence 25, Appl
29	534	66.5	499	3	US-09-049-672A-1	Sequence 1, Appl
30	488.5	60.8	172	4	US-09-472-087-7	Sequence 7, Appl
31	488.5	60.8	172	4	US-09-472-087-86	Sequence 86, Appl
32	467.5	58.2	473	3	US-09-049-672A-4	Sequence 4, Appl
33	465.5	58.0	832	3	US-08-630-820-7	Sequence 7, Appl
34	465.5	58.0	832	4	US-09-273-453-7	Sequence 7, Appl
35	461.5	57.5	241	4	US-09-726-219A-187	Sequence 187, App
36	461.5	57.5	255	3	US-09-171-945-57	Sequence 57, Appl
37	456.5	56.8	167	4	US-09-472-087-74	Sequence 74, Appl
38	456.5	56.8	463	4	US-09-472-087-1	Sequence 1, Appl
39	456.5	56.8	463	4	US-09-472-087-63	Sequence 63, Appl
40	456.5	56.8	463	4	US-09-472-087-64	Sequence 64, Appl
41	452	56.3	166	4	US-09-472-087-75	Sequence 75, Appl
42	452	56.3	464	4	US-09-472-087-2	Sequence 2, Appl
43	452	56.3	464	4	US-09-472-087-66	Sequence 66, Appl
44	451.5	56.2	273	3	US-08-397-411-6	Sequence 6, Appl
45	451.5	56.2	446	3	US-08-397-411-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-996-288-210
; Sequence 210, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 210
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-210

Query Match 72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy 2 PQTTLTCTFSGFSLITRGVGVDMIRQPPGKALQWLALIYWNDDKRYSPSLKSLRTITK 61
Db 14 PQTTLTCTFSGFSLSLTAGMSVGVIRQPPGKALEWLADIWDDKDYNPSLKSLRTITK 73

Qy 62 DTSKNQVVLWNNMDPVDTATYCAHFFDSSGGYPPFDSWGQGLVSVSSASTGKPSVFP 121
Db 74 DTSKNQVVLWNNMDPVDTATYCAHFFDSSGGYPPFDSWGQGLVSVSSASTGKPSVFP 130

Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 2
US-09-996-288-238
; Sequence 238, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288

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; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-238

Query Match          72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy  2 PQTTLTCTFSGSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db  14 PTQTLLTCTFSGSLTAGSVGWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLISK 73

Qy  62 DTSKNQVLTWMTNMDPVDATYYCAHHFFDSSGGYYPFDSMGQGTLSVSSASTKGPSVFP 121
Db  74 DTSKNQVLTWMTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130

Qy  122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db  131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 3
US-09-996-288-240
; Sequence 240, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-240

Query Match          72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy  2 PQTTLTCTFSGSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db  14 PTQTLLTCTFSGSLTAGSVGWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLISK 73

Qy  62 DTSKNQVLTWMTNMDPVDATYYCAHHFFDSSGGYYPFDSMGQGTLSVSSASTKGPSVFP 121
Db  74 DTSKNQVLTWMTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130

Qy  122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db  131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 4
US-09-996-288-242
; Sequence 242, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
```

```
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 242
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-242

Query Match          72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy  2 PQTTLTCTFSGSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db  14 PTQTLLTCTFSGSLTAGSVGWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLISK 73

Qy  62 DTSKNQVLTWMTNMDPVDATYYCAHHFFDSSGGYYPFDSMGQGTLSVSSASTKGPSVFP 121
Db  74 DTSKNQVLTWMTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130

Qy  122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db  131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 5
US-09-996-288-244
; Sequence 244, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 244
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-244

Query Match          72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy  2 PQTTLTCTFSGSLITRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLITK 61
Db  14 PTQTLLTCTFSGSLTAGSVGWIRQPPGKALEWLADIWDDKKDYNFSLKSLRLISK 73

Qy  62 DTSKNQVLTWMTNMDPVDATYYCAHHFFDSSGGYYPFDSMGQGTLSVSSASTKGPSVFP 121
Db  74 DTSKNQVLTWMTNMDPADTATYYCARDMI--TNFY-FDVWGQGTTVTVSSASTKGPSVFP 130

Qy  122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db  131 LAPSSKSTSGTAAALGCLVKDYFPEPVT 158

RESULT 6
US-09-996-288-246
; Sequence 246, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
```

; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 246
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-246

Query Match 72.5%; Score 582.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 2.5e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy 2 PQTTLTCTGSGSLITRGVGVWDWIROPKQKALQWLALIYWNDDKRYSPSLKSLRLITTK 61
Db 14 PTQTLTCTGSGSLITRGVGVWDWIROPKQKALEWLADIWDDKDYNPSPSLKSLRLITSK 73
Qy 62 DTSKNQVVLWTNMDPVDATATYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADTATYCARMI--TNYF-FDVWGQGTVTTVSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

RESULT 7
US-09-996-288-208
; Sequence 208, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 208
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-208

Query Match 72.4%; Score 581.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 3.1e-49;
Matches 113; Conservative 11; Mismatches 21; Indels 3; Gaps 2;

Qy 2 PQTTLTCTGSGSLITRGVGVWDWIROPKQKALQWLALIYWNDDKRYSPSLKSLRLITTK 61
Db 14 PTQTLTCTGSGSLITRGVGVWDWIROPKQKALEWLADIWDDKDYNPSPSLKSLRLITSK 73
Qy 62 DTSKNQVVLWTNMDPVDATATYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADTATYCARSMI--TNYF-FDVWGQGTVTTVSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

RESULT 8
US-09-996-288-232
; Sequence 232, Application US/09996288

; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-232

Query Match 72.2%; Score 579.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 5e-49;
Matches 113; Conservative 10; Mismatches 22; Indels 3; Gaps 1;

Qy 2 PQTTLTCTGSGSLITRGVGVWDWIROPKQKALQWLALIYWNDDKRYSPSLKSLRLITTK 61
Db 14 PTQTLTCTGSGSLITRGVGVWDWIROPKQKALEWLADIWDDKDYNPSPSLKSLRLITSK 73
Qy 62 DTSKNQVVLWTNMDPVDATATYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADTATYCAR--DMIFNWFYDVWGQGTVTTVSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

RESULT 9
US-09-996-288-234
; Sequence 234, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-234

Query Match 72.2%; Score 579.5; DB 4; Length 450;
Best Local Similarity 76.4%; Pred. No. 5e-49;
Matches 113; Conservative 10; Mismatches 22; Indels 3; Gaps 1;

Qy 2 PQTTLTCTGSGSLITRGVGVWDWIROPKQKALQWLALIYWNDDKRYSPSLKSLRLITTK 61
Db 14 PTQTLTCTGSGSLITRGVGVWDWIROPKQKALEWLADIWDDKDYNPSPSLKSLRLITSK 73
Qy 62 DTSKNQVVLWTNMDPVDATATYCAHHFFDSSGGYYPFDSWGQGLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADTATYCAR--DMIFNWFYDVWGQGTVTTVSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

RESULT 14

US-09-996-288-254
; Sequence 254, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 254
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-254

Query Match 72.0%; Score 578.5; DB 4; Length 450;
Best Local Similarity 75.7%; Pred. No. 6.2e-49;
Matches 112; Conservative 10; Mismatches 23; Indels 3; Gaps 1;

Qy 2 PQTTLTCTSGFSLTRGVGVWIRPPGKALQWLAIYWNDDKRYSPSLKRLTITK 61
Db 14 PTQTLTCTSGFSLTAGSVGVIRPPGKALEWLADIWDDKKHYNPSLKDLRLTISK 73
Qy 62 DTSKNQVVLWTNMDPVDATYYCAHFFDSSGGYYPDSWGOGTLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADTATYYCAR---DMIFNFYFDVMGOGTTVTVSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

RESULT 15

US-09-996-288-256
; Sequence 256, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 256
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-256

Query Match 72.0%; Score 578.5; DB 4; Length 450;
Best Local Similarity 75.7%; Pred. No. 6.2e-49;
Matches 112; Conservative 10; Mismatches 23; Indels 3; Gaps 1;

Qy 2 PQTTLTCTSGFSLTRGVGVWIRPPGKALQWLAIYWNDDKRYSPSLKRLTITK 61
Db 14 PTQTLTCTSGFSLTAGSVGVIRPPGKALEWLADIWDDKKHYNPSLKDLRLTISK 73

Qy 62 DTSKNQVVLWTNMDPVDATYYCAHFFDSSGGYYPDSWGOGTLVSVSSASTKGPSVFP 121
Db 74 DTSKNQVVLKVTNMDPADTATYYCAR---DMIFNFYFDVMGOGTTVTVSSASTKGPSVFP 130
Qy 122 LAPCSRSTSESTAALGCLVKDYFPEPVT 149
Db 131 LAPSSKSTSGGTAALGCLVKDYFPEPVT 158

Search completed: March 8, 2005, 05:54:11
Job time : 16.3835 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 10.5183 Seconds
(without alignments)
1353.842 Million cells updates/sec

Title: US-09-784-950-36

Perfect score: 772

Sequence: 1 VTQSPLSLSTPGQPASISCSQSLSVHSGNTLYWYVKPQSPKPLIYRVSNRPSGV 148

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	573	74.2	219	2 S16112	Ig kappa chain V r
2	568	73.6	219	2 S38865	Ig kappa chain - m
3	567	73.4	219	2 S52028	Ig kappa chain - m
4	567	73.4	219	2 PC4203	Ig kappa chain (mo
5	564	73.1	197	2 S29593	Ig kappa chain (WM
6	564	73.1	217	2 S42772	Ig kappa chain - m
7	548	71.0	225	2 J10029	Ig kappa chain pre
8	522	67.6	215	2 J20242	Ig kappa chain NIG
9	515	66.7	215	2 J20244	Ig kappa chain NIG
10	506	65.5	215	2 A23746	Ig kappa chain V-I
11	501	64.9	121	2 S40371	Ig kappa chain - h
12	498.5	64.6	240	2 S06084	Ig kappa chain pre
13	495	64.1	135	2 S40342	Ig kappa chain - h
14	490.5	63.5	214	2 S68212	Ig kappa chain (Ma
15	490.5	63.5	220	2 A31790	Ig kappa chain V r
16	489.5	63.4	210	2 A56169	Ig kappa chain V r
17	489	63.3	124	2 S03876	Ig kappa chain V-I
18	488	63.2	125	2 S40356	Ig kappa chain - h
19	488	63.2	215	2 J20243	Ig kappa chain NIG
20	485	62.8	120	2 S42266	Ig kappa chain V-J
21	484	62.7	136	2 S40357	Ig kappa chain V-I
22	478.5	62.0	216	2 J20241	Ig kappa chain Am3
23	475.5	61.6	218	2 S68241	Ig kappa chain V r
24	475.5	61.6	218	2 J25810	Ig kappa chain V r
25	469	60.8	112	2 S58206	Ig kappa chain V r
26	466	60.4	112	2 S58207	Ig kappa chain V-I
27	465	60.2	113	1 K2HUTW	Ig kappa chain V-I
28	462	59.8	132	2 S26882	Ig kappa chain pre
29	458.5	59.4	140	2 S22658	Ig kappa chain pre

30 458 59.3 117 1 K2HUCM Ig kappa chain pre
31 457 59.2 126 2 S40312 Ig kappa chain - h
32 457 59.2 128 2 S40373 Ig kappa chain - h
33 456.5 59.1 130 2 S40321 Ig kappa chain - h
34 455 58.9 115 2 S38715 Ig kappa chain V r
35 453 58.7 118 2 PT0359 Ig kappa chain V r
36 451 58.4 115 2 S60666 Ig kappa chain V r
37 450 58.3 112 2 E27887 Ig kappa chain V r
38 449.5 58.2 131 2 S40355 Ig kappa chain - h
39 448 58.0 131 2 B34904 Ig kappa chain pre
40 447.5 58.0 126 2 S40339 Ig kappa chain - h
41 447 57.9 131 2 D29380 Ig kappa chain pre
42 445 57.6 112 2 F27887 Ig kappa chain V r
43 445 57.6 114 2 A32967 Ig kappa chain V-I
44 445 57.6 131 2 B30577 Ig kappa chain pre
45 444 57.5 112 2 S53750 antibody Fab Jel 1

ALIGNMENTS

RESULT 1

S16112
Ig kappa chain V region (G2a) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S16112
R;Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.; F
Biol. Chem. Hoppe-Seyler 372, 451-453, 1991
A;Title: Primary structure of the murine monoclonal IGC2a antibody mAb735 against alpha(2
A;Reference number: S16112; MUID:92000313; PMID:1910583
A;Accession: S16112
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-219 <BIT>
A;Cross-references: UNIPROT:Q8VC16; UNIPROT:Q99M37
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 74.2%; Score 573; DB 2; Length 219;
Best Local Similarity 74.3%; Pred. No. 3.1e-41;
Matches 107; Conservative 16; Mismatches 21; Indels 0; Gaps 0;
Oy 1 VTQSPLSLSTPGQPASISCSQSLSVHSGNTLYWYVKPQSPKPLIYRVSNRPSGV 60
Db 4 MTQTPLSLPSVSLGDAQSISCRSSQSLVHSGNTLYWYVKPQSPKPLIYRVSNRPSGV 63
Oy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGGTKVRIKRTVAAPSVFIF 120
Db 64 PDRFSGSGSGTDFTLKISRVEAEDVGLYYFCQGHVPTFGGGRLEIKRAADAAPTVSIF 123
Oy 121 PPSDEQLKSGTASVVCLLNNFYP 144
Db 124 PPSSEQLTSGGASVVCFLNNFYPK 147

RESULT 2

S38865
Ig kappa chain - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001
C;Accession: S38865
R;Kipp, B.; Becker, W.; Schlaak, M.
submitted to the EMBL Data Library, November 1993
A;Description: Combination of a defined specificity and desired isotype by cloning of an
A;Reference number: S38864
A;Accession: S38865
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-219 <KIP>
A;Cross-references: EMBL:Z27396; NID:g416538; PIDN:CAAB1787.1; PID:g416539
C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 73.6%; Score 568; DB 2; Length 219;
Best Local Similarity 75.0%; Pred. No. 8.1e-41;
Matches 108; Conservative 16; Mismatches 20; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGQASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIYEAFNRFSGV 60

Db 4 MTQSPSLSVSLGDAQASISCRSSQSIHVHTNGNTLYLWYLOKPGSLPKLLIYVSNRFSGV 63

Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVEIKRTVAAPSVPFIF 120

Db 64 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVEIKRTVAAPSVPFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPR 144

Db 124 PPSSEQLTSGGASVVCFLNNFYPK 147

RESULT 3

S52028

Ig kappa chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000

C;Accession: S52028

R;van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.;
submitted to the EMBL Data Library, August 1994

A;Description: Coordinate expression of antibody subunit genes yields high levels of fur

A;Reference number: S52028

A;Accession: S52028

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-219 <NAV>

A;Cross-references: EMBL:L35138; NID:g522336; PIDN:AAA67525.1; PID:g522337

A;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;16-95/Domain: immunoglobulin homology <IMM>

Query Match 73.4%; Score 567; DB 2; Length 219;

Best Local Similarity 75.0%; Pred. No. 9.8e-41;

Matches 108; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGQASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIYEAFNRFSGV 60

Db 4 MTQSPSLSVSLGDAQASISCRSSQSIHVHTNGNTLYLWYLOKPGQSPKLLIYKVSNRFSGV 63

Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVEIKRTVAAPSVPFIF 120

Db 64 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVEIKRTVAAPSVPFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPR 144

Db 124 PPSSEQLTSGGASVVCFLNNFYPK 147

RESULT 4

PC4203

Ig kappa chain (monoclonal antibody Maba34) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000

C;Accession: PC4203

R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.

Gene 173, 257-259, 1996

A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mc

A;Reference number: PC4202; MUID:97082978; PMID:8964510

A;Accession: PC4203

A;Molecule type: mRNA

A;Residues: 1-219 <KWA>

A;Cross-references: GB:U29147; NID:g1594225; PIDN:AAC52821.1; PID:g1594226

A;Superfamily: This protein is specific for human plasma apolipoprotein A-I of high-density

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;1-112/Domain: V region #status predicted <VRG>

F;113-219/Domain: C region #status predicted <CRG>

Query Match

Best Local Similarity 74.3%; Pred. No. 9.8e-41;

Matches 107; Conservative 16; Mismatches 21; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGQASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIYEAFNRFSGV 60

Db 4 MTQSPSLSVSLGDAQASISCRSSQSIHVHTNGNTLYLWYLOKPGQSPKLLIYKVSNRFSGV 63

Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVEIKRTVAAPSVPFIF 120

Db 64 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVEIKRTVAAPSVPFIF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPR 144

Db 124 PPSSEQLTSGGASVVCFLNNFYPK 147

RESULT 5

S29593

Ig kappa chain (WM65) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000

C;Accession: S29593

R;Seymour, R.

submitted to the EMBL Data Library, February 1991

A;Reference number: S29593

A;Accession: S29593

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-197 <SEY>

A;Cross-references: EMBL:X57856; NID:g52588; PIDN:CAA40991.1; PID:g52589

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 73.1%; Score 564; DB 2; Length 197;

Matches 106; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

Qy 1 VTQSPSLSVTPGQASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIYEAFNRFSGV 60

Db 19 MTQAPFIPVTPGESASISCRSSQSLHSDGTYLYWYLOKPGQPPOLLIYRMSNLASGV 78

Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVEIKRTVAAPSVPFIF 120

Db 79 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSTELPFTFGGKTKVEIKRTVAAPSVPFIF 138

Qy 121 PPSDEQLKSGTASVVCLLNNFYPR 144

Db 139 PPSSEQLTSGGASVVCFLNNFYPK 162

RESULT 6

S42772

Ig kappa chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C;Accession: S42772

R;Schellekens, G.A.

submitted to the EMBL Data Library, November 1993

A;Reference number: S42771

A;Accession: S42772

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-217 <SCH>

A;Cross-references: EMBL:X75536; NID:g414143; PIDN:CAA53226.1; PID:g414144

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;14-93/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 73.1%; Score 564; DB 2; Length 217;

Matches 106; Conservative 17; Mismatches 21; Indels 0; Gaps 0;


```
Qy 1 VTQSPLSLSTVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAFFNRFSGV 60
Db 2 MTQSPLSLSTVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYKVSSTRFSGV 61
Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 120
Db 62 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 121
Qy 121 PPSDEQLKSGTASVVCLLNNFYPR 144
Db 122 PPSDEQLKSGTASVVCFLNNFYPR 145

RESULT 7
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desayard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor
A:Reference number: JL0029; MUID:88171315; PMID:3127529
A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Cross-references: UNIPROT:Q99M37
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
ect except for four positions shown above
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-106/Domain: Ig kappa chain #status predicted <ILC>
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <JIR>
F:120-225/Domain: C region #status predicted <COR>

Query Match 71.0%; Score 548; DB 2; Length 225;
Best Local Similarity 72.2%; Pred. No. 4e-39;
Matches 104; Conservative 17; Mismatches 23; Indels 0; Gaps 0;

Qy 1 VTQSPLSLSTVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAFFNRFSGV 60
Db 10 MTQSPLSLSTVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYKVSSTRFSGV 69
Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 120
Db 70 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 129
Qy 121 PPSDEQLKSGTASVVCLLNNFYPR 144
Db 130 PPSDEQLKSGTASVVCFLNNFYPR 153

RESULT 8
JL0242
Ig kappa chain NIG26 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0242
R:Alim, M.A.; Yamaki, S.; Hosain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mul
A:Reference number: JE0241
A:Accession: JE0242
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-91/Domain: immunoglobulin homology <IMM>
```

```
Query Match 67.6%; Score 522; DB 2; Length 215;
Best Local Similarity 68.2%; Pred. No. 5.9e-37;
Matches 101; Conservative 19; Mismatches 24; Indels 4; Gaps 1;

Qy 1 VTQSPLSLSTVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAFFNRFSGV 60
Db 4 LTQSPGLSLSPGERATLSRASQSV---SNNYLANVQKPGQAPSLIIYDASSTRATGI 59
Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 120
Db 60 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 119
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 120 PPSDEQLKSGTASVVCFLNNFYPRKERV 147

RESULT 9
JE0244
Ig kappa chain NIG2 precursor - human
C:Species: Homo sapiens (man)
C>Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0244
R:Alim, M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T.
submitted to JIPID, November 1998
A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
A:Reference number: JE0243
A:Accession: JE0244
A:Molecule type: protein
A:Residues: 1-215 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match 66.7%; Score 515; DB 2; Length 215;
Best Local Similarity 69.1%; Pred. No. 2.3e-36;
Matches 103; Conservative 19; Mismatches 21; Indels 6; Gaps 3;

Qy 1 VTQSPLSLSTVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAFFNRFSGV 60
Db 4 LTQSPATLSVSPGERATLSRASQS-VHSN---LAWYQKPGQAPRLIIYRSTRATGI 58
Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQ-SIELPFTFGGKTKVEIKRTVAAPSVPF 119
Db 59 PARFSGSGSGTDFTLTITSSIQSEDFALYYCOQYNTWPPLTFGGGKTKVEIKRTVAAPSVPF 118
Qy 120 FPPSDEQLKSGTASVVCFLNNFYPRKERV 148
Db 119 FPPSDEQLKSGTASVVCFLNNFYPRKERV 147

RESULT 10
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C>Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Ghiso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunogl
A:Reference number: A23746; MUID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 65.5%; Score 506; DB 2; Length 215;
Best Local Similarity 68.2%; Pred. No. 1.3e-35;
Matches 101; Conservative 18; Mismatches 25; Indels 4; Gaps 1;

Qy 1 VTQSPLSLSTVTPGQPASISCKSSQSLHSDGKTYLYWYLPKPGQPOLLIIYEAFFNRFSGV 60
```

Db 4 LTQSPATLSLSPGRATLSGASQSV-----SSNYLAWYQQKPGQAPRLIIYDASSRATGI 59
Qy 61 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 120
Db 60 PDRESGSGGTDFTLTISRLEPEDFAVYYGQYGSPLTFGGGKTKVEIKRTVAAPSVFIF 119

Qy 121 PPSDEQLKSGTASVVCLNLFYPRKERV 148
Db 120 PPSDEQLKSGTASVVGLNLFYPRKAV 147

RESULT 11
S40371
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C/Accession: S40371
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40371
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-121 <KLE>
A/Cross-references: EMBL:X72481; NID:g441430; PIDN:CAA51149.1; PID:g441431
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/13-92/Domain: immunoglobulin homology <IMM>

Query Match 64.9%; Score 501; DB 2; Length 121;
Best Local Similarity 80.2%; Pred. No. 1.9e-35;
Matches 97; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIIYEA FNRFSGV 60
Db 1 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGKSPQLLIYLGSKRASGV 60
Qy 61 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 120
Db 61 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 120

Qy 121 P 121
Db 121 P 121

RESULT 12
S06084
Ig kappa chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C/Accession: S06084
R/Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7992, 1989
A/Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A/Reference number: S06084; MUID:90016888; PMID:2508067
A/Accession: S06084
A/Molecule type: mRNA
A/Residues: 1-240 <CRO>
A/Cross-references: EMBL:X16129; NID:g56457; PIDN:CAA34256.1; PID:g56458
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-240/Product: Ig kappa chain #status predicted <MAT>
F/153-222/Domain: immunoglobulin homology <IMM>

Query Match 64.6%; Score 498.5; DB 2; Length 240;
Best Local Similarity 66.9%; Pred. No. 6.3e-35;
Matches 97; Conservative 19; Mismatches 28; Indels 1; Gaps 1;
Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIIYEA FNRFSG 59

Db 24 MTQSPSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQQKPGSQPKLLIYWASTRQSG 83
Qy 60 VPRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 119
Db 84 VPRFSGSGGTDFTLTISRLEPEDFAVYYGQYGSPLTFGGGKTKVEIKRTVAAPSVFIF 143
Qy 120 PPSDEQLKSGTASVVCLNLFYPR 144
Db 144 PPSDEQLATGGASVVCLMNFYPR 168

RESULT 13
S40342
Ig kappa chain - human
C/Species: Homo sapiens (man)
C/Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
C/Accession: S40342
R/Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A/Title: Expressed human immunoglobulin chi genes and their hypermutation.
A/Reference number: S40312; MUID:94080891; PMID:8258341
A/Accession: S40342
A/Status: preliminary; translation not shown
A/Molecule type: mRNA
A/Residues: 1-135 <KLE>
A/Cross-references: UNIPROT:QGNK0; EMBL:X72452; NID:g441372; PID:g441373
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/29-108/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 495; DB 2; Length 135;
Best Local Similarity 82.8%; Pred. No. 6.9e-35;
Matches 96; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIIYEA FNRFSGV 60
Db 17 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGKSPQLLIYLGSKRASGV 76
Qy 61 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPS 116
Db 77 PDRESGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPS 132

RESULT 14
S68212

Ig kappa chain (Mab03-1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C/Accession: S68212
R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A/Title: Thermolabile peroxidase activity with a recombinant antibody L chain-porphyrin
A/Reference number: S68211; MUID:96085223; PMID:7498516
A/Accession: S68212
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-214 <TKA>
A/Cross-references: EMBL:D29668
C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 63.5%; Score 490.5; DB 2; Length 214;
Best Local Similarity 66.9%; Pred. No. 2.7e-34;
Matches 97; Conservative 17; Mismatches 30; Indels 1; Gaps 1;
Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIIYEA FNRFSG 59
Db 4 MTQSPSLAVSAGETVTINCKSSQSLFYSGNQKNYLAWYQQKPGSQPKLLIYWASTRQSG 63
Qy 60 VPRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 119
Db 64 VPRFSGSGGTDFTLTISRLEPEDFAVYYGQYGSPLTFGGGKTKVEIKRTVAAPSVFIF 123

Qy 120 FPPSDEQLKSGTASVVCILNNFYPR 144
Db 124 FPPSSEQLTSGASVVCFLNNFYPK 148

RESULT 15

A31790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R;Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an an
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M23626; GB:J04061; NID:g533234; PID:AAA39162.1; PID:g533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;16-96/Domain: immunoglobulin homology <IMM>

Query Match 63.5%; Score 490.5; DB 2; Length 220;
Best Local Similarity 66.2%; Pred. No. 2.7e-34;
Matches 96; Conservative 16; Mismatches 32; Indels 1; Gaps 1;
Qy 1 VTQSPLSLSVTPGQPASISCKSSQSLHS-DGKTYLYWYLOKPGQPOLLIIYEAFNRFSG 59
Db 4 MTQSPSSLTVTAGEKVTWTSCTSSQSLFNSGKQKNYLTWYQKPGQPPKVLIIYWASTRESG 63
Qy 60 VPDPSGSGSGTDFTLKISRVEADVGLYYCMQSIELPFTGGGTYKVEIKRTVAAPSVP 119
Db 64 VPDRTGSGSGTDFTLTSSVQAEADLAVYYCQNDYSNPLTFGGGTYKLEKRAADAAPT VSI 123
Qy 120 FPPSDEQLKSGTASVVCILNNFYPR 144
Db 124 FPPSSEQLTSGASVVCFLNNFYPK 148

Search completed: March 8, 2005, 06:39:29
Job time : 11.5683 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 55.2705 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-36

Perfect score: 772

Sequence: 1 VTQSPLSVTPGQPASISC.....SGTASVCLNNFPRKERV 148

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	651	84.3	239	2	Q8NEKO	Q8nek0 homo sapien
2	637.5	82.6	240	2	Q8PIH6	Q8pih6 homo sapien
3	621	80.4	239	2	Q8P491	Q8p491 homo sapien
4	607	78.6	239	2	Q8TCD0	Q8tcd0 homo sapien
5	570	73.8	219	2	Q65ZC0	Q65zc0 mus musculus
6	532	68.9	235	2	Q6GMV9	Q6gmv9 homo sapien
7	516.5	66.9	236	2	Q8PIL8	Q8pil8 homo sapien
8	507.5	65.7	236	2	Q8P5S8	Q8p5s8 homo sapien
9	504	65.3	235	2	Q8PJF2	Q8pjf2 homo sapien
10	496	64.2	235	2	Q6GMW0	Q6gmw0 homo sapien
11	495.5	64.2	236	2	Q6GMX0	Q6gmx0 homo sapien
12	493.5	63.9	234	2	Q72473	Q72473 homo sapien
13	493.5	63.9	236	2	Q6GMX8	Q6gmx8 homo sapien
14	492.5	63.8	236	2	Q6GMW1	Q6gmw1 homo sapien
15	485.5	62.9	236	2	Q6PIH7	Q6pih7 homo sapien
16	475.5	61.6	236	2	Q6GMX9	Q6gmx9 homo sapien
17	475.5	61.6	236	2	Q6PIT5	Q6pit5 homo sapien
18	473.5	61.3	238	2	Q66J87	Q66j87 mus musculus
19	468.5	60.7	236	2	Q723Y4	Q723y4 homo sapien
20	465	60.2	113	1	KV2D HUMAN	P01617 homo sapien
21	458	59.3	117	1	KV2E HUMAN	P06309 homo sapien
22	458	59.3	243	2	Q6NTU5	Q6ntu5 xenopus lae
23	446.5	57.8	236	2	Q6PIH4	Q6pih4 homo sapien
24	443.5	57.4	115	1	KV2A HUMAN	P01614 homo sapien
25	439.5	56.9	112	1	KV2C HUMAN	P01616 homo sapien
26	438	56.7	248	2	Q65ZQ7	Q65zq7 mus sp. b3
27	436.5	56.2	237	2	Q7SZ36	Q7sz36 xenopus lae
28	434	56.2	113	1	KV2G MOUSE	P01631 mus musculus
29	433.5	56.2	236	2	Q7TS98	Q7ts98 mus musculus
30	433	56.1	133	1	KV2F HUMAN	P06310 homo sapien
31	431.5	55.9	241	2	Q63ZX4	Q63zx4 mus musculus

32	427	55.3	112	2	Q6LEM8	Q6lem8 mus musculus
33	427	55.3	113	1	KV2E_MOUSE	P03976 mus musculus
34	427	55.3	113	1	KV2F_MOUSE	P01630 mus musculus
35	419	54.3	113	1	KV2B HUMAN	P01615 homo sapien
36	415.5	53.8	114	2	Q9UL80	Q9ul80 homo sapien
37	403	52.2	112	1	KV2D_MOUSE	P01629 mus musculus
38	390.5	50.6	134	1	KV4C_HUMAN	P06314 homo sapien
39	385	49.9	113	1	KV2C_MOUSE	P01628 mus musculus
40	378	49.0	112	1	KV2A_MOUSE	P01626 mus musculus
41	376	48.7	133	1	KV4B HUMAN	P06313 homo sapien
42	374.5	48.5	114	1	KV4A_HUMAN	P01625 homo sapien
43	372.5	48.3	108	1	KV1_CANFA	P01618 canis famil
44	364.5	47.2	111	1	KV3W_MOUSE	P01665 mus musculus
45	364.5	47.2	262	2	Q65Z11	Q65z11 mus musculus

ALIGNMENTS

RESULT 1

ID	Q8NEKO	PRELIMINARY;	PRT;	239 AA.
AC	Q8NEKO;			
DT	01-OCT-2002 (TrEMBLrel. 22, Created)			
DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DB	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uadin T.B., Toehiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Iqbal N.A., Peters G.J., Abramson R.D., Mullahy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Prostate;			
RA	Strausberg R.;			
RA	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC030814; AAH30814.1; -.			
DR	PIR; S23638; S23638.			
DR	PIR; S34091; S34091.			
DR	PIR; S40342; S40342.			
DR	PIR; S40357; S40357.			
DR	HSSP; P01834; 117Z.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig ci.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig v.			
DR	Pfam; PF07654; C1-set; 1.			
DR	SMART; SM00406; IGv; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			

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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26024 MW; F5E20AD3B0552COA CRC64;

Query Match 84.3%; Score 651; DB 2; Length 239;
Best Local Similarity 84.5%; Pred. No. 2.5e-57;
Matches 125; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 VTQSPLSLVTPGPASISCKSSQSLLHSDGKTYLYWLOKPGOPPOLLIYEAFFNRFSV 60
DB 24 MTQSPFLSLVTPGPASISCKSSQSLLHSDGTYNDWLOKPGOPPOLLIYLGNSRASGV 83
QY 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYCYMQSIELPFTFGGTVKVEIKRTVAAPSFI 120
DB 84 PDRFSGSGSGTDFTLKISRVEAEDVGLYCYMQSIELPFTFGGTVKVEIKRTVAAPSFI 143
QY 121 PPSDEQLKSGTASVCLNNFYPRKERV 148
DB 144 PPSDEQLKSGTASVCLNNFYPRKERV 171

RESULT 2
Q6PIH6 PRELIMINARY; PRT; 240 AA.
AC Q6PIH6
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034142; AAH34142.1; -.
DR HSSP; P01837; 1XB5.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
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DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 240 AA; 26234 MW; 188D4DD8BB781EC4 CRC64;

Query Match 82.6%; Score 637.5; DB 2; Length 240;
Best Local Similarity 82.6%; Pred. No. 5.7e-56;
Matches 123; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

QY 1 VTQSPLSLVTPGPASISCKSSQSLLHSDGKTYLYWLOKPGOPPOLLIYEAFFNRFSV 60
DB 24 MAQSPFLSLVTPGPASISCKSSQSLLHSGNYFDWLOKPGOPPOLLIYWGNSRASGV 83
QY 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYCYMQSIELPFTFGGTVKVEIKRTVAAPSFI 119
DB 84 PDRFSGSGSGTDFTLKISRVEAEDVGLYCYMQSIELPFTFGGTVKVEIKRTVAAPSFI 143
QY 120 PPSDEQLKSGTASVCLNNFYPRKERV 148
DB 144 PPSDEQLKSGTASVCLNNFYPRKERV 172

RESULT 3
Q6P491 PRELIMINARY; PRT; 239 AA.
AC Q6P491
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC063599; AAH63599.1; -.
DR HSSP; P01837; 1XCU.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
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Db 24 LTQSPGTLSPGERATLSRASQSL----SSSYLAWYQQKPGQAPRLIIYGVSSRATGI 79
Qy 61 PDRFSGSGGDTFTLKISRVEAEDVGLYYCMQ-SIELPFTFGGKTKVEIKRTVAAPSVEI 119
Db 80 PDRFSGSGGDTFTLTISRLPEDPAVYCCQYGTSGRDTFTGGTRLDIKRTVAAPSVEI 139
Qy 120 FPPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 140 FPPSDEQLKSGTASVVCLLNNFYPREAKV 168

RESULT 8
Q6P5S8 PRELIMINARY; PRT; 236 AA.
ID Q6P5S8
AC Q6P5S8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSU=Glandular pool- thyroid;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSU=Glandular pool- thyroid;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062704; AAH62704.1; -.
DR HSSP; P01837; 1KCU
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25773 MW; 953E37BEB4FF5F27 CRC64;

Query Match 65.7%; Score 507.5; DB 2; Length 236;
Best Local Similarity 66.4%; Pred. No. 7, 1e-43;
Matches 99; Conservative 23; Mismatches 22; Indels 5; Gaps 2;

Qy 1 VTQSPLSLSVTFGQPASISCKSSQLHSDGKTYLYWYLOKPGQPQLLIYEAENRFSGV 60
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Db 24 LTQSPGTLSPGERATLSRASQTFVSS----HLAWYQQKPGQAPRLIIYGVSSRATGI 79
Qy 61 PDRFSGSGGDTFTLKISRVEAEDVGLYYCMQSIELP-FTFGGKTKVEIKRTVAAPSVEI 119
Db 80 PDRFSGSGGDTFTLTITRLPEPDAVYFCQYGTSPSLFTGGGTRVEIKRTVAAPSVEI 139
Qy 120 FPPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 140 FPPSDEQLKSGTASVVCLLNNFYPREAKV 168

RESULT 9
Q6PJF2 PRELIMINARY; PRT; 235 AA.
ID Q6PJF2
AC Q6PJF2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSU=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSU=Lung;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC016380; AAH16380.1; -.
DR HSSP; P01837; 1KCU
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.c1.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25520 MW; F33A145A396BA285 CRC64;

Query Match 65.3%; Score 504; DB 2; Length 235;
Best Local Similarity 65.5%; Pred. No. 1, 6e-42;
Matches 97; Conservative 22; Mismatches 25; Indels 4; Gaps 1;
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QY 1 VTQSPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLOKQGPOLLIIYAFNRFSGV 60
Db 24 LTQSPATLSVPGERATLSRASQISNN-----SSAYLAWYQKPGQAPRLMFGSSRATGI 79
QY 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 120
Db 80 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFIF 139
QY 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 140 PPSDEQLKSGTASVVCLLNNFYPRKERV 167

RESULT 10
Q6GMW0 PRELIMINARY; PRT; 235 AA.
ID Q6GMW0 AC Q6GMW0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH73792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
DR KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36BD4133F5 CRC64;

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Query Match 64.2%; Score 496; DB 2; Length 235;
 Best Local Similarity 64.4%; Pred. No. 1e-41;
 Matches 96; Conservative 27; Mismatches 20; Indels 6; Gaps 2;

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QY 1 VTQSPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLOKQGPOLLIIYAFNRFSGV 60
Db 24 MTQSPATLSVPGERATLSRASQISNN-----LAWYQQRPGQAPRELLIYGASSRVGTI 78
QY 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVFI 119
Db 79 PGRFSGSGGTEFTLSTISLSQSEDFAVFYCCQYNDWLLYTFGQGTLEIKRTVAAPSVFI 138
QY 120 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 139 PPSDEQLKSGTASVVCLLNNFYPRKERV 167

RESULT 11
Q6GMX0 PRELIMINARY; PRT; 236 AA.
ID Q6GMX0 AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
DR KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

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Query Match 64.2%; Score 495.5; DB 2; Length 236;
 Best Local Similarity 65.5%; Pred. No. 1.2e-41;

Matches 97; Conservative 15; Mismatches 31; Indels 5; Gaps 1;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIIYEAFFRSGV 60
 Db 26 MTQSPSSLSASVGRVITTCRASQNI-----NNYLNWYQLKPGKAPNLLIYAASLSQSGV 80
 Qy 61 PDPSGSGSGDFTLTKISRVEAEADVGLYCMQSIETELPFTGGTKVEIKRTVAAPSVFIF 120
 Db 81 PSRFGSGSGDFTLTKISRVEAEADVGLYCMQSIETELPFTGGTKVEIKRTVAAPSVFIF 140
 Qy 121 PPSDEQLKSGTASVVCLLNNFPYPRKERV 148
 Db 141 PPSDEQLKSGTASVVCLLNNFPYPRKERV 168

RESULT 12
 Q72473
 ID Q72473 PRELIMINARY; PRT; 234 AA.
 AC Q72473
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Lung;
 RC Strausberg R.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC056256; AAH56256.1; -.
 DR HSSP; P01834; 1HEZ.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 2.
 DR PROSITE; PS0290; IG.MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 63.9%; Score 493.5; DB 2; Length 234;
 Best Local Similarity 66.2%; Pred. No. 1.8e-41;
 Matches 98; Conservative 15; Mismatches 30; Indels 5; Gaps 1;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIIYEAFFRSGV 60
 Db 24 MTQSPSSLSASVGRVITTCRASQNI-----GSLAWYQKPGKAPOLLIIYAASLQSGV 78
 Qy 61 PDPSGSGSGDFTLTKISRVEAEADVGLYCMQSIETELPFTGGTKVEIKRTVAAPSVFIF 120
 Db 79 PSRFGSGSGDFTLTKISRVEAEADVGLYCMQSIETELPFTGGTKVEIKRTVAAPSVFIF 138
 Qy 121 PPSDEQLKSGTASVVCLLNNFPYPRKERV 148
 Db 139 PPSDEQLKSGTASVVCLLNNFPYPRKERV 166

RESULT 13
 Q6GMX8
 ID Q6GMX8 PRELIMINARY; PRT; 236 AA.
 AC Q6GMX8
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 EX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Primary B-Cells;
 RC Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC073764; AAH73764.1; -.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003597; IG-cl.
 DR InterPro; IPR003006; IG.MHC.
 DR InterPro; IPR003596; IG.v.
 DR Pfam; PF07654; Cl-set; 1.
 DR Pfam; PF00047; IG; 2.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 2.
 DR PROSITE; PS0290; IG.MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;

Query Match 63.9%; Score 493.5; DB 2; Length 236;
 Best Local Similarity 64.9%; Pred. No. 1.8e-41;
 Matches 96; Conservative 19; Mismatches 28; Indels 5; Gaps 1;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 68.6168 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-36
Perfect score: 772
Sequence: 1 VTQSPLSLSTPGQPASISC.....SGTASVCLLNFPYRKERV 148

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	772	100.0	148	2 AAY34315	Aay34315 IgG antib
2	704	91.2	168	8 ADK52426	Adk52426 Human ant
3	679.5	88.0	238	2 AAR93554	Aar93554 Monoclonal
4	662	85.8	241	3 AAY96303	Aay96303 Human IGF
5	661	85.6	247	5 ABG70338	Abg70338 Human MDD
6	657	85.1	238	8 ADL93653	Adl93653 Human CD4
7	656	85.0	238	8 ADL93649	Adl93649 Human CD4
8	653	84.6	238	8 ADL93654	Adl93654 Human CD4
9	652	84.5	219	6 ABP58286	Abp58286 Humanised
10	652	84.5	238	6 ABP58288	Abp58288 Humanised
11	650	84.2	238	8 ADL93650	Adl93650 Human CD4
12	649	84.1	239	3 AAY82611	Aay82611 Human PTH
13	649	84.1	239	7 ADL23139	Adl23139 Mouse/hum
14	648	83.9	219	6 ABR39464	Abr39464 Humanised
15	648	83.9	219	6 ABU08310	Abu08310 Humanised
16	648	83.9	219	6 ABR39792	Abr39792 Humanised
17	648	83.9	219	6 ABB80108	Abb80108 Light cha
18	648	83.9	219	7 ADE94065	Ade94065 Humanised
19	648	83.9	219	8 ADN61713	Adn61713 Humanised
20	648	83.9	238	4 AAU07744	Aau07744 Humanised
21	648	83.9	238	6 ABR39842	Abr39842 Humanised
22	647	83.8	219	8 ADR16817	Adr16817 Human bre
23	647	83.8	238	4 AAB72235	Aab72235 Humanised
24	647	83.8	238	4 AAB72231	Aab72231 Humanised
25	647	83.8	238	4 AAB72227	Aab72227 Humanised

26	647	83.8	238	4 AAB72233	Aab72233 Humanised
27	644	83.4	239	3 AAY82615	Aay82615 Human PTH
28	643	83.3	239	2 AAW71876	Aaw71876 Anti-huma
29	643	83.3	239	2 AAW71878	Aaw71878 Anti-huma
30	643	83.3	239	3 AAB12913	Aab12913 Anti-huma
31	643	83.3	239	3 AAB12915	Aab12915 Anti-huma
32	643	83.3	239	7 ADE28461	Ade28461 Human ant
33	641	83.0	239	7 ADE28421	Ade28421 Human ant
34	640	82.9	219	7 ADJ32138	Adj32138 Human int
35	639.5	82.8	175	8 ADK52414	Adk52414 Human ant
36	639	82.8	239	2 AAW71879	Aaw71879 Anti-huma
37	639	82.8	239	2 AAW71877	Aaw71877 Anti-huma
38	639	82.8	239	3 AAB12914	Aab12914 Anti-huma
39	639	82.8	239	3 AAB12916	Aab12916 Anti-huma
40	639	82.8	239	7 ADE28405	Ade28405 Human ant
41	638.5	82.7	237	8 ADL93658	Adl93658 Human CD4
42	638.5	82.7	237	8 ADL93651	Adl93651 Human CD4
43	638	82.6	239	7 ADE28465	Ade28465 Human ant
44	637	82.5	238	2 AAW14937	Aaw14937 Murine an
45	637	82.5	238	2 AAW14942	Aaw14942 3F4 Human

ALIGNMENTS

RESULT 1
AAY34315
ID AAY34315 standard; protein; 148 AA.
XX AC AAY34315;
XX DT 19-NOV-1999 (first entry)
XX DE IG antibody 2.4.4 kappa chain sequence.
XX KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX OS Homo sapiens.
XX PN WO9945031-A2.
XX PD 10-SEP-1999.
XX PF 03-MAR-1999; 99WO-US004583.
XX PR 03-MAR-1998; 98US-00034607.
XX PR 03-FEB-1999; 99US-00244253.
(ABGE-) ABGENIX INC.
Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
WPI; 1999-540816/45.
N-PSDB; AAZ20416.
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX Claim 61; Fig 30; 245pp; English.
CC This sequence represents the kappa chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 MAB
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 148 AA;

Query Match 100.0%; Score 772; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 2.le-54;
Matches 148; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQSPLSLVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIVEAFNRESGV 60
DB 1 VTQSPLSLVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIVEAFNRESGV 60
QY 61 PDRFSGSGSGTDFTLKISRVEADVGLYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 120
DB 61 PDRFSGSGSGTDFTLKISRVEADVGLYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 120
QY 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
DB 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148

RESULT 2
ADK52426
ID ADK52426 standard; protein; 168 AA.
XX AC ADK52426;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human anti-MCP-1 variable region light chain #33.
XX
KW monocyte chemo-attractant protein-1; MCP-1; Cytostatic; Antiarthritic;
KW Antirheumatic; Nephrotropic; Antiarteriosclerotic; Antiposoriatic;
KW Vasotropic; Immunosuppressive; Neuroprotective; neoplastic;
KW Inflammatory condition; cancer; arthritis; multiple sclerosis;
KW anti-MCP-1; heavy chain; light chain.
XX
OS Homo sapiens.
XX
PN W02004016769-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US026232.
XX
PR 19-AUG-2002; 2002US-0404802P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Gudas JM, Haak-Frendscho M, Foord O, Liang ML, Ahluwalia K;
PI Bhakta S;
XX
DR WPI; 2004-203794/19.
DR N-PSDB; ADK52425.
XX
PT New human monoclonal antibody that binds to monocyte chemo-attractant
PT protein-1 and is immobilized on an insoluble matrix; useful for
PT diagnosing or treating neoplastic or inflammatory diseases, e.g. cancer,
PT rheumatoid arthritis or psoriasis.
XX
PS Claim 2; SEQ ID NO 132; 154pp; English.
XX
CC The present invention relates to a human monoclonal antibody that binds
CC to monocyte chemo-attractant protein-1 (MCP-1). The antibody is useful
CC for the preparation of a medicament useful for treating neoplastic or
CC inflammatory conditions. The neoplastic disease is selected from breast
CC cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer or prostate cancer. The inflammatory condition is
CC selected from rheumatoid arthritis, glomerulonephritis, atherosclerosis,
CC psoriasis, restenosis, autoimmune disease or multiple sclerosis. The
CC antibodies are also useful for diagnosing the above diseases. It is also

CC useful for the determining the level of MCP-1 and MCP-1 family members in
CC patient samples. The present sequence represents a human anti-MCP-1
CC variable region light chain sequence.
XX
SQ Sequence 168 AA;

Query Match 91.2%; Score 704; DB 8; Length 168;
Best Local Similarity 89.9%; Pred. No. 6.9e-49;
Matches 133; Conservative 9; Mismatches 6; Indels 0; Gaps 0;

QY 1 VTQSPLSLVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIVEAFNRESGV 60
DB 16 MTQTPLSLVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPOLLIVEAFNRESGV 75
QY 61 PDRFSGSGSGTDFTLKISRVEADVGLYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 120
DB 76 PDRFSGSGSGTDFTLKISRVEADVGLYCMQSIELPFTFGGKTKVEIKRTVAAPS VFIF 135
QY 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
DB 136 PPSDEQLKSGTASVVCLLNNFYPRKERV 163

RESULT 3
AAR93554
ID AAR93554 standard; protein; 238 AA.
XX AC AAR93554;
XX
DT 20-AUG-1996 (first entry)
XX
DE Monoclonal antibody DNA light chain against 65 kD hCMV antigen.
XX
KW Polymerase chain reaction; primer; amplify; PCR; light chain; MAb;
KW 65 kD antigen; human cytomegalovirus; hCMV; heavy chain; diagnosis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..20
FT /note= "Signal peptide"
FT Protein 21..238
FT /note= "Mature light chain"
XX
PN JP08038178-A.
XX
PD 13-FEB-1996.
XX
PF 20-FEB-1995; 95JP-00030742.
XX
PR 18-FEB-1994; 94JP-00021628.
XX
PA (TANA/) TANAKA H.
PA (NISN) NISSHINO IND INC.
XX
DR WPI; 1996-154852/16.
DR N-PSDB; AAT18060.
XX
PT Human monoclonal antibody binds to cytomegalovirus 65 kD antigen -
PT produced by primer amplification, used in the diagnosis of hCMV
PT infection.
XX
PS Claim 5; Page 19; 22pp; Japanese.
XX
CC The sequences given in AAR93553-54 represent the heavy and light chains
CC respectively of a monoclonal antibody against a 65 kD antigen of human
CC cytomegalovirus (hCMV). The DNA's encoding these sequences were amplified
CC using the sequences given in AAT18040-58. The monoclonal antibody may be
CC used in the diagnosis of hCMV
XX
SQ Sequence 238 AA;

Query Match 88.0%; Score 679.5; DB 2; Length 238;

Best Local Similarity 88.5%; Pred. No. 9,1e-47;
Matches 131; Conservative 8; Mismatches 8; Indels 1; Gaps 1;
Qy 1 VTQPLSLSVTPGQPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYEAFNRPSGV 60
Db 24 MTQPLSLSVTPGQPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYEVSNRPSGV 83
Qy 61 PDRFSGSGSGDFTLKISRVEAEDVGLYVCMQSIETLP--FTFGGKTKVEIKRTVAAPSVFIP 120
Db 84 PDRFSGSGSGDFTLKISRVEAEDVGLYVCMQSIETLP--FTFGGKTKVEIKRTVAAPSVFIP 142
Qy 121 PPSDEQLKSGTASVVCLLNNFYPKERV 148
Db 143 PPSDEQLKSGTASVVCLLNNFYPKERV 170
RESULT 4
AAY96303
ID AAY96303 standard; protein; 241 AA.
XX AAY96303;
AC AAY96303;
DT 16-AUG-2000 (first entry)
XX Human IGFAM-15 immunoglobulin.
XX Human; immunoglobulin; IGFAM-15; IGFAM; immune disorder; cancer;
KW infection; inflammation; haematopoiesis; AIDS; allergy.
XX Homo sapiens.
XX Key Location/Qualifiers
FT Peptide 1..20
FT Protein 21..241 /label= signal_peptide
FT Protein 21..241 /label= IGFAM-15
FT Domain 36..115
FT Domain 154..223 /label= Ig_domain
FT Domain 154..223 /label= Ig_domain
XX WO200029583-A2.
XX 25-MAY-2000.
XX 19-NOV-1999; 99WO-US027566.
XX 19-NOV-1998; 98US-00195853.
XX 22-DEC-1998; 98US-0113633P.
XX 07-APR-1999; 99US-0128194P.
XX (INCY-) INCYTE PHARM INC.
XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
PI Lu DAM, Lal P, Hillman JL, Yang J;
XX WPI; 2000-387796/33.
DR N-PSDB; AAA27395.
XX Immunoglobulin superfamily proteins, the agonist and antagonist of the
PT protein is useful for preventing and treating disorders associated with
PT altered levels of the protein such as cancer, immune system disorders.
XX Claim 1; Page 89-90; 105pp; English.
XX The present sequence is the human immunoglobulin superfamily protein
CC IGFAM-15. Its gene was isolated from a cDNA library of colon tissue. It
CC is expressed in reproductive, gastrointestinal, haematopoietic and immune
CC and cardiovascular tissue, where cancer and inflammation are common. The
CC gene, protein, its antibodies, agonists and antagonists are suitable for
CC diagnosing and treating many diseases, including cancer, immune system
CC disorders (such as inflammation, AIDS, allergies, anaemia, Crohn's
CC arteriosclerosis, asthma, atherosclerosis, cholecystitis, Crohn's

CC disease, diabetes mellitus, emphysema, Graves' disease, hepatitis, multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma, CC systemic lupus erythematosus and ulcerative colitis), complications of CC cancer, haemodialysis and extracorporeal circulation, trauma and CC haematopoietic cancer (such as leukaemia) and infections caused by CC bacteria, viruses, fungi or parasites
XX Sequence 241 AA;
SQ Query Match 85.8%; Score 662; DB 3; Length 241;
Best Local Similarity 83.3%; Pred. No. 2.3e-45;
Matches 125; Conservative 17; Mismatches 6; Indels 2; Gaps 1;
Qy 1 VTQPLSLSVTPGQPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYEAFNRPSGV 60
Db 24 LTQPLSLSVTPGQPASISCKSSQSLHSDGKTYLYWLQKPGQPQLLIYEVSNRPSGV 83
Qy 61 PDRFSGSGSGDFTLKISRVEAEDVGLYVCMQSIETLP--FTFGGKTKVEIKRTVAAPSVF 118
Db 84 PDRFSGSGSGDFTLKISRVEAEDVGLYVCMQSIETLP--FTFGGKTKVEIKRTVAAPSVF 143
Qy 119 IFPPSDEQLKSGTASVVCLLNNFYPKERV 148
Db 144 IFPPSDEQLKSGTASVVCLLNNFYPKERV 173
RESULT 5
ABG70338
ID ABG70338 standard; protein; 247 AA.
XX ABG70338;
AC ABG70338;
DT 21-OCT-2002 (first entry)
XX Human MDDT protein Incyte ID No: LI:1171219.2.orf3:2001JAN12.
XX Human; molecule for disease detection and treatment; MDDT; cancer;
KW cell proliferative disorder; arteriosclerosis; cirrhosis; asthma;
KW autoimmune disorder; inflammatory disorder; Crohn's disease;
KW multiple sclerosis; cytostatic; antiarteriosclerotic; antiinflammatory;
KW hepatotropic; immunosuppressive; antiasthmatic.
XX Homo sapiens.
XX WO200255738-A2.
XX 18-JUL-2002.
XX 09-JAN-2002; 2002WO-US001008.
XX 12-JAN-2001; 2001US-0261622P.
PR 16-JAN-2001; 2001US-0261865P.
PR 17-JAN-2001; 2001US-0262208P.
PR 17-JAN-2001; 2001US-0262209P.
PR 17-JAN-2001; 2001US-0262326P.
PR 19-JAN-2001; 2001US-0263063P.
PR 19-JAN-2001; 2001US-0263065P.
PR 19-JAN-2001; 2001US-0263329P.
XX (INCY-) INCYTE GENOMICS INC.
XX Panzer SR, Lincoln SE, Altus CM, Dufour GE, Hillman JL, Jones AL;
PI Dam TC, Liu TF, Harris B, Flores V, Daffo A, Marwaha R, Chen AJ;
PI Chang SC, Gerstein EH, Peralta CH, David MH, Lewis SA;
XX WPI; 2002-590679/63.
DR N-PSDB; ABS51811.
XX New disease detection and treatment molecule (MDDT) polynucleotides and
PT polypeptides, useful in diagnosing, studying, preventing or treating
PT diseases associated with MDDT expression, e.g. autoimmune or inflammatory
PT disorders.
XX

PS Claim 27; Page 125-126; 129pp; English.

XX The present invention relates to the isolation of novel human molecules

CC for disease detection and treatment (MDDT), and the polynucleotide

CC sequences (mdt) encoding them. The MDDT polypeptides may be used to

CC screen for molecules that bind to, or are bound by the encoded

CC polypeptides, and to develop a transcript image of a tissue or cell type.

CC Probes comprising at least 20 nucleotides of the mdt polynucleotide may

CC be used to assess the toxicity of a test compound. The MDDT polypeptides

CC and mdt polynucleotides are useful in the diagnosis, study, prevention

CC and treatment of diseases associated with the expression of molecules for

CC disease detection and treatment. Such disorders include cell

CC proliferative disorders (e.g. arteriosclerosis, cirrhosis, or cancers),

CC and autoimmune/inflammatory disorders (e.g. asthma, Crohn's disease, or

CC multiple sclerosis). The mdt polynucleotides may also be used as

CC molecule markers, in microarrays, and in somatic or germline gene

CC therapy. ABG70306-ABG70341 represent the MDDT proteins of the invention

XX

SQ Sequence 247 AA;

Query Match 85.6%; Score 661; DB 5; Length 247;

Best Local Similarity 84.5%; Pred. No. 2.9e-45;

Matches 125; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYAFNRPSGV 60

Db 32 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYLGSSRASGV 91

Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPFIF 120

Db 92 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPFIF 151

Qy 121 PPSDEQLKSGTASVVCLLNNFPYRKERV 148

Db 152 PPSDEQLKSGTASVVCLLNNFPYRKERV 179

RESULT 6

ADL93653

ID ADL93653 standard; protein; 238 AA.

AC ADL93653;

XX

XX 17-JUN-2004 (first entry)

DT

DE Human CD44-binding antibody light chain BE-D7-kappa-light SEQ ID NO:148.

XX human; CD44; light chain immunoglobulin variable domain;

KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;

KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;

KW dermatological; vasotropic; neuroprotective; antibody therapy;

KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;

KW graft versus host response; multiple sclerosis; neoplastic disorder;

XX cancer; antibody.

OS Homo sapiens.

XX

XX WO2004024750-A2.

PN

PD 25-MAR-2004.

XX

XX 15-SEP-2003; 2003WO-US029318.

XX

XX 13-SEP-2002; 2002US-0410758P.

PR

PR 09-MAY-2003; 2003US-0469123P.

XX

XX (DYAX-) DYAX CORP.

PA

XX Rondon IJ, Edge A, Baribault Kent R;

PI

XX WPI; 2004-270003/25.

DR

XX New protein comprising a light chain (LC) immunoglobulin variable domain

PT

PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,

PT useful for preparing a composition for treating inflammatory or

PT neoplastic disorders.

XX

XX Disclosure; SEQ ID NO 148; 128pp; English.

PS

XX The invention relates to a novel isolated protein comprising a light

CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)

CC immunoglobulin variable domain sequence that form an antigen binding site

CC with binding affinity for the human CD44 extracellular domain and where

CC CD3 of the LC variable domain sequence. A protein of the invention has

CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,

CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,

CC and may have a use in antibody therapy. The protein is useful for

CC preparing a composition for treating inflammatory disorders, e.g.,

CC rheumatoid arthritis, lupus, restenosis, graft versus host response or

CC multiple sclerosis or neoplastic disorder, which is a malignant or

CC metastatic cancer. The present sequence represents a human CD44-binding

CC antibody light chain.

XX

SQ Sequence 238 AA;

Query Match 85.1%; Score 657; DB 8; Length 238;

Best Local Similarity 85.1%; Pred. No. 5.8e-45;

Matches 126; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYAFNRPSGV 60

Db 23 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYLGSSRASGV 82

Qy 61 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPFIF 120

Db 83 PDRFSGSGSGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPFIF 142

Qy 121 PPSDEQLKSGTASVVCLLNNFPYRKERV 148

Db 143 PPSDEQLKSGTASVVCLLNNFPYRKERV 170

RESULT 7

ADL93649

ID ADL93649 standard; protein; 238 AA.

AC ADL93649;

XX

XX 17-JUN-2004 (first entry)

DT

XX Human CD44-binding antibody light chain HAE-A3-kappa-light SEQ ID NO:144.

DE human; CD44; light chain immunoglobulin variable domain;

XX heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;

KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;

KW dermatological; vasotropic; neuroprotective; antibody therapy;

KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;

KW graft versus host response; multiple sclerosis; neoplastic disorder;

XX cancer; antibody.

OS Homo sapiens.

XX

XX WO2004024750-A2.

PN

PD 25-MAR-2004.

XX

XX 15-SEP-2003; 2003WO-US029318.

XX

XX 13-SEP-2002; 2002US-0410758P.

PR

PR 09-MAY-2003; 2003US-0469123P.

XX

XX (DYAX-) DYAX CORP.

PA

XX Rondon IJ, Edge A, Baribault Kent R;

PI

XX WPI; 2004-270003/25.

DR

XX New protein comprising a light chain (LC) immunoglobulin variable domain
 PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
 PT useful for preparing a composition for treating inflammatory or
 PT neoplastic disorders.
 XX Disclosure; SEQ ID NO 144; 128pp; English.
 XX
 CC The invention relates to a novel isolated protein comprising a light
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
 CC immunoglobulin variable domain sequence that form an antigen binding site
 CC with binding affinity for the human CD44 extracellular domain and where
 CC CDR3 of the LC variable domain sequence. A protein of the invention has
 CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
 CC and may have a use in antibody therapy. The protein is useful for
 CC preparing a composition for treating inflammatory disorders, e.g.,
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
 CC multiple sclerosis or neoplastic disorder, which is a malignant or
 CC metastatic cancer. The present sequence represents a human CD44-binding
 CC antibody light chain.
 XX Sequence 238 AA;
 SQ
 Query Match 85.0%; Score 656; DB 8; Length 238;
 Best Local Similarity 85.1%; Pred. No. 7e-45;
 Matches 126; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
 QY 1 VTQPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRPSGV 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 23 MTQSPSLPVTTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYLSNRASGV 82
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVPFIF 120
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 83 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQALQTPPTFGGKTKVEIKRTVAAPSVPFIF 142
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 143 PPSDEQLKSGTASVVCLLNNFYPRKRV 170
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 RESULT 8
 ID ADL93654 standard; protein; 238 AA.
 XX ADL93654;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE Human CD44-binding antibody light chain BE-H10-kappa-light SEQ ID NO:149.
 XX
 KW human; CD44; light chain immunoglobulin variable domain;
 KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;
 KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
 KW dermatological; vasotropic; neuroprotective; antibody therapy;
 KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
 KW graft versus host response; multiple sclerosis; neoplastic disorder;
 KW cancer; antibody.
 XX
 OS Homo sapiens.
 OS
 FN WO2004024750-A2.
 XX
 PD 25-MAR-2004.
 XX
 PF 15-SEP-2003; 2003WO-US029318.
 XX
 PR 13-SEP-2002; 2002US-0410758P.
 PR 09-MAY-2003; 2003US-0469123P.
 XX
 PA (DYAX-) DYAX CORP.
 XX
 FI Rondon IJ, Edge A, Baribault Kent R;

XX WPI; 2004-270003/25.
 XX
 PT New protein comprising a light chain (LC) immunoglobulin variable domain
 PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
 PT useful for preparing a composition for treating inflammatory or
 PT neoplastic disorders.
 XX Disclosure; SEQ ID NO 149; 128pp; English.
 XX
 CC The invention relates to a novel isolated protein comprising a light
 CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
 CC immunoglobulin variable domain sequence that form an antigen binding site
 CC with binding affinity for the human CD44 extracellular domain and where
 CC CDR3 of the LC variable domain sequence. A protein of the invention has
 CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,
 CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
 CC and may have a use in antibody therapy. The protein is useful for
 CC preparing a composition for treating inflammatory disorders, e.g.,
 CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
 CC multiple sclerosis or neoplastic disorder, which is a malignant or
 CC metastatic cancer. The present sequence represents a human CD44-binding
 CC antibody light chain.
 XX Sequence 238 AA;
 SQ
 Query Match 84.6%; Score 653; DB 8; Length 238;
 Best Local Similarity 84.5%; Pred. No. 1.2e-44;
 Matches 125; Conservative 11; Mismatches 12; Indels 0; Gaps 0;
 QY 1 VTQPSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRPSGV 60
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 23 MTQSPSLPVTTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYLSNRASGV 82
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVPFIF 120
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 83 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQALQTPPTFGGKTKVEIKRTVAAPSVPFIF 142
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 QY 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 Db 143 PPSDEQLKSGTASVVCLLNNFYPRKRV 170
 :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
 RESULT 9
 ID ABP58286 standard; protein; 219 AA.
 XX ABP58286;
 XX
 DT 23-OCT-2003 (revised)
 DT 31-MAR-2003 (first entry)
 XX
 DE Humanised 10D5 antibody light chain.
 XX
 KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
 KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
 KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; neurotropic.
 XX
 OS Mus sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Region 1..113
 FT /note= "light chain variable region"
 FT Region 24..39
 FT /note= "CDR1"
 FT Region 55..61
 FT /note= "CDR2"
 FT Region 94..102
 FT /note= "CDR3"
 XX
 FN WO200288307-A2.


```
RESULT 11
ADL93650
ID ADL93650 standard; protein; 238 AA.
XX AC ADL93650;
XX DT 17-JUN-2004 (first entry)
XX DE Human CD44-binding antibody light chain HAE-G2-kappa-light SEQ ID NO:145.
XX KW human; CD44; light chain immunoglobulin variable domain;
XX KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;
XX KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
XX KW dermatological; vasotropic; neuroprotective; antibody therapy;
XX KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
XX KW graft versus host response; multiple sclerosis; neoplastic disorder;
XX KW cancer; antibody.
XX OS Homo sapiens.
XX PN WO2004024750-A2.
XX PD 25-MAR-2004.
XX PF 15-SEP-2003; 2003WO-US029318.
XX PR 13-SEP-2002; 2002US-0410758P.
XX PR 09-MAY-2003; 2003US-0469123P.
XX PA (DYAX-) DYAX CORP.
XX PI Rondon IJ, Edge A, Baribault Kent R;
XX DR WPI; 2004-270003/25.
XX PT New protein comprising a light chain (LC) immunoglobulin variable domain
XX PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
XX PT useful for preparing a composition for treating inflammatory or
XX PT neoplastic disorders.
XX PS Disclosure; SEQ ID NO 145; 128pp; English.
XX CC The invention relates to a novel isolated protein comprising a light
XX CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
XX CC immunoglobulin variable domain sequence that form an antigen binding site
XX CC with binding affinity for the human CD44 extracellular domain and where
XX CC CD44 is the variable domain sequence. A protein of the invention has
XX CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,
XX CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
XX CC and may have a use in antibody therapy. The protein is useful for
XX CC preparing a composition for treating inflammatory disorders, e.g.,
XX CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
XX CC multiple sclerosis or neoplastic disorder, which is a malignant or
XX CC metastatic cancer. The present sequence represents a human CD44-binding
XX CC antibody light chain.
XX SQ Sequence 238 AA;
Query Match 84.2%; Score 650; DB 8; Length 238;
Best Local Similarity 83.8%; Pred. No. 2.1e-44;
Matches 124; Conservative 12; Mismatches 12; Indels 0; Gaps 0;
Qy 1 VTQPSLSVTPGPASISCKSSQSLHSDGKTYLYWYVLPKPGQPPQLLIYEAFFNRFSGV 60
Dy 23 MTQSPSLPVTTPGPASISCKSSQSLHSDGKTYLYWYVLPKPGQPPQLLIYGSNRASGV 82
Qy 61 PDPSGSGSGDFTLKISRVEAEDVGLYVCMQSTELPTFGGKTKVEIKRTVAAPSVFIF 120
Dy 83 PDPSGSGSGDFTLKISRVEAEDVGLYVCMQSTELPTFGGKTKVEIKRTVAAPSVFIF 142
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Dy 143 PPSDEQLKSGTASVVCLLNNFYPRKERV 170
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RESULT 12
AAY82611
ID AAY82611 standard; protein; 239 AA.
XX AC AAY82611;
XX DT 02-AUG-2000 (first entry)
XX DE Human PTHrP monoclonal antibody clone 16E12-6 protein SEQ ID NO:6.
XX KW Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
XX KW hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
XX KW fracture; cachexia; tooth disease; periodontal disease; gingivitis; sepsis;
XX KW systemic inflammatory response syndrome; SIRS; hypophosphataemia;
XX KW antiarthritic; cytostatic; antiinflammatory.
XX OS Homo sapiens.
XX PN JP2000080100-A.
XX PD 21-MAR-2000.
XX PF 12-OCT-1998; 98JP-00304793.
XX PR 17-JUN-1998; 98JP-00188196.
XX PR 26-JUN-1998; 98JP-00196729.
XX PA (NISB) JAPAN TOBACCO INC.
XX DR WPI; 2000-286723/25.
XX DR N-ESDB; AAA13921.
XX PT A human monoclonal antibody to parathyroid hormone related protein. -
XX PT useful for treating hypercalcaemia, rheumatoid arthritis, cancer of bone
XX PT including metastasis, and pain.
XX PS Claim 31; Page 34-35; 88pp; Japanese.
XX CC The present invention describes a human monoclonal antibody to
XX CC parathyroid hormone related protein (PTHrP). The monoclonal antibody or
XX CC its fragments, following the stimulation of PTHrP has the following
XX CC properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
XX CC the release of calcium from bone; or (c) inhibits elevation of blood
XX CC calcium content. The monoclonal antibody can be used in the treatment of
XX CC hypercalcaemia, rheumatoid arthritis, cancer of bone including
XX CC metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
XX CC diseases and gingivitis, sepsis, systemic inflammatory response syndrome
XX CC (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
XX CC antiinflammatory activities. The present sequence represents a human
XX CC PTHrP monoclonal antibody clone protein sequence from the present
XX CC invention
XX SQ Sequence 239 AA;
Query Match 84.1%; Score 649; DB 3; Length 239;
Best Local Similarity 82.4%; Pred. No. 2.6e-44;
Matches 122; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
Qy 1 VTQPSLSVTPGPASISCKSSQSLHSDGKTYLYWYVLPKPGQPPQLLIYEAFFNRFSGV 60
Dy 24 MTQSPSLPVTTPGPASISCKSSQSLHSDGKTYLYWYVLPKPGQPPQLLIYGSNRASGV 83
Qy 61 PDPSGSGSGDFTLKISRVEAEDVGLYVCMQSTELPTFGGKTKVEIKRTVAAPSVFIF 120
Dy 84 PDPSGSGSGDFTLKISRVEAEDVGLYVCMQSTELPTFGGKTKVEIKRTVAAPSVFIF 143
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Dy 144 PPSDEQLKSGTASVVCLLNNFYPRKERV 171
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RESULT 13
ADL23139
ID ADL23139 standard; protein; 239 AA.
XX
AC ADL23139;
DT 20-MAY-2004 (first entry)
XX
DE Mouse/human ING-1 antibody light chain, low/medium risk engineered.
XX
KW Human; mouse; mutein; bactericidal/permeability-increasing protein; BPI;
KW Ep-CAM; CAB2.1; recombinant polypeptide production; ING-1; antibody;
KW anti-CD18 antibody; cosmetic product; mutant.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
OS Synthetic.
XX
PN US2003203447-A1.
XX
PD 30-OCT-2003.
XX
PF 31-MAR-2003; 2003US-00404724.
XX
PR 29-MAR-2002; 2002US-0368530P.
XX
PA (HORW/) HORWITZ A H.
XX
PI Horwitz AH;
XX
XX WPI; 2003-875646/81.
DR N-PSDB; ADL23138.
DR
XX
PT Producing recombinant polypeptide, useful for treating or diagnosing
PT comprises culturing cells transformed or transfected with a vector
PT comprising multiple copies of a transcription unit separated by a
PT selective marker gene.
XX
PS Example 6; SEQ ID NO 12; 133pp; English.
XX
CC The invention relates to producing a recombinant polypeptide comprising
CC culturing cells, which have been transformed or transfected with a
CC vector, or its segment comprising multiple copies of a transcription unit
CC separated by at least one selective marker gene, where the transcription
CC unit encodes a polypeptide under selective conditions. Also included are
CC a vector or segment comprising multiple copies of a transcription unit
CC separated by at least one selective marker gene where the transcription
CC unit encodes a polypeptide, a host cell comprising an expression vector
CC or segment and a stable cell line comprising an expression vector or
CC segment. Each transcription unit is under the control of its own promoter
CC and 3' untranslated region, where the promoter is an SV40, HSV, bovine
CC growth hormone, thymidine kinase, MP5V, mouse beta globin, human EFl, MSV
CC -LTR, RSV, MMTV-LTR, CMV, MLV, Chinese hamster elongation factor or mouse
CC Abelson LTR promoter. The expression vector further comprises multiple
CC enhancers. The transcription unit also encodes two different subunits of
CC a multimeric protein, an immunoglobulin light and heavy chain
CC polypeptides or at least the variable regions of the immunoglobulin light
CC and heavy chain polypeptides. It further encodes a BPI protein
CC (bactericidal/permeability-increasing protein) product. The protein
CC product BPI protein fragment, BPI analogue, BPI variant or BPI-derived
CC peptide. The transcription unit encodes an rBPI21 and is under the
CC control of an hCMV promoter and mouse light chain 3' untranslated region,
CC where the vector further comprises 0, 1 or 2 copies of a human heavy
CC chain enhancer and either a gpt or neo gene. Other genes suitable for
CC expression using the method of the invention are Ep-CAM and CAB2.1 (both
CC not defined). The immunoglobulin may be the ING-1 chimaeric mouse/human
CC antibody (or humanised versions or proline substitution mutants) or an
CC anti-CD18 antibody. The method is useful for producing recombinant
CC polypeptide. Recombinant polypeptide compositions are useful in
CC therapies, in diagnostic procedures or as tools in preventive medicine.
CC Recombinant polypeptides are also found in a wide array of both health
CC and cosmetic products, used to increase the quality of life. Complex

CC polypeptide products are also routinely used in research laboratories
CC both as end products of analyses and as agents in assays for the study or
CC preparation of other molecules. Advantages of the present invention
CC includes increased recombinant polypeptide production, increased
CC production efficiency, greater control and/or regulation over the
CC qualities of the polypeptide expressed, increased stability of cell
CC lines, and/or decreased costs for materials, reagents and/or other
CC resources. The present sequence represents a mutated (humanised or
CC proline mutant) light or heavy chain from a antibody gene suitable for
CC inclusion in the transcription unit of the invention.
XX
SQ Sequence 239 AA;
Query Match 84.1%; Score 649; DB 7; Length 239;
Best Local Similarity 83.1%; Pred. No. 2.6e-44;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
Qy 1 VTQSPLSLVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIYEAPNRFSGV 60
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Db 24 MTQSPLSLVTPGPGSISCRSSKSLHSGITLYWYLOKPGQSPOLLIYQMSNRASGV 83
Qy 61 PDRFSSGSGTDFTLKISRVEAEDVGLYYCMQSIELPFTGGGTVKVEIKETVAAPSVEIF 120
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 84 PDRFSSGSGTDFTLKISRVEAEDVGLYYCAQNLELPRTFGGGTVKVEIKETVAAPSVEIF 143
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 144 PPSDEQLKSGTASVVCLLNNFYPRKERV 171
RESULT 14
ABR39464
ID ABR39464 standard; protein; 219 AA.
XX
AC ABR39464;
XX
DT 12-JUN-2003 (first entry)
XX
DE Humanised anti-Abeta antibody 266 light chain.
XX
KW Amyloid-beta; Abeta; antibody 266; nootropic; neuroprotective; CDR;
KW immunostimulant.
XX
OS Homo sapiens.
XX
PN WO2003016467-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US021324.
XX
PR 17-AUG-2001; 2001US-0313576P.
PR 28-MAY-2002; 2002US-0383851P.
XX
XX (ELIL) LILLY & CO ELI.
PI Bales KR, Paul SM;
XX
XX WPI; 2003-289975/28.
XX
PT Treating or reducing the progression of diseases associated with amyloid-
PT beta peptide, e.g. Alzheimer's disease, vascular dementia or mild
PT cognitive impairment, comprises administering an anti-amyloid-beta
PT peptide antibody.
XX
PS Disclosure; Page 19-20; 84pp; English.
XX
CC The invention relates to treating cognitive symptoms or reducing disease
CC progression in a subject having a condition or disease associated with
CC amyloid-beta peptide (Abeta). The method involves administering an amount
CC of an anti-Abeta antibody that has greater affinity for soluble Abeta
CC than 10⁻⁹ M, that has affinity (KD) for soluble Abeta1-40 or Abeta1-42
CC higher than 10⁻⁹ M, or that has greater affinity for soluble Abeta than

CC antibody 266 has. The method or the anti-Abeta antibody is useful in
CC preparing a medicament for treating cognitive symptoms or reducing
CC disease progression in a subject having a condition or disease associated
CC with Abeta. The condition or disease is Alzheimer's disease, Down's
CC syndrome, cerebral amyloid angiopathy, vascular dementia, or mild
CC cognitive impairment. The present sequence represents a humanised anti-
CC Abeta antibody 266 light chain
XX
SQ Sequence 219 AA;

Query Match 83.9%; Score 648; DB 6; Length 219;
Best Local Similarity 83.1%; Pred. No. 2.8e-44;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYVLOKPGQPOLLIVEAFNRFSGV 60
Db 4 MTQSPSLSLPVTLGQPASISCRSSQSLIYSDGNAYLHWFLOKPGQSPRLLIYKVNRFSGV 63
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVPFIF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVPFIF 123
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPRKAV 151

RESULT 15
ABU08310
ID ABU08310 standard; protein; 219 AA.
XX
AC ABU08310;
XX
DT 22-MAY-2003 (first entry)
XX
DE Humanised 266 antibody light chain.
XX
KW Mouse; cognition; Abeta peptide associated disorder; anti-Abeta antibody;
KW cognitive impairment; Alzheimer's disease; Down's syndrome;
KW cerebral amyloid angiopathy; vascular dementia; neurotropic;
KW mild cognitive impairment; antibody 266; light chain; humanised; mutant;
KW muten.
XX
OS Mus sp.
OS Synthetic.
XX
FN WO2003015691-A2.
XX
PD 27-FEB-2003.
XX
PF 14-AUG-2002; 2002WO-US021323.
XX
PR 17-AUG-2001; 2001US-0313222P.
PR 28-MAY-2002; 2002US-0383846P.
XX
PA (ELIL) LILLY & CO ELI.
XX
PI Bales KR, Dodart JF, Paul SM;
XX
XX WPI; 2003-268234/26.
XX
PT Effecting rapid improvement of cognition in a subject having Alzheimer's
PT disease, Down's syndrome, cerebral amyloid angiopathy, or mild cognitive
PT impairment, comprises administering anti-A beta antibody.
XX
PS Disclosure; Page 20-21; 85pp; English.
XX

The present invention relates to a method for effecting rapid improvement
of cognition in a subject having a condition or disease related to the
Abeta peptide. The method comprises administering an anti-Abeta antibody.
The method is useful for treating cognitive impairments associated with
Abeta peptide including those involved in Alzheimer's disease, Down's
syndrome, cerebral amyloid angiopathy, certain vascular dementia, and

CC certain forms of mild cognitive impairment. The anti-Abeta antibody is
CC useful for preparing a medicament for effecting rapid improvement in
CC cognition in a subject having Alzheimer's disease, Down's syndrome,
CC cerebral amyloid angiopathy, or mild cognitive impairment. The present
CC sequence represents a preferred light chain for a humanised 266 antibody
XX
SQ Sequence 219 AA;

Query Match 83.9%; Score 648; DB 6; Length 219;
Best Local Similarity 83.1%; Pred. No. 2.8e-44;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;
Qy 1 VTQSPSLSVTPGPASISCKSSQSLHSDGKTYLYVLOKPGQPOLLIVEAFNRFSGV 60
Db 4 MTQSPSLSLPVTLGQPASISCRSSQSLIYSDGNAYLHWFLOKPGQSPRLLIYKVNRFSGV 63
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVPFIF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVPFIF 123
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPRKAV 151

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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	661	85.6	247	US-10-466-164-69	Sequence 69, Appl
2	657	85.1	238	US-10-663-244-148	Sequence 148, App
3	656	85.0	238	US-10-663-244-144	Sequence 144, App
4	653	84.6	238	US-10-663-244-149	Sequence 149, App
5	650	84.2	238	US-10-663-244-145	Sequence 145, App
6	649	84.1	239	US-10-404-724-12	Sequence 12, Appl
7	649	84.1	239	US-10-816-276-8	Sequence 8, Appl
8	648	83.9	219	US-10-226-435A-11	Sequence 11, Appl
9	648	83.9	219	US-10-487-322-11	Sequence 11, Appl
10	647	83.8	219	US-10-698-041-4	Sequence 4, Appl
11	644	83.4	173	US-10-309-762-175	Sequence 175, App
12	643	83.3	239	US-10-292-088-40	Sequence 40, Appl
13	641	83.0	239	US-10-292-088-32	Sequence 32, Appl

14	640	82.9	219	10	US-09-972-656-92	Sequence 92, Appl
15	639	82.8	239	15	US-10-292-088-16	Sequence 16, Appl
16	638.5	82.7	237	16	US-10-663-244-146	Sequence 146, App
17	638.5	82.7	237	16	US-10-663-244-153	Sequence 153, App
18	638	82.6	239	15	US-10-292-088-56	Sequence 56, Appl
19	636	82.4	238	16	US-10-663-244-147	Sequence 147, App
20	636	82.4	239	15	US-10-292-088-8	Sequence 8, Appl
21	636	82.4	239	15	US-10-292-088-80	Sequence 80, Appl
22	636	82.4	239	15	US-10-292-088-102	Sequence 102, App
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24	634	82.1	239	10	US-09-924-340-8	Sequence 8, Appl
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26	634	82.1	239	10	US-09-999-570-8	Sequence 8, Appl
27	634	82.1	239	14	US-10-000-489-8	Sequence 8, Appl
28	634	82.1	239	14	US-10-000-986-8	Sequence 8, Appl
29	634	82.1	239	14	US-10-154-678-8	Sequence 8, Appl
30	634	82.1	239	15	US-10-404-724-45	Sequence 45, Appl
31	634	82.1	239	15	US-10-404-724-49	Sequence 49, Appl
32	634	82.1	239	17	US-10-816-276-41	Sequence 41, Appl
33	634	82.1	239	17	US-10-816-276-45	Sequence 45, Appl
34	634	82.1	239	17	US-10-838-854-8	Sequence 8, Appl
35	633.5	82.1	220	9	US-09-822-698A-24	Sequence 24, Appl
36	632.5	81.9	237	16	US-10-663-244-152	Sequence 152, App
37	632	81.9	239	15	US-10-404-724-47	Sequence 47, Appl
38	632	81.9	239	17	US-10-816-276-43	Sequence 43, Appl
39	628	81.3	239	15	US-10-108-260A-4028	Sequence 4028, App
40	626	81.1	239	9	US-09-758-173-6	Sequence 6, Appl
41	626	81.1	239	9	US-09-948-429B-6	Sequence 6, Appl
42	626	81.1	239	13	US-10-124-905-6	Sequence 6, Appl
43	626	81.1	239	14	US-10-124-807-6	Sequence 6, Appl
44	626	81.1	239	14	US-10-291-532-6	Sequence 41, Appl
45	626	81.1	239	15	US-10-404-724-41	

ALIGNMENTS

RESULT 1
US-10-466-164-69
; Sequence 69, Application US/10466164
; Publication No. US20040058365A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE CORPORATION; PANZER, Scott R.;
; APPLICANT: LINCOLN, Stephen E.; ALTUS, Christina M.;
; APPLICANT: DUFOUR, Gerard E.; JACKSON, Jennifer L.;
; APPLICANT: JONES, Anissa L.; DAM, Tam C.;
; APPLICANT: LIU, Tommy F.; HARRIS, Bernard;
; APPLICANT: FLORES, Vincent Z.; DAPPO, Abel;
; APPLICANT: MARWAHA, Rakesh; CHEN, Alice J.;
; APPLICANT: CHANG, Simon C.; GERSTIN, Jr., Edward H.;
; APPLICANT: PERALTA, Careyna H.; DAVID, Marie H.;
; APPLICANT: LEWIS, Samantha A.
; TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
; FILE REFERENCE: PT-1215 PCT
; CURRENT APPLICATION NUMBER: US/10/466,164
; PRIOR FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: PCT/US02/01008
; PRIOR FILING DATE: 2002-01-09
; PRIOR APPLICATION NUMBER: US 60/261,865
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/263,065
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/263,329
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/262,209
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,208
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/262,326
; PRIOR FILING DATE: 2001-01-17
; PRIOR APPLICATION NUMBER: US 60/263,063
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/261,622

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; PRIOR FILING DATE: 2001-01-12
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: PERL Program
; SEQ ID NO 69
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20040058365A1 LI:1171219.2.orf3.2001JAN12
US-10-666-164-69

Query Match      85.6%; Score 661; DB 15; Length 247;
Best Local Similarity 84.5%; Pred. No. 2.4e-44;
Matches 125; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
32 MTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYLGSSRASGV 91

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
92 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 151

Qy 121 PPSDEQLKSGTASVVCLLNFPYPRKERV 148
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
152 PPSDEQLKSGTASVVCLLNFPYPRKERV 179

RESULT 2
US-10-663-244-148
; Sequence 148, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-148

Query Match      85.1%; Score 657; DB 16; Length 238;
Best Local Similarity 85.1%; Pred. No. 4.9e-44;
Matches 126; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 MTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYLGSSRASGV 82

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 142

Qy 121 PPSDEQLKSGTASVVCLLNFPYPRKERV 148
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
143 PPSDEQLKSGTASVVCLLNFPYPRKERV 170

RESULT 3
US-10-663-244-149
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149

Query Match      84.6%; Score 653; DB 16; Length 238;
Best Local Similarity 84.5%; Pred. No. 1e-43;
Matches 125; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
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US-10-663-244-144
; Sequence 144, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-144

Query Match      85.0%; Score 656; DB 16; Length 238;
Best Local Similarity 85.1%; Pred. No. 5.8e-44;
Matches 126; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
23 MTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYLGSSRASGV 82

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
83 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPTFGGKTKVEIKRTVAAPSVPFIF 142

Qy 121 PPSDEQLKSGTASVVCLLNFPYPRKERV 148
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
143 PPSDEQLKSGTASVVCLLNFPYPRKERV 170

RESULT 4
US-10-663-244-149
; Sequence 149, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-149

Query Match      84.6%; Score 653; DB 16; Length 238;
Best Local Similarity 84.5%; Pred. No. 1e-43;
Matches 125; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTGPGPASPISCKSSQSLHSDGKTYLYWYLOKPGQPPOLLIIYEAFNRFSGV 60
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;
; ORGANISM: Homo Sapiens
US-10-404-724-12

Query Match      84.1%; Score 649; DB 15; Length 239;
Best Local Similarity 83.1%; Pred. No. 2.1e-43;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPGASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 60
Db 24 MTQSPLSLVTPGPGASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 83
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120
Db 84 PDRFSSSGGTDFTLKISRVEAEDVGLYYCAQNLPRFTFGGKTKVEIKRTVAAPSVFIF 143
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPRKERV 171

RESULT 7
US-10-816-276-8
; Sequence 8, Application US/10816276
; Publication No. US2005000907A1
; GENERAL INFORMATION:
; APPLICANT: Better, Marc D.
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Human Engineered to Antibodies to Ep-CAM
; FILE REFERENCE: 14923US02
; CURRENT APPLICATION NUMBER: US/10/816,276
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: 60/459,334
; PRIOR FILING DATE: 2003-03-31
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 8
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-816-276-8

Query Match      84.1%; Score 649; DB 17; Length 239;
Best Local Similarity 83.1%; Pred. No. 2.1e-43;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPGASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 60
Db 24 MTQSPLSLVTPGPGASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 83
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120
Db 84 PDRFSSSGGTDFTLKISRVEAEDVGLYYCAQNLPRFTFGGKTKVEIKRTVAAPSVFIF 143
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPRKERV 171

RESULT 8
US-10-226-435A-11
; Sequence 11, Application US/10226435A
; Publication No. US20040043418A1
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY AND COMPANY
; TITLE OF INVENTION: Humanized Antibodies that Sequester Amyloid Beta Peptide
; FILE REFERENCE: 8792/293
; CURRENT APPLICATION NUMBER: US/10/226,435A
; CURRENT FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/06191
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,601
; PRIOR FILING DATE: 2000-02-24
; CURRENT APPLICATION NUMBER: 60/254,465
;

;
; ORGANISM: Homo Sapiens
US-10-404-724-12

Query Match      84.2%; Score 650; DB 16; Length 238;
Best Local Similarity 83.8%; Pred. No. 1.7e-43;
Matches 124; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPGASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 60
Db 23 MTQSPLSLVTPGPGASISCKSSQSLHSDGKTYLYWYLOKPGQPPQLLIYEAFNRFSGV 82
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120
Db 83 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQALQTPWTFGGKTKLEIKRTVAAPSVFIF 142
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKERV 148
Db 143 PPSDEQLKSGTASVVCLLNNFYPRKERV 170

RESULT 6
US-10-404-724-12
; Sequence 12, Application US/10404724
; Publication No. US20030203447A1
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Arnold H.
; TITLE OF INVENTION: Methods and Materials For Increasing Expression of Recombinant
; TITLE OF INVENTION: Polypeptides
; FILE REFERENCE: 13698US01
; CURRENT APPLICATION NUMBER: US/10/404,724
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/368,530
; PRIOR FILING DATE: 2002-03-29
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-145
; Sequence 145, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-145
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; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/254,498
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibodies
US-10-226-435A-11

Query Match      83.9%; Score 648; DB 15; Length 219;
Best Local Similarity 83.1%; Pred. No. 2.3e-43;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEAAPNRFSGV 60
Db 4 MTQSPLSLPTVLTGQPASISCKSSQSLIYSDGNAYLHWFLOKPGQSPRLIIYKVSNRFSGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPKERV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPKERV 151

RESULT 9
US-10-487-322-11
; Sequence 11, Application US/10487322
; Publication No. US2004019289A1
; GENERAL INFORMATION:
; APPLICANT: ELI LILLY AND COMPANY
; TITLE OF INVENTION: ANTI-AB ANTIBODIES
; FILE REFERENCE: X-15113
; CURRENT APPLICATION NUMBER: US/10/487,322
; CURRENT FILING DATE: 2004-02-17
; PRIOR APPLICATION NUMBER: 60/313,234
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanized antibody
; NAME/KEY: MISC_FEATURE
; LOCATION: (1)..(219)
; OTHER INFORMATION: HUMANIZED ANTIBODY LIGHT CHAIN
US-10-487-322-11

Query Match      83.9%; Score 648; DB 16; Length 219;
Best Local Similarity 83.1%; Pred. No. 2.3e-43;
Matches 123; Conservative 13; Mismatches 12; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEAAPNRFSGV 60
Db 4 MTQSPLSLPTVLTGQPASISCKSSQSLIYSDGNAYLHWFLOKPGQSPRLIIYKVSNRFSGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPKERV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPKERV 151
```

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RESULT 10
US-10-698-041-4
; Sequence 4, Application US/10698041
; Publication No. US2004015172A1
; GENERAL INFORMATION:
; APPLICANT: Coronella-Wood, Julia
; TITLE OF INVENTION: Antibody Fab Fragments Specific for Breast Cancer
; FILE REFERENCE: 5051.057
; CURRENT APPLICATION NUMBER: US/10/698,041
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: US 60/423,052
; PRIOR FILING DATE: 2002-10-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-041-4

Query Match      83.8%; Score 647; DB 16; Length 219;
Best Local Similarity 83.1%; Pred. No. 2.7e-43;
Matches 123; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEAAPNRFSGV 60
Db 4 MTQSPLSLPTVLTGQPASISCKSSQSLHSDGKTYLYWYLOKPGQSPOLLIIYLGFNASGV 63

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 123

Qy 121 PPSDEQLKSGTASVVCLLNNFYPKERV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPKERV 151

RESULT 11
US-10-309-762-175
; Sequence 175, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
; APPLICANT: Gudas, Jean
; APPLICANT: Foltz, Ian
; APPLICANT: Handa, Masahisa
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXYIC ANHYDRASE IX
; FILE REFERENCE: ARGENIX.027A
; CURRENT APPLICATION NUMBER: US/10/309,762
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/337275
; PRIOR FILING DATE: 2001-12-03
; NUMBER OF SEQ ID NOS: 246
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-309-762-175

Query Match      83.4%; Score 644; DB 15; Length 173;
Best Local Similarity 81.8%; Pred. No. 3.7e-43;
Matches 121; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEAAPNRFSGV 60
Db 20 MTQTPLSLPTVLTGQPASISCKSSQSLVHSDGNTYLSWMLQQRPGQPPRLIIYKISNRFSGV 79

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 120
Db 80 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIQLPFTFGGKTKVEIKRTVAAPSVPF 139
```

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 140 PPSDEQLKSGTASVVCLLNNFYPREAKV 167

RESULT 12

US-10-292-088-40
; Sequence 40, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-40

Query Match 83.3%; Score 643; DB 15; Length 239;
Best Local Similarity 83.1%; Pred. No. 6.1e-43;
Matches 123; Conservative 12; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPQLLIYEAFNRFSGV 60
Db 24 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPQLLIYLSNRASGV 83
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFTGGGTVKVEIKRTVAAPSVFIF 120
Db 84 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFTGGGTVKVEIKRTVAAPSVFIF 143

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPREAKV 171

RESULT 13

US-10-292-088-32
; Sequence 32, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-32

Query Match 83.0%; Score 641; DB 15; Length 239;
Best Local Similarity 81.8%; Pred. No. 8.8e-43;
Matches 121; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPQLLIYEAFNRFSGV 60
Db 24 MTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPQLLIYLSNRASGV 83
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFTGGGTVKVEIKRTVAAPSVFIF 120
Db 84 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFTGGGTVKVEIKRTVAAPSVFIF 143
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPREAKV 171

RESULT 14

US-09-972-656-92
; Sequence 92, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 92
; LENGTH: 219
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-92

Query Match 82.9%; Score 640; DB 10; Length 219;
Best Local Similarity 81.8%; Pred. No. 9.7e-43;
Matches 121; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 VTQSPLSLVTPGPASISCKSSQSLHSDGKTYLYWYLPKPGQPQLLIYEAFNRFSGV 60
Db 4 MHTPLSSPVLTPGPASISCKSSQSLHSDGNTYLSMLHQRPGQPRLLIYKISNRFSGV 63
Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFTGGGTVKVEIKRTVAAPSVFIF 120
Db 64 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPTFTGGGTVKVEIKRTVAAPSVFIF 123
Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 124 PPSDEQLKSGTASVVCLLNNFYPREAKV 151

RESULT 15

US-10-292-088-16
; Sequence 16, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-292-088-16

Query Match	82.8%	Score 639;	DB 15;	Length 239;
Best Local Similarity	83.1%;	Pred. No. 1.3e-42;		
Matches 123; Conservative 12;	Mismatches 13;	Indels 0;	Gaps 0;	
Qy	1	VTQSPLSLVPTGPGASISCKSSOSLHSDGKTYLVYLOKPGOPPOLLIYEAFNRPSGV	60	
Dd	24	MTQSPFLSLPVTGPGFAPGISCRSSSLLYSNGYNFDWYLOKPGOSPQLLIYLGSNRASGV	83	
Qy	61	PDRFSGSGSGTDFTLKISRVEAEDVGYLYCMQSIELPFTEGGGTKEVKIRTAAPSIFYIF	120	
Dd	84	PDRFSGSGSGTDFTLKISRVEAEDVGYYCYMAQLQTPTRTFGGTKEVKIRTAAPSIFYIF	143	
Qy	121	PPSEQLKSGTASVVCLLNFFPKRERV	148	
Dd	144	PPSEQLKSGTASVVCLLNFFPREAKV	171	

Search completed: March 8, 2005, 07:05:56
Job time : 78.5397 secs


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RESULT 2
US-08-487-550-6
; Sequence 6, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-550-6

Query Match      81.1%; Score 626; DB 3; Length 239;
Best Local Similarity 80.4%; Pred. No. 1.1e-56;
Matches 119; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFSGV 60
Db 24 MTQSPLSLPTPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVSNRDSGV 83

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120
Db 84 PDRFSGSGAGTDFTLKISAVEADVGVYFCGGTTRTPPTFGGKTKVEIKRTVAAPSVFIF 143

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPREAKV 171

RESULT 3
US-09-526-098-6
; Sequence 6, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
```

```
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-526-098-6

Query Match      81.1%; Score 626; DB 4; Length 239;
Best Local Similarity 80.4%; Pred. No. 1.1e-56;
Matches 119; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFSGV 60
Db 24 MTQSPLSLPTPGEPASISCRSSQSLKHSNGDTFLSWYQKPGQPRLIIYKVSNRDSGV 83

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120
Db 84 PDRFSGSGAGTDFTLKISAVEADVGVYFCGGTTRTPPTFGGKTKVEIKRTVAAPSVFIF 143

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 144 PPSDEQLKSGTASVVCLLNNFYPREAKV 171

RESULT 4
US-09-383-916-6
; Sequence 6, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/383,916

FILING DATE: 26-AUG-1999

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/487,550

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Teskin, Robin L.

REGISTRATION NUMBER: 35,030

REFERENCE/DOCKET NUMBER: 012712-131

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6620

TELEFAX: 703-836-2021

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 239 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-383-916-6

Query Match 81.1%; Score 626; DB 4; Length 239;

Best Local Similarity 80.4%; Pred. No. 1.1e-56;

Matches 119; Conservative 13; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTFPGOPASISCKSSQSLHSDGKTYLYWYLRQPGOPQLLIYEAFNRSGV 60

Db 24 MTQSPLSLPITPGPAPASISCKSSQSLHSDGKTYLYWYLRQPGOPQLLIYKVNRSQGV 83

Qy 61 PDRFSGSGGDTFTLKISRVEADVGYYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120

Db 84 PDRFSGSGAGDTFTLKISAVEADVGYYFCQGTPTPTFTFGGKTKVEIKRTVAAPSVFIF 143

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148

Db 144 PPSDEQLKSGTASVVCLLNNFYPRKRV 171

RESULT 5

US-09-698-705-10

Sequence 10, Application US/09698705

Patent No. 6824780

GENERAL INFORMATION:

APPLICANT: Devaux, B.

APPLICANT: Keller, G.

APPLICANT: Koepfen, H.

APPLICANT: Lasky, L.

TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use

FILE REFERENCE: P1777R1

CURRENT APPLICATION NUMBER: US/09/698,705

PRIOR FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/162,558

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: US 60/182,872

PRIOR FILING DATE: 2000-02-16

NUMBER OF SEQ ID NOS: 25

SEQ ID NO 10

LENGTH: 238

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: sequence is chimeric mouse/human

US-09-698-705-10

Query Match 79.4%; Score 613; DB 4; Length 238;

Best Local Similarity 77.0%; Pred. No. 2.5e-55;

Matches 114; Conservative 18; Mismatches 16; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTFPGOPASISCKSSQSLHSDGKTYLYWYLRQPGOPQLLIYEAFNRSGV 60

Db 23 MTQAAPSVFPTPGESVSIKSSQSLHSDGKTYLYWYLRQPGOPQLLIYRMNLSAGV 82

Qy 61 PDRFSGSGGDTFTLKISRVEADVGYYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIF 120

Db 83 PDRFSGSGGTAFTLRISRVEADVGYYCQLHLEYPTFGGKTKLELKRVAAPSVFIF 142

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148

Db 143 PPSDEQLKSGTASVVCLLNNFYPRKRV 170

RESULT 6

US-09-472-087-26

Sequence 26, Application US/09472087

Patent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, ELLEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PFI

CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 26

LENGTH: 133

TYPE: PRT

ORGANISM: Homo sapiens

US-09-472-087-26

Query Match 79.0%; Score 610; DB 4; Length 133;

Best Local Similarity 86.5%; Pred. No. 2.5e-55;

Matches 115; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 12 PGQPASISCKSSQSLHSDGKTYLYWYLRQPGOPQLLIYEAFNRFSVDPDRFSGSGGT 71

Db 1 PGEPASISCKSSQSLHSDGKTYLYWYLRQPGOPQLLIYLSNRASVDPDRFSGSGGT 60

Qy 72 DFTLKISRVEADVGYYCMQSIELPFTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGT 131

Db 61 DFTLKISRVEADVGYYCMQALQTLPTFTFGGKTKVEIKRTVAAPSVFIFPPSDEQLKSGT 120

Qy 132 ASVVCLNNFYPR 144

Db 121 ASVVCLNNFYPR 133

RESULT 7

US-09-472-087-116

Sequence 116, Application US/09472087

Patent No. 6682736

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, ELLEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PFI

CURRENT APPLICATION NUMBER: US/09/472,087

CURRENT FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: 60/113,647

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 116
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-116

Query Match      79.0%; Score 610; DB 4; Length 133;
Best Local Similarity 86.5%; Pred. No. 2.5e-55;
Matches 115; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 12 PGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFGVDPDRFGSGSGT 71
Db 1 PGEPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYLGSRASGVDPDRFGSGSGT 60

Qy 72 DFTLKISRVAEDVGLYYCWSIELPFTFGGTVKRTVAAPSVFIPPSDEQLKSGT 131
Db 61 DFTLKISRVAEDVGLYYCWSIELPFTFGGTVKRTVAAPSVFIPPSDEQLKSGT 120

Qy 132 ASVVCLLNFFPR 144
Db 121 ASVVCLLNFFPR 133

RESULT 8
US-09-698-705-12
; Sequence 12, Application US/09698705
; Patent No. 6824780
; GENERAL INFORMATION:
; APPLICANT: Devaux, B.
; APPLICANT: Keller, G.
; APPLICANT: Koepfen, H.
; APPLICANT: Lasky, L.
; TITLE OF INVENTION: Anti-Tumor Antibody Compositions and Methods of Use
; FILE REFERENCE: P177R1
; CURRENT APPLICATION NUMBER: US/09/698,705
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,558
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 60/182,872
; PRIOR FILING DATE: 2000-02-16
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 12
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: sequence is chimeric mouse/human
US-09-698-705-12

Query Match      78.5%; Score 606; DB 4; Length 218;
Best Local Similarity 79.7%; Pred. No. 1.2e-54;
Matches 118; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFGSV 60
Db 4 MTQTPLSVTIGQPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYVSTLDSGV 63

Qy 61 PDRFGSGSGTDFTLKISRVAEDVGLYYCWSIELPFTFGGTVKRTVAAPSVFIF 120
Db 64 PDRFTGSGSGTDFTLKISRVAEDVGLYYCWSIELPFTFGGTVKRTVAAPSVFIF 123

Qy 121 PSDEQLKSGTASVVCLLNFFPRKERV 148
Db 124 PSDEQLKSGTASVVCLLNFFPRKERV 151

RESULT 9
US-08-398-613A-56
; Sequence 56, Application US/08398613A
; Patent No. 5677426
; GENERAL INFORMATION:
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
{
```

```
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment of Inflammatory I
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,613A
; FILING DATE: 01-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 874P1-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1489
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-398-613A-56

Query Match      78.2%; Score 604; DB 1; Length 242;
Best Local Similarity 76.4%; Pred. No. 2.1e-54;
Matches 113; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYEAFNRFGSV 60
Db 27 MTQTPLSVLPGDQASISCKSSQSLHSDGKTYLYWYLOKPGQPQLLIYKVSNRFGSV 86

Qy 61 PDRFGSGSGTDFTLKISRVAEDVGLYYCWSIELPFTFGGTVKRTVAAPSVFIF 120
Db 87 PDRFGSGSGTDFTLKISRVAEDVGLYYCWSIELPFTFGGTVKRTVAAPSVFIF 146

Qy 121 PSDEQLKSGTASVVCLLNFFPRKERV 148
Db 147 PSSEQLKSGTASVVCLLNFFPRKERV 174

RESULT 10
US-08-398-612A-56
; Sequence 56, Application US/08398612A
; Patent No. 5686070
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
```

```

; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,612A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-398-612A-56

Query Match 78.2%; Score 604; DB 1; Length 242;
Best Local Similarity 76.4%; Pred. No. 2.1e-54;
Matches 113; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPQLIYEAFNRFSGV 60
Db 27 MTQTPLSLPVLGDPQASISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVNRFSGV 86

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGTTKVEIKRTVAAPSVEIF 120
Db 87 PDRFSGSGGTDFTLKISRVEAEDVGLYFCQSQSTHVPLTFGAGTKLELKRAVAAPTVEIF 146

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 147 PPSDEQLKSGTASVVCLLNNFYPREAKV 174

RESULT 11
US-08-398-611A-56
; Sequence 56, Application US/08398611A
; Patent No. 5702946
; GENERAL INFORMATION:
; APPLICANT: Doershuk, Claire M.
; APPLICANT: Fong, Sherman
; APPLICANT: Hebert, Caroline Alice
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Leong, Steven R.
; TITLE OF INVENTION: Anti-IL-8 Monoclonal Antibodies for Treatment
; TITLE OF INVENTION: Of Inflammatory Disorders
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,611A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-398-612A-56

Query Match 78.2%; Score 604; DB 1; Length 242;
Best Local Similarity 76.4%; Pred. No. 2.1e-54;
Matches 113; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPQLIYEAFNRFSGV 60
Db 27 MTQTPLSLPVLGDPQASISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVNRFSGV 86

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGTTKVEIKRTVAAPSVEIF 120
Db 87 PDRFSGSGGTDFTLKISRVEAEDVGLYFCQSQSTHVPLTFGAGTKLELKRAVAAPTVEIF 146

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 147 PPSDEQLKSGTASVVCLLNNFYPREAKV 174

RESULT 12
US-08-491-334A-56
; Sequence 56, Application US/08491334A
; Patent No. 5874080
; GENERAL INFORMATION:
; APPLICANT: Hebert, Caroline A.
; APPLICANT: Kabakoff, Rhona C.
; APPLICANT: Moore, Mark W.
; TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
; TITLE OF INVENTION: Disorders and Asthma
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,334A
; FILING DATE: 27-Jun-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-398-611A-56
```

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; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,611A
; FILING DATE: 01-MAR-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-398-611A-56

Query Match 78.2%; Score 604; DB 1; Length 242;
Best Local Similarity 76.4%; Pred. No. 2.1e-54;
Matches 113; Conservative 17; Mismatches 18; Indels 0; Gaps 0;

Qy 1 VTQSPLSVTPGQPASISCKSSQSLHSDGKTYLYWYLOKPGOPPQLIYEAFNRFSGV 60
Db 27 MTQTPLSLPVLGDPQASISCRSSQSLVHGIGNTYLHWYLOKPGQSPKLLIYKVNRFSGV 86

Qy 61 PDRFSGSGGTDFTLKISRVEAEDVGLYYCMQSIELPFTFGGTTKVEIKRTVAAPSVEIF 120
Db 87 PDRFSGSGGTDFTLKISRVEAEDVGLYFCQSQSTHVPLTFGAGTKLELKRAVAAPTVEIF 146

Qy 121 PPSDEQLKSGTASVVCLLNNFYPRKRV 148
Db 147 PPSDEQLKSGTASVVCLLNNFYPREAKV 174

RESULT 12
US-08-491-334A-56
; Sequence 56, Application US/08491334A
; Patent No. 5874080
; GENERAL INFORMATION:
; APPLICANT: Hebert, Caroline A.
; APPLICANT: Kabakoff, Rhona C.
; APPLICANT: Moore, Mark W.
; TITLE OF INVENTION: IL-8 Antagonists for Treatment of Inflammatory
; TITLE OF INVENTION: Disorders and Asthma
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/491,334A
; FILING DATE: 27-Jun-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/398611
; FILING DATE: 01-MAR-1995
; APPLICATION NUMBER: 08/205864
; FILING DATE: 03-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Love, Richard B.
; REGISTRATION NUMBER: 34,659
; REFERENCE/DOCKET NUMBER: P0874P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-5530
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 56:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 242 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-398-611A-56
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Qy 121 PPSDEQLKSGTASVVCLLNFPKRV 148
 Db 147 PPSSEQLKSGTASVVCLLNFPREKV 174

RESULT 15

US-09-026-985-42
 ; Sequence 42, Application US/09026985
 ; Patent No. 6133426
 ; GENERAL INFORMATION:
 ; APPLICANT: Gonzalez, Tania R.
 ; APPLICANT: Leong, Steven R.
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and
 ; TITLE OF INVENTION: Humanized Anti-IL-8 Monoclonal Antibodies
 ; NUMBER OF SEQUENCES: 72
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/026,985
 ; FILING DATE: 20-Feb-1998
 ; CLASSIFICATION:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Love, Richard B.
 ; REGISTRATION NUMBER: 34,659
 ; REFERENCE/DOCKET NUMBER: P1085R3-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-5530
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 242 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-09-026-985-42

Query Match 78.2%; Score 604; DB 3; Length 242;
 Best Local Similarity 76.4%; Pred. No. 2.1e-54;
 Matches 113; Conservative 17; Mismatches 18; Indels 0; Gaps 0;
 Qy 1 VTQSPLSLSVTPGPASISCKSSQSLHSDGKTYLYWYLOKPGQPOLLIIYEAFNPSGV 60
 Db 27 MTQTPLSLPSVLGQASISCKSSQSLVHGIGNTYLHWYLOKPGSPKLLIYKVSNRPSGV 86
 Qy 61 PDRFSGSGSGDFTLKISRVEAEDVGLYYCMQSIELPPTFGGKTKVEIKRTVAAPSVPF 120
 Db 87 PDRFSGSGSGDFTLKISRVEAEDLGLYFCQSQTHVPLTFGAGTKLELKRAVAAPTVPF 146
 Qy 121 PPSDEQLKSGTASVVCLLNFPKRV 148
 Db 147 PPSSEQLKSGTASVVCLLNFPREKV 174

Search completed: March 8, 2005, 05:54:12
 Job time : 17.2736 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 12.295 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-37

Perfect score: 912
Sequence: 1 GEGLVKPGGSLRLSCAASGF.....SWNSGALTSGVHTFPAVLQ 173

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR.79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637.5	69.9	548	2 S38864	Ig epsilon chain C
2	637	69.8	213	2 S68213	Ig heavy chain (Ma
3	617	67.7	143	2 S23624	Ig heavy chain V r
4	601.5	66.0	254	2 B31790	Ig heavy chain V r
5	568.5	62.3	220	2 S68211	Ig heavy chain (Ma
6	568.5	62.3	444	2 PC4436	monoclonal antibod
7	555.5	60.9	241	2 S69131	Ig heavy chain (DO
8	546	59.9	220	2 A49444	Ig gamma-1 heavy c
9	544	59.6	125	2 S30531	Ig heavy chain V r
10	528.5	57.9	469	2 S37483	Ig gamma-2a chain
11	517.5	56.7	141	2 S31669	Ig heavy chain V r
12	516	56.6	246	2 S38950	Ig gamma chain - m
13	516	56.6	446	2 S40295	Ig gamma-2a chain
14	515.5	56.5	470	2 S22080	Ig heavy chain pre
15	507	55.6	231	2 PC4155	Ig heavy chain V r
16	505.5	55.4	214	2 PC4202	Ig gamma-2b chain
17	501	54.9	221	2 S49220	monoclonal antibod
18	499.5	54.8	110	2 PH1652	Ig gamma-1 chain -
19	497.5	54.6	147	2 I37780	Ig heavy chain V r
20	496.5	54.4	128	2 S26790	Ig variable region
21	496	54.4	119	2 S31107	Ig heavy chain - h
22	496	54.4	123	2 S26794	Ig heavy chain V r
23	495.5	54.3	112	2 S26794	Ig heavy chain V r
24	494	54.2	160	2 S05271	Ig heavy chain pre
25	491.5	53.9	120	2 S48798	Ig heavy chain V r
26	490	53.7	117	2 S34012	Ig heavy chain V r
27	490	53.7	119	2 C36005	Ig heavy chain V r
28	490	53.7	474	1 G2MS11	Ig gamma-2b chain
29	488.5	53.6	128	2 S26786	Ig heavy chain V r

30	486.5	53.3	114	2 S31120	Ig heavy chain - h
31	486	53.3	568	2 A34891	Ig heavy chain pre
32	485	53.2	140	2 S31588	Ig heavy chain V r
33	484.5	53.1	249	2 S69340	Ig heavy chain VH1
34	483	53.0	119	2 D36005	Ig heavy chain V r
35	483	53.0	127	2 S38489	Ig heavy chain - h
36	483	53.0	138	2 S31666	Ig heavy chain V r
37	483	53.0	509	2 S17597	Ig delta chain (WI
38	483	53.0	549	2 S04845	Ig heavy chain pre
39	481.5	52.8	118	2 S31105	Ig heavy chain (su
40	481	52.7	152	2 B26471	Ig heavy chain pre
41	479.5	52.6	124	2 S20782	Ig heavy chain V r
42	479	52.5	119	2 S31108	Ig heavy chain - h
43	479	52.5	121	2 S36005	Ig heavy chain V r
44	478.5	52.5	475	2 S01321	Ig gamma-2b chain
45	478	52.4	123	2 S31114	Ig heavy chain - h

ALIGNMENTS

RESULT 1

S38864

Ig epsilon chain C region - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C/Accession: S38864

R/Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A/Description: Combination of a defined specificity and desired isotype by cloning of an

A/Reference number: S38864

A/Accession: S38864

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-548 <KIP>

A/Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAAB1788.1; PID:g940782

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 69.9%; Score 637.5; DB 2; Length 548;

Beat Local Similarity 71.1%; Pred. No. 1.3e-41;

Matches 123; Conservative 17; Mismatches 32; Indels 1; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNWVRQAPGKGLWVSSISSSSYIYADSVKGR 60

Db 8 GGDLVKPGGSLRLSCAASGFTFSYSGMSWVRQIPDKRLEWVATISSGGTYTYYPDSVKGR 67

Qy 61 FTISRDNKNSLYLQMSLRADTAIVYCARDSSGWYEDYDYGQGLTVTVSSASTKGP 120

Db 68 FTISRDNKNTLYLQMSLSKSEDTAMYYCARQGVSTM-IRPAYWGQGLTVTVSAGKTPPP 126

Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTSWNSGALTSGVHTFPAVLQ 173

Db 127 SVYFLAPCSAAQTNSMTLGLVKVGFPEPTVTVWNSGSLSSGVHTFPAVLQ 179

RESULT 2

S68213

Ig heavy chain (Mab03-1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C/Accession: S68213

R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.

FEBS Lett. 375, 273-276, 1995

A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin

A/Reference number: S68211; MUID:96085223; PMID:7498516

A/Accession: S68213

A/Status: preliminary; nucleic acid sequence not shown

A/Molecule type: mRNA

A/Residues: 1-213 <TAK>

A/Cross-references: UNIPROT:Q91Z05; EMBL:D29667

C/Superfamily: immunoglobulin C region; immunoglobulin homology

F:137-201/Domain: immunoglobulin homology <IMM>

```
Query Match          69.8%; Score 637; DB 2; Length 213;
Best Local Similarity 71.7%; Pred. No. 5.4e-42;
Matches 124; Conservative 18; Mismatches 27; Indels 4; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSYIYADSVKGR 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 8 GGGVLVPGGSLRLSCAASGFTFSYSGMVRQPTDKRLEWVAISGGGYIYVDSVKGR 67
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYWGQGTLLTVSSASTKGP 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 FTISRDNKNTLFLQMTSLRSEDAMYYCAR---SWLLP-FDYWGQGTLLTVSSAKTTPP 123
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWSGALTSGVHTTTPAVLQS 173
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 124 SVFPLAPCGDPTGSSVTGLCLVKGYFPEPVTVWNSGSLSSSVHTTTPALLQS 176
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
S23624
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S23624
R/Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A/Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A/Reference number: S23623; MUID:92156804; PMID:1740665
A/Accession: S23624
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-143 <OLE>
A/Cross-references: EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PID:g32013
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          67.7%; Score 617; DB 2; Length 143;
Best Local Similarity 89.3%; Pred. No. 1.2e-40;
Matches 125; Conservative 3; Mismatches 8; Indels 4; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSYIYADSVKGR 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 8 GGGVLVPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSYSSSSSYIYADSVKGR 67
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYWGQGTLLTVSSASTKGP 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 FTISRDNKNSLYLQMSLRAEDTAVYYCAR--SGYRG--DYWGQGTLLTVSSASTKGP 123
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 SVFPLAPCSRSTSESTAALG 140
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 124 SVFPLAPCSRSTSGTAAALG 143
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 4
B31790
Ig heavy chain V region (17/9) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C/Accession: B31790
R/Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A/Title: Preliminary crystallographic data, primary sequence, and binding data for an
A/Reference number: A92886; MUID:89034213; PMID:3182835
A/Accession: B31790
A/Molecule type: mRNA
A/Residues: 1-254 <SCH>
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match          66.0%; Score 601.5; DB 2; Length 254;
Best Local Similarity 67.4%; Pred. No. 3.4e-39;
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Matches 122; Conservative 22; Mismatches 28; Indels 9; Gaps 5;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSYIYADSVKGR 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 8 GGGVLVPGGSLRLSCAASGFTFSYSGMVRQPTDKRLEWVAISGGGYIYVDSVKGR 67
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYWGQGTLLTVSSASTKGP 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 68 FTISRDNKNTLFLQMSLSEDSAMYYCAR-RERYDENGFAVWGQGTLLTVSSAAKTTP 126
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 121 SVFPLAPCSR--STSSSTAALGCLVKDYFPEPTV--SW-----NSGALTSG-VHTTTPAVLQ 172
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 127 SVFPLAPVCGXDDTGTSSVTGLCLVKGYFPEPVTLTXWXXXNXXSGSLSSGXVHTTTPAVLQ 186
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 173 s 173
Db 187 s 187

RESULT 5
S68211
Ig heavy chain (Mab13-1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000
C/Accession: S68211
R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A/Reference number: S68211; MUID:96085223; PMID:7498516
A/Accession: S68211
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-220 <TAK>
A/Cross-references: EMBL:D29669; NID:g473958; PIDN:BA06140.1; PID:g473959
A/Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequence
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F/136-200/Domain: immunoglobulin homology <IMM>

Query Match          62.1%; Score 568.5; DB 2; Length 220;
Best Local Similarity 64.8%; Pred. No. 1e-36;
Matches 113; Conservative 22; Mismatches 35; Indels 5; Gaps 4;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSIS-SSSSY-IYYADSVK 58
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 GGGVLVPGNSLKLSCLTSGTFSNYRMHLRQPGKRELIATVTKSDNYGAKYAESVR 63
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 59 GRTFISRDNAXNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYWGQGTLLTVSSASTK 118
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 GRTFISRDDSKSVLYLQMNRLREEDTATYYCCR--TPWVY-AMDCWGQGTSVIVSSAKTT 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 119 GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNWSGALTSGVHTTTPAVLQS 173
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 121 PPSVYPLAPGSAQAQTNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQS 175
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C/Accession: PC4436
R/Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.;
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A/Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A/Reference number: JCS810; MUID:98063277; PMID:9398605
A/Accession: PC4436
A/Molecule type: protein
A/Residues: 1-444 <AKA>
C/Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F/251-320/Domain: immunoglobulin homology <IMM>
F/22/Disulfide bonds: interchain (to 98) #status predicted
F/99/Disulfide bonds: interchain (to 109) #status predicted
```


Query Match 62.3%; Score 568.5; DB 2; Length 444;
Best Local Similarity 64.6%; Pred. No. 2.1e-36;
Matches 113; Conservative 22; Mismatches 35; Indels 5; Gaps 4;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYNNWVRQAPGKGLWVSSIS-SSSSV-IYYADSVK 58
Db 8 GGGVLRPENSUKLSCLTSGFTFSYNNWVRQAPGKGLWIAIVIKSDNYGAKYASVR 67

Qy 59 GRFTISRDNAKNSLYLQMSLRADTAIVYICARDSSGWYEDYFDYWGQGLTVTVSSASTK 118
Db 68 GRFTISRDSSKSYLVQNLRLREEDTATYYCCR--TPWVY-AMDCWGGGTSVIVSSAKTT 124

Qy 119 GPSVFPPLAPCSRSTSESTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPFPAVLQS 173
Db 125 PPSVYPLAPGSAQTNSMTVIGCLVKGYFPPPTVTVSNWNSGSLSGVHTFPFPAVLQS 179

RESULT 7
S69131
Ig heavy chain (DOT) - human (fragment)
N:Alternate names: anti-riboflavin IgG Fd fragment
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C:Accession: S69131
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A:Reference number: S69130; MUID:95255298; PMID:7737190
A:Accession: S69131
A:Molecule type: protein
A:Residues: 1-241 <STO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>
F:140-205/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 60.9%; Score 555.5; DB 2; Length 241;
Best Local Similarity 62.9%; Pred. No. 1.1e-35;
Matches 105; Conservative 25; Mismatches 36; Indels 1; Gaps 1;

Qy 7 PGGLRLSCAASGFTFSYNNWVRQAPGKGLWVSSISSSSSSIYYADSVKGRFTISRD 66
Db 14 PGASVRISSCKASGAFENYIHWVRQAPGLGLEWMGIFNPVAGAV-SSEKFRDLVMSSD 72

Qy 67 NAKNSLYLQMSLRADTAIVYICARDSSGWYEDYFDYWGQGLTVTVSSASTKGPSVPLA 126
Db 73 TSANTVSNQLRLNSDDTGRYFCARVYDFQYGMVWQGGTTVIVSSASTKGPSVPLA 132

Qy 127 PCSRSTSESTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPFPAVLQS 173
Db 133 PCSRSTSESTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPFPAVLQS 179

RESULT 8
A49444
Ig gamma-1 heavy chain (New) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999
C:Accession: A49444
R:Saul, F.A.; Poljak, R.J.
Proteins 14, 363-371, 1992
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res
A:Reference number: A49444; MUID:93066153; PMID:1438175
A:Accession: A49444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-220 <SAU>
A:Note: this sequence modified after extraction from NCBI backbone
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin

F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 59.9%; Score 546; DB 2; Length 220;
Best Local Similarity 60.2%; Pred. No. 5.4e-35;
Matches 109; Conservative 21; Mismatches 31; Indels 20; Gaps 4;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYNNWVRQAPGKGLWVSSISSSSSSIYYA----- 54

Db 8 GGLVLRPSQSLTSTCTVSGTSDDYVYTWVRQPPGRGLEWII-----GYFFYTGTTLLD 60

Qy 55 DSVKGRFTISRDNAKNSLYLQMSLRADTAIVYICARD--SSGWYEDYFDYWGQGLTVTV 112

Db 61 PSLRGRVTMLVNTSKNQFSLRLSSVTAADTAIVYICARNLIAGG-----IDWVGQGLTVTV 115

Qy 113 SSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPFPAVLQ 172

Db 116 SSASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPPPTVTVSNWNSGALTSGVHTFPFPAVLQ 175

Qy 173 S 173

Db 176 S 176

RESULT 9

S30531

Ig heavy chain V region - human

C:Species: Homo sapiens (man)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: S30531

R:Marlette, X.

submitted to the EMBL Data Library, October 1992

A:Reference number: S30520

A:Accession: S30531

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-125 <MAR>

A:Cross-references: UNIPROT:Q9UL91; EMBL:Z18317

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 59.6%; Score 544; DB 2; Length 125;

Best Local Similarity 89.8%; Pred. No. 4.2e-35;

Matches 106; Conservative 3; Mismatches 5; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYNNWVRQAPGKGLWVSSISSSSSSIYYADSVKGR 60

Db 8 GGLVQVFGSLRLSCAASGFTFSYNNWVRQAPGKGLWISYSSSSSTIYYADSVKGR 67

Qy 61 FTISRDNAKNSLYLQMSLRADTAIVYICAR----DSSGWYEDYFDYWGQGLTVTVSS 114

Db 68 FTISRDNAKNSLYLQMSLRADTAIVYICARSRNYDSSGYSHYFDYWGQGLTVTVSS 125

RESULT 10

S37483

Ig gamma-2a chain - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S37483

R:Ducancel, F.F.D.

submitted to the EMBL Data Library, February 1993

A:Reference number: S37483

A:Accession: S37483

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-469 <DUC>

A:Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 57.9%; Score 528.5; DB 2; Length 469;

Best Local Similarity 56.1%; Pred. No. 2.6e-33;
Matches 97; Conservative 33; Mismatches 42; Indels 1; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAAGTFFSSYSNNVVRQAPKGKLEWVSSISSSSSYYIYADSVKGR 60
Db 27 GPELVKPGASVKISCKASGYFTDYYINWVKRQPGQLRWIGWYIPASGNTKYNENPKG 86

QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYICARDSSGWYEDFYWGQGTTLVTSSASTKGP 120
Db 87 ATLTVDTSSSTAYWQLSSLTSEDVAVFCAR-ANGATATLLDYWGQGTTLVTSSAKTAP 145

QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPPAVLQS 173
Db 146 SVYPLAPVCGDITGSSVTLGCLVKGYFPEPVTLTWNSSLSGSGVHTFPPAVLQS 198

RESULT 11
S31669
Ig heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
A/Description: Mechanisms that generate human immunoglobulin diversity operate from the
R/Cuisinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A/Reference number: S31585
A/Accession: S31669
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-141 <CDI>
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology <IMM>

Query Match 56.7%; Score 517.5; DB 2; Length 141;
Best Local Similarity 89.7%; Pred. No. 5.2e-33;
Matches 104; Conservative 3; Mismatches 6; Indels 3; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAAGTFFSSYSNNVVRQAPKGKLEWVSSISSSSSYYIYADSVKGR 60
Db 27 GGLVLPKPGSLRLSCAAGTFFSSYSNNVVRQAPKGKLEWVSSISSSSSYYIYADSVKGR 86

QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYICARDS--SGWYEDFYWGQGTTLVTSS 114
Db 87 FTISRDNKNSLYLQWNSLRAEDTAVYICARGHLTG-EKGYFDLWGRGTLVTSS 141

RESULT 12
S38950
Ig gamma chain - mouse
C/Species: Mus musculus (house mouse)
C/Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
A/Accession: S38950
R/Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bit
Biol. Chem. Hoppe-Seyler 374, 993-1000, 1993
A/Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
A/Reference number: S38950; MUID:94128242; PMID:8297501
A/Accession: S38950
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-246 <KLE>
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: immunoglobulin
F;137-201/Domain: immunoglobulin homology <IMM>

Query Match 56.6%; Score 516; DB 2; Length 246;
Best Local Similarity 54.9%; Pred. No. 1.2e-32;
Matches 95; Conservative 32; Mismatches 42; Indels 4; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAAGTFFSSYSNNVVRQAPKGKLEWVSSISSSSSYYIYADSVKGR 60
Db 8 GPELVKPGASVKISCKASGYFTDYYIHWVKRQPGEGLEWIGWYIPGSGNTKYNKPKG 67

QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYICARDSSGWYEDFYWGQGTTLVTSSASTKGP 120
Db 68 ATLTVDTSSSTAYWQLSSLTSEDVAVYFCARGG----KFMADYWGQGTSTVTSSAKTAP 123

QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPPAVLQS 173
Db 124 SVYPLAPVCGDITGSSVTLGCLVKGYFPEPVTLTWNSSLSGSGVHTFPPAVLQS 176

RESULT 13
S40295
Ig gamma-2a chain (mAb735) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 09-Jul-2004
A/Accession: S40295
R/Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bit
submitted to the EMBL Data Library, January 1993
A/Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A/Reference number: S40295
A/Accession: S40295
A/Molecule type: protein
A/Residues: 1-446 <KLE>
A/Cross-references: UNIPROT:Q99L25
C/Genetics:
A/Map position: 12
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F;1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F;1-117/Domain: V-D-J region <VDJ>
F;118-446/Domain: C region <CHR>
F;118-214/Domain: C1 region <CH1>
F;215-230/Region: hinge
F;231-340/Domain: C2 region <CH2>
F;341-446/Domain: C3 region <CH3>
F;360-427/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F;22-96,144-199,261-321,367-425/Disulfide bonds: #status predicted
F;132/Disulfide bonds: interchain (to light chain) #status predicted
F;224,227,229/Disulfide bonds: interchain #status predicted
F;237/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 56.6%; Score 516; DB 2; Length 446;
Best Local Similarity 54.9%; Pred. No. 2.2e-32;
Matches 95; Conservative 32; Mismatches 42; Indels 4; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAAGTFFSSYSNNVVRQAPKGKLEWVSSISSSSSYYIYADSVKGR 60
Db 8 GPELVKPGASVKISCKASGYFTDYYIHWVKRQPGEGLEWIGWYIPGSGNTKYNKPKG 67

QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYICARDSSGWYEDFYWGQGTTLVTSSASTKGP 120
Db 68 ATLTVDTSSSTAYWQLSSLTSEDVAVYFCARGG----KFMADYWGQGTSTVTSSAKTAP 123

QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPPPTVSNWNSGALTSGVHTFPPAVLQS 173
Db 124 SVYPLAPVCGDITGSSVTLGCLVKGYFPEPVTLTWNSSLSGSGVHTFPPAVLQS 176

RESULT 14
S22080
Ig heavy chain precursor (B/MT. 4A.17.H5.A5) - bovine
N/Alternate names: Ig gamma-1 chain C region (clone 8.10)
C/Species: Bos primigenius taurus (cattle)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
A/Accession: S22080; S06610; A31303
R/Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A/Reference number: S22080
A/Accession: S22080
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-470 <SAN>

[illegible]

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 64.6068 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-37
Perfect score: 912
Sequence: 1 GEGLVKGGSLRLSCAASGF.....SWNSGALTGVHTFPVAVLQS 173

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	805	88.3	464	2	Q6MZU6	Q6mzu6 homo sapien
2	785	86.1	470	2	Q6PJA4	Q6pja4 homo sapien
3	764.5	83.8	473	2	Q6MZV7	Q6mzv7 homo sapien
4	744	81.6	478	2	Q6PI81	Q6pi81 homo sapien
5	743.5	81.5	465	2	Q6P6C4	Q6p6c4 homo sapien
6	723	79.3	472	2	Q6N089	Q6n089 homo sapien
7	719.5	78.9	475	2	Q6MZQ6	Q6mzq6 homo sapien
8	715.5	78.5	544	2	Q6PJ95	Q6pj95 homo sapien
9	707	77.5	480	2	Q6N094	Q6n094 homo sapien
10	687	75.3	470	2	Q7Z5W1	Q7z5w1 homo sapien
11	686	75.2	466	2	Q6IN78	Q6in78 homo sapien
12	681.5	74.7	475	2	Q6GMW7	Q6gmw7 homo sapien
13	679	74.5	521	2	Q6N4Y9	Q6n4y9 homo sapien
14	676	74.1	466	2	Q6N096	Q6n096 homo sapien
15	670	73.5	493	2	Q68CN4	Q68cn4 homo sapien
16	641	70.3	417	2	Q6N093	Q6n093 homo sapien
17	639.5	70.1	473	2	Q6P055	Q6p055 homo sapien
18	638.5	70.0	473	2	Q6I205	Q6i205 mus musculus
19	635	69.6	482	2	Q7Z351	Q7z351 homo sapien
20	624.5	68.5	481	2	Q6N097	Q6n097 homo sapien
21	623.5	68.4	518	2	Q6N030	Q6n030 homo sapien
22	622.5	68.3	471	2	Q66K04	Q66k04 mus musculus
23	603	66.1	606	2	Q6GMV2	Q6gmv2 homo sapien
24	602.5	66.1	475	2	Q6N095	Q6n095 homo sapien
25	596	65.4	464	2	Q6PIP8	Q6pip8 mus musculus
26	592	64.9	458	2	Q65ZQ1	Q65zq1 homo sapien
27	591.5	64.9	469	2	Q7Z7P5	Q7z7p5 homo sapien
28	587.5	64.4	597	2	Q96BB9	Q96bb9 homo sapien
29	583	63.9	476	2	Q6GMX1	Q6gmx1 homo sapien
30	580.5	63.7	465	2	Q6GMX6	Q6gmx6 homo sapien
31	579.5	63.5	494	2	Q96K68	Q96k68 homo sapien

32	573	62.8	613	2	Q8WUK1	Q8wuk1 homo sapien
33	572.5	62.8	473	2	Q8TC63	Q8tc63 homo sapien
34	570	62.5	208	2	Q6ZP87	Q6zpb7 homo sapien
35	567	62.2	573	2	Q8WU38	Q8wu38 homo sapien
36	565	62.0	480	2	Q6PJF1	Q6pjf1 homo sapien
37	559	61.3	473	2	Q9D8L4	Q9d8l4 mus musculus
38	557	61.1	476	2	Q6MZX7	Q6mzx7 homo sapien
39	539.5	59.2	463	2	Q99LC4	Q99lc4 mus musculus
40	536.5	58.8	487	2	Q99KA4	Q99ka4 mus musculus
41	534.5	58.6	465	2	Q6PJB2	Q6pjb2 mus musculus
42	533.5	58.5	593	2	Q6INM5	Q6inm5 xenopus lae
43	529	58.0	493	2	Q6GMX2	Q6gmx2 homo sapien
44	527	57.8	614	2	Q6DDQ7	Q6ddq7 xenopus lae
45	526	57.7	472	2	Q6PJA7	Q6pja7 mus musculus

ALIGNMENTS

RESULT 1
Q6MZU6 PRELIMINARY; PRT; 464 AA.
AC Q6MZU6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DB Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloeker H., Boescher M., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAE45931.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-Cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2; 3.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 88.3%; Score 805; DB 2; Length 464;

Best Local Similarity 91.4%; Pred. No. 1.2e-65;

Matches 159; Conservative 2; Mismatches 9; Indels 4; Gaps 3;

Qy	1	GEGLVKGGSLRLSCAASGFTFSSYSMNVRQAPKGLEWVSSISS-SSSYIYVADSVKG	59
Db	27	GGGLVKGGLSLRLSCAASGFTFSSYSMNVRQAPKGLEWVSSFSRRGGSYEYVADSVKG	86
Qy	60	RFTISRDNKNSLYLQWNSLRADTAIVYICARDSSGWYDFDYWGQGLTVTVSSASTKG	119
Db	87	RFTISRDNKNSLYLQWNSLRADTAIVYICARD-LGWFG--LDYWGQGLTVTVSSASTKG	143
Qy	120	PSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNNGALTSVHTFPAVLQS	173
Db	144	PSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVWSNNGALTSVHTFPAVLQS	197

RESULT 2


```

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DSC-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC041037; AAH41037.1; -.
DR HSPP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 81.6%; Score 744; DB 2; Length 478;
Best Local Similarity 80.1%; Pred. No. 5.1e-60;
Matches 145; Conservative 10; Mismatches 18; Indels 8; Gaps 1;

QY 1 GEGLVKPGSLRLSCAASGFTFSYSMNVRQAPGKLEWVSSISSSSYIYVADSVKGR 60
Db 27 GGGVLVQPGSLRLSCAASGFTFSYSMNVRQAPGKLEWVSSISSSSYIYVADSVKGR 86
QY 61 FTISRDNAKNSLYLQMSRLRAEDTAVYICAREPSTMTTNADYYFYFMDVWGKTTVV 112
Db 87 FTISRDNAKNSLYLQMSRLRAEDTAVYICAREPSTMTTNADYYFYFMDVWGKTTVV 146
QY 113 SSASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 172
Db 147 SSASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 206
QY 173 S 173
Db 207 S 207

RESULT 5
Q6P6C4 PRELIMINARY; PRT; 465 AA.
AC Q6P6C4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBT_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Spleen;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RC SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC062335; AAH62335.1; -.
DR HSPP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDD89348ADC37E6D CRC64;

Query Match 81.5%; Score 743.5; DB 2; Length 465;
Best Local Similarity 83.0%; Pred. No. 5.5e-60;
Matches 142; Conservative 11; Mismatches 17; Indels 1; Gaps 1;

QY 3 GLVKPGSLRLSCAASGFTFSYSMNVRQAPGKLEWVSSISSSSYIYVADSVKGRFT 62
Db 29 GLVKPGSLRLSCAASGFTFSYSMNVRQAPGKLEWVSSISSSSYIYVADSVKGRFT 88
QY 63 ISRDNAKNSLYLQMSRLRAEDTAVYICARDSSGWYEDYFDYWGQGLTVVSSASTKGPSV 122
Db 89 ISRDNAKNSLYLQMSRLRAEDTAVYICAREIPGG-RCFYDFWGHGTLTVVSSASTKGPSV 147
QY 123 FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 173
Db 148 FPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 198

RESULT 6
Q6N089 PRELIMINARY; PRT; 472 AA.
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686P15220.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBT_TaxID=9606;
RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE=Spleen;

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RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BX640627; CAE45781.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein_
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 79.3%; Score 723; DB 2; Length 472;
Best Local Similarity 81.1%; Pred. No. 4.3e-58;
Matches 142; Conservative 10; Mismatches 21; Indels 2; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNWVRQAPGKGLWVSSISSSSSYYIYADSVKGR 60
Db 27 GGGVLVQPGSLRLSCAASGFTFDYAHVWVRQAPGKGLWVSGISWNSGIAYADSVKGR 86
Qy 61 FTISRDNKNSLYLQMSLRADDTAVYVCARD--SSGWYEDYFYWGQGLVTVSSASTK 118
Db 87 FTISRDNKNSLYLQMSLRADDTALYCAKEIGHNFYFGMDVWGQGLVTVSSASTK 146
Qy 119 GPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQS 173
Db 147 GPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQS 201

RESULT 7
Q6MZQ6 PRELIMINARY; PRT; 475 AA.
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686G11190.
GN Name=DKFZp686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; BX640947; CAE45972.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.

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SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A264F8BE CRC64;

Query Match 78.9%; Score 719.5; DB 2; Length 475;
Best Local Similarity 78.5%; Pred. No. 9.1e-58;
Matches 142; Conservative 11; Mismatches 17; Indels 11; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNWVRQAPGKGLWVSSISSSSSYYIYADSVKGR 60
Db 27 GGGVLVQPGSLRLSCAASGFTFRYAMWVRQAPGKGLWVSGISWNSGVNTYIYADSVKGR 86
Qy 61 FTISRDNKNSLYLQMSLRADDTAVYVCARDSSGWYEDYFYWGQGLVTV 112
Db 87 FTISGDIINTLYLQMSLRADDTAVYVCARD---YRDYQVSPAYWYFVWGRGTLVS 143
Qy 113 SSASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQ 172
Db 144 SAASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPVTWNSGALTSGVHTFPAVLQ 203
Qy 173 S 173
Db 204 S 204

RESULT 8
Q6PU95 PRELIMINARY; PRT; 544 AA.
ID Q6PU95
AC Q6PU95;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC019046; AAH19046.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.

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DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;

Query Match 78.5%; Score 715.5; DB 2; Length 544;
Best Local Similarity 78.1%; Pred. No. 2.5e-57;
Matches 139; Conservative 11; Mismatches 23; Indels 5; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSMNWVRQAPGKGLWVSSISSSSYIYADSVKGR 60
Db 27 GGVVQPGSSRLRLSCAASGFTFSYSGMHWVRQAPGKGLWVAVSYDESCKYKAAVKGR 86
Qy 61 FTISRDNAKNSLYLQMNSLRADTAIVYCARDSSGWYED-----YFDYWGQGLTVTVSSA 115
Db 87 FTISRDNSKNTLSLQMNSLRVEDTAIVYCAKQKQKPNWSNFWLTFNFDWSGRGTLTVTVSSA 146
Qy 116 STKGPSVPEPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 173
Db 147 STKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQS 204

RESULT 9
Q6N094 PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFP686001196;
GN Homo sapiens (Human);
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human esophagus tumor;
RC The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Pobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAE45776.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35ABC18 CRC64;

Query Match 77.5%; Score 707; DB 2; Length 480;
Best Local Similarity 74.1%; Pred. No. 1.3e-56;
Matches 137; Conservative 15; Mismatches 19; Indels 14; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSMNWVRQAPGKGLWVSSISSSSYIYADSVKGR 60
Db 27 GGVVQPGSSRLRLSCAASGFTFSYSGMHWVRQAPGKGLWVAVSYDESCKYKAAVKGR 86
Qy 61 FTISRDNAKNSLYLQMNSLRADTAIVYCARDSSGWYED-----YFDYWGQGLTVTVSSA 108
Db 87 FTISRDNAKNSLYLQMNSLRVDTAIVYCARGLK--WVPAGTSTSGPVHNFDPWGGT 144
Qy 109 LVTSSASTKGPSVPEPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 169
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Db 145 LVTSSASTKGPSVPEPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFP 204
Qy 169 AVLQS 173
Db 205 AVLQS 209

RESULT 10
Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Human esophagus tumor;
RC The German Human cDNA Consortium;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.C., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RL "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP TISSUE=Human esophagus tumor;
RC The German Human cDNA Consortium;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC053984; AAH53984.1; -.
DR HSSP; P01857; 1HZH.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 75.3%; Score 687; DB 2; Length 470;
Best Local Similarity 77.6%; Pred. No. 8.8e-55;
Matches 135; Conservative 11; Mismatches 26; Indels 2; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSMNWVRQAPGKGLWVSSISSSSYIYADSVKGR 60
Db 27 GGVVQPGGSLRLSCVAGFTFLNNYDMHWVRQGIQKGLWVSKIGTAGDR--YIAGSVKGR 85
Qy 61 FTISRDNAKNSLYLQMNSLRADTAIVYCARDSSGWYEDYFDYWGQGLTVTVSSASTKG 119
Db 86 FTISRENKOSLYLQMNSLRVGDAAVYICARGAGRWAPLGFADIWGQGLTVTVSSASTKG 145
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QY 120 PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWMSGALTSGVHTFPAVLQ 173
|||||:|||||
Db 146 PSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWMSGALTSGVHTFPAVLQ 199
|||||:|||||

RESULT 11
O6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCEDE81076E CRC64;

Query Match 75.2%; Score 686; DB 2; Length 466;
Best Local Similarity 79.7%; Pred. No. 1.1e-54;
Matches 141; Conservative 7; Mismatches 17; Indels 12; Gaps 3;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMWVRQAPGKGLVWSISSSSYI-----YYADS 56
|||||:|||||
Db 27 GGGLIQGGSLTSLCAASGLTVSSNMWVRQAPGKGLVWSLV-----YIGGATYYADS 81
|||||:|||||

QY 57 VKGRFTISRDNKNSLYQMNSLRADTAIVYCAR-----DSSGWYEDYFDYWGQGLTVTVSSAS 116
|||||:|||||

Db 82 VKGRFTISRDNKNSLYQMNSLRADTAIVYCAR-----GNVVPAPAWGQGLTVTVSSAS 138
|||||:|||||
QY 117 TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTWMSGALTSGVHTFPAVLQ 173
|||||:|||||
Db 139 TKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTWMSGALTSGVHTFPAVLQ 195
|||||:|||||

RESULT 12
O6GNW7 PRELIMINARY; PRT; 475 AA.
AC Q6GNW7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00407; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 51987 MW; 2A1FE55D736860F8 CRC64;

Query Match 74.7%; Score 681.5; DB 2; Length 475;
Best Local Similarity 76.4%; Pred. No. 2.9e-54;
Matches 136; Conservative 12; Mismatches 25; Indels 5; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMWVRQAPGKGLVWSISSSSYIYADSVKGR 60
|||||:|||||
Db 27 GGGLVKPGGSLRLSCVSAFTLSRHANHWVRQAPGKGLVSGISNSENSYIYADSVKGR 86
|||||:|||||

QY 61 FTISRDNKNSLYQMNSLRADTAIVYCAR-----DSSGWYEDYFDYWGQGLTVTVSSA 115
|||||:|||||
```


Search completed: March 8, 2005, 06:35:55
Job time : 64.6068 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 80.2075 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-37

Perfect score: 912

Sequence: 1 GEGLVKGGSLRLSCAASGF.....SWNSGALTGVHPTPAVLQS 173

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	912	100.0	173	2 AAY34306	Ay34306 IgG antib
2	799.5	87.7	475	7 ADM47075	Adm47075 Mouse ant
3	798.5	87.6	443	2 AAW13564	Aaw13564 Humanised
4	794	87.1	470	5 ABG77158	Abg77158 Germline
5	794	87.1	470	8 ADR28580	Adr28580 Human ant
6	793	87.0	465	7 ADQ93783	Add93783 Monoclonal
7	791	86.7	444	6 ABR55342	Abr55342 Amino aci
8	788.5	86.5	468	8 ADL93666	Adl93666 Human CD4
9	785	86.1	469	8 ADL93669	Adl93669 Human CD4
10	780	85.5	469	8 ADL93662	Adl93662 Human CD4
11	778.5	85.4	473	5 ABG77162	Abg77162 Germline
12	778.5	85.4	473	8 ADR28584	Adr28584 Human ant
13	777.5	85.3	224	6 ABR01511	Abr01511 Human ant
14	777	85.2	224	7 ADJ32114	Adj32114 Human int
15	776.5	85.1	467	6 ABP71365	Abp71365 Anti-OPGL
16	776	85.1	470	5 ABG77157	Abg77157 Amino aci
17	776	85.1	470	8 ADR28579	Adr28579 Human ant
18	770.5	84.5	444	6 AAE35327	Aae35327 Humanised
19	770.5	84.5	444	6 AAE34876	Aae34876 BiWA4/8 a
20	770.5	84.5	444	8 ADL15443	Adl15443 Humanised
21	770.5	84.5	444	8 ADOO0851	Ado00851 Humanised
22	770	84.4	222	7 ADJ32120	Adj32120 Human int
23	770	84.4	470	5 ABG77161	Abg77161 Amino aci
24	770	84.4	470	8 ADR28583	Adr28583 Human ant
25	767	84.1	217	6 ABR01509	Abr01509 Human ant

26	767	84.1	249	6 ABR55323	Abr55323 Amino aci
27	767	84.1	484	6 ABR55341	Abr55341 Amino aci
28	766.5	84.0	449	5 AAO18400	Aao18400 Mature nu
29	766.5	84.0	697	8 ADQ07403	Adq07403 hCBEl1/hB
30	766.5	84.0	697	8 ADQ12180	Adq12180 Heavy cha
31	766.5	84.0	701	8 ADQ07409	Adq07409 hCBEl1 mo
32	766.5	84.0	701	8 ADQ12186	Adq12186 Heavy cha
33	766	84.0	451	8 ADH34584	Adh34584 008 heavy
34	765	83.9	463	8 ADL93665	Adl93665 Human CD4
35	764.5	83.8	222	6 ABR01515	Abr01515 Human ant
36	764.5	83.8	462	8 ADL93670	Adl93670 Human CD4
37	763.5	83.7	628	6 ABJ38670	Abj38670 Fab expre
38	763.5	83.7	638	6 ADA89103	Ada89103 Phage dis
39	763.5	83.7	638	6 ADA90139	Ada90139 Anti-Abet
40	763.5	83.7	638	6 ADA91410	Ada91410 Anti-Abet
41	763.5	83.7	747	7 ADG74355	Adg74355 MSPRO lig
42	763	83.7	217	6 ABR01504	Abr01504 Human ant
43	763	83.7	467	2 AAR80617	Aar80617 Anti-huma
44	762.5	83.6	466	8 ADL93667	Adl93667 Human CD4
45	760	83.3	221	6 ABR01534	Abr01534 Human ant

ALIGNMENTS

RESULT 1

AAY34306

ID AAY34306 standard; protein; 173 AA.

AC AAY34306;

DT 19-NOV-1999 (first entry)

DE IG antibody 2.1.1 heavy chain sequence.

KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

OS Homo sapiens.

PN WO9945031-A2.

PD 10-SEP-1999.

PF 03-MAR-1999; 99WO-US004583.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

PA (ABGE-) ABGENIX INC.

PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

DR WPI; 1999-540816/45.

DR N-PSDB; AAZ20407.

XX New monoclonal antibody, used for treating e.g. graft versus host
XX disease, cancer, autoimmune diseases and inflammatory diseases.

XX Claim 60; Fig 31; 245pp; English.

CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAb) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 MAb
CC by the IGM MAb ABX-CBL, providing that the antibody is not CBL1. The MAb
CC can selectively kill activated T-cells, activated B-cells or resting or
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
 CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
 XX
 SQ Sequence 173 AA;
 Query Match 100.0%; Score 912; DB 2; Length 173;
 Best Local Similarity 100.0%; Pred. No. 6.7e-70;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLWVSSISSSSSYYIYADSVKGR 60
 |||||
 DB 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLWVSSISSSSSYYIYADSVKGR 60
 |||||
 QY 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWTEDYFDYWGQGTTLVTVSSASTKGP 120
 |||||
 DB 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWTEDYFDYWGQGTTLVTVSSASTKGP 120
 |||||
 QY 121 SVFPLAPCSRSTSTSTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173
 |||||
 DB 121 SVFPLAPCSRSTSTSTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173
 |||||
 RESULT 2
 ADM47075
 ID ADM47075 standard; protein; 475 AA.
 XX
 AC ADM47075;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE Mouse anti-human G-CSF antibody heavy chain protein.
 XX
 KW methylotroph yeast; mammalian sugar chain; OCH1; alpha-1;
 KW 6-mannosyl transferase; alpha-1; 2-mannosidase;
 KW orotidin-5'-phosphate decarboxylase; URA3;
 KW phosphoribosyl-amino-imidazole succinocarboxamide synthase; ADE1;
 KW imidazole-glycerol-phosphate dehydratase; HIS3;
 KW 3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PRB1;
 KW PEP4; YPS1; KTR1; MN9; AOX; GAPDH; mannosyl transferase;
 KW glyceraldehyde 3-phosphate dehydrogenase; mannose glycoprotein.
 XX
 OS Mus sp.
 XX
 XX WO2003091431-A1.
 XX
 XX 06-NOV-2003.
 XX
 XX 28-APR-2003; 2003WO-JP005464.
 XX
 XX 26-APR-2002; 2002JP-00127677.
 XX
 XX (KIRI) KIRIN BEER KK.
 XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX Kobayashi K, Kitagawa Y, Kameda T, Kawashima N, Jigami Y;
 PI Chiba Y;
 XX
 XX WPI; 2003-854401/79.
 XX
 XX Producing methylotroph yeast that expresses mammalian sugar chains by
 PT disrupting the OCH1 gene and inserting an alpha-1,2-mannosidase gene.
 PT
 XX Example 28; SEQ ID NO 94; 247pp; Japanese.
 PS
 XX The invention relates to the production of a methylotroph yeast that
 CC produces mammalian sugar chains, comprising disrupting the OCH1 gene in
 CC the yeast that encodes for alpha-1,6-mannosyl transferase and inserting
 CC and expressing the alpha-1,2-mannosidase gene. The specification also
 CC includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase
 CC (URA3); (b) phosphoribosyl-amino-imidazole succinocarboxamide synthase
 CC (ADE1); (c) imidazole-glycerol-phosphate dehydratase (HIS3); (d) 3-
 CC isopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase
 CC (OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRB1); and (h)

CC aspartic protease (YPS1), mannosyl transferase (KTR1 or MN9), alcohol
 CC oxidase (AOX) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene
 CC sequences. The yeast is used for the production of human and mammalian
 CC high mannose glycoproteins with high yield and purity. The method is also
 CC useful for producing hybrid or complex sugar chains containing mammalian
 CC type chains. This sequence represents a mouse anti-human G-CSF antibody
 CC heavy chain used in the invention.
 XX
 SQ Sequence 475 AA;
 Query Match 87.7%; Score 799.5; DB 7; Length 475;
 Best Local Similarity 89.9%; Pred. No. 8.6e-60;
 Matches 160; Conservative 1; Mismatches 12; Indels 5; Gaps 2;
 QY 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLWVSSISSSSSYYIYADSVKGR 60
 |||||
 DB 27 GGGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLWVSSISSSSSYYIYADSVKGR 86
 |||||
 QY 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWTEDYFDYWGQGTTLVTVSSA 115
 |||||
 DB 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARDRIIMVRGVYVYGMVWGQGTTLVTVSSA 146
 |||||
 QY 116 STKGPSVFPPLAPCSRSTSTSTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173
 |||||
 DB 147 STKGPSVFPPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 204
 |||||
 RESULT 3
 AAW13564
 ID AAW13564 standard; protein; 443 AA.
 XX
 AC AAW13564;
 XX
 DT 17-OCT-2003 (revised)
 DT 03-JUN-1997 (first entry)
 XX
 DE Humanised anti-L-selectin antibody HuDreg 55 heavy chain.
 XX
 KW L-selectin; humanised antibody; HuDreg 55; acute organ damage;
 KW organ failure; poly-trauma; haemorrhagic-traumatic shock.
 XX
 OS Mus; sp.
 OS Homo sapiens.
 OS Chimeric.
 XX
 XX WO9706822-A1.
 XX
 XX 27-FEB-1997.
 XX
 XX 14-AUG-1996; 96WO-US013152.
 XX
 XX 17-AUG-1995; 95EP-00112895.
 XX 19-SEP-1995; 95EP-00114696.
 XX 27-DEC-1995; 95US-00578953.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 XX (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 XX Haselbeck A, Schumacher G, Co M, Martin U;
 XX
 XX WPI; 1997-165036/15.
 XX N-PSDB; AAT61281.
 XX
 XX Using anti-selectin antibody to prevent acute organ damage and multiple
 PT organ failure - during extracorporeal circulation or following
 PT polytrauma, e. g. haemorrhagic-traumatic shock.
 XX
 XX Disclosure; Page 34-36; 52pp; English.
 XX
 XX Humanised anti-L-selectin antibody HuDreg 55 comprises 2 heavy chains
 CC each having the sequence given in AAW13564 and 2 light chains each having
 CC the sequence given in AAW13563. These are encoded by the cDNA clones
 CC given in AAT61281 and AAT61280. HuDreg 55 can be used to prevent multiple

CC organ failure associated with polytrauma and for the prevention of acute
 CC organ damage associated with extracorporeal blood circulation. The
 CC antibody inhibits interaction between the carbohydrate-recognising domain
 CC of the selectin and the corresponding cell surface receptor. (Updated on
 CC 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 443 AA;

Query Match 87.6%; Score 798.5; DB 2; Length 443;
 Best Local Similarity 89.0%; Pred. No. 9.6e-60;
 Matches 154; Conservative 8; Mismatches 6; Indels 5; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSSISSSSYIYYADSVKGR 60
 Db 8 GGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSSISSSSYIYYADSVKGR 66
 QY 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWEDYDYGQGLVTVSSASTKGP 120
 Db 67 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWEDYDYGQGLVTVSSASTKGP 122
 QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
 Db 123 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 175

RESULT 4

ABG77158
 ID ABG77158 standard; protein; 470 AA.

AC ABG77158;

DT 24-OCT-2002 (first entry)

DE Germline protein sequence of anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6.

KW Insulin-like growth factor I receptor; antibody; human; cytostatic;
 KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour;
 KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
 KW acromegaly; gigantism; psoriasis; atherosclerosis.

OS Homo sapiens.

PN WO200253596-A2.

XX 11-JUL-2002.

XX 20-DEC-2001; 2001WO-US051113.

XX 05-JAN-2001; 2001US-0259927P.

XX (PFIZ) PFIZER INC.

XX (ABGE-) ABGENIX INC.

PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;

XX WPI; 2002-575410/61.

XX Novel humanized, chimeric monoclonal antibody that specifically binds to
 PT insulin-like growth factor I (IGF-I) receptor useful for inhibiting
 PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.

PS Disclosure; Fig 19B; 172pp; English.

XX This invention relates to a novel humanised, chimeric or human monoclonal
 CC antibody or its antigen binding portion that specifically binds to
 CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the
 CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
 CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
 CC phosphorylation. The antibodies of the invention are useful for
 CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
 CC subject. The antibody or its antigen-binding portion is also useful for
 CC treating cancer in a human. The method for this further involves an anti
 CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The

CC antibodies may also be useful for increasing IGF-IR activity and thus
 CC restoring IGF-IR activity in a condition characterised by low IGF-IR
 CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
 CC also useful for inducing apoptosis of specific cells in a patient, and to
 CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,
 CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
 CC minimise the immunogenic and allergic responses intrinsic to mouse or
 CC mouse-derivatised monoclonal antibodies and thus increase the efficacy
 CC and safety of the administered antibodies. The present sequence
 CC represents an anti-insulin-like growth factor I receptor antibody of the
 CC invention

XX SQ Sequence 470 AA;

Query Match 87.1%; Score 794; DB 5; Length 470;
 Best Local Similarity 87.0%; Pred. No. 2.5e-59;
 Matches 154; Conservative 8; Mismatches 11; Indels 4; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSSISSSSYIYYADSVKGR 60
 Db 27 GGLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSSISSSSYIYYADSVKGR 86
 QY 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWEDYDYGQGLVTVSSAS 116
 Db 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWEDYDYGQGLVTVSSAS 146
 QY 117 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
 Db 147 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 203

RESULT 5

ADR28580
 ID ADR28580 standard; protein; 470 AA.

AC ADR28580;

XX 18-NOV-2004 (first entry)

DE Human anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6 protein SEQ ID NO:46.

KW aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;
 KW T-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;
 KW neurodegenerative disorder; human;

KW anti-insulin-like growth factor I receptor antibody;

KW anti-IGF-IR antibody; cytostatic; immunosuppressive; endocrine;

KW vasotropic; neuroprotective; nootropic; antithyroid; vaccine;

KW gene therapy.

XX Homo sapiens.

XX WO2004071529-A2.

XX 26-AUG-2004.

XX 03-FEB-2004; 2004WO-IB000366.

XX 13-FEB-2003; 2003US-0447353P.

XX (PFIZ) PFIZER PROD INC.

XX Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;

XX Cusmano JD, Guyot DJ, Page KL;

XX WPI; 2004-625776/60.

XX Treating or preventing aging or a disorder (e.g. multiple myeloma,
 PT autoimmune disease or neurodegenerative disorder) in humans comprises
 PT administering an amount of a human anti-insulin-like growth factor I
 PT receptor antibody.

XX Disclosure; SEQ ID NO 46; 105pp; English.

CC The present invention describes a method for treating or preventing aging
CC or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
CC ischaemia or neurodegenerative disorder) in a mammal. The method
CC comprises administering to the mammal an amount of a human anti-insulin-
CC like growth factor I receptor (IGF-IR) antibody. Also described is a
CC pharmaceutical composition for treating or preventing the above-mentioned
CC disorder in a mammal, comprising an amount of the human anti-IGF-IR
CC antibody and a pharmaceutical carrier. The composition has cytostatic,
CC immunosuppressive, endocrine, vasotropic, neuroprotective, and
CC antithyroid activities, and can be used in vaccines and in gene therapy.
CC The method and composition are useful for preventing or treating aging or
CC a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
CC ischaemia or neurodegenerative disorder) in mammals, such as humans. The
CC human IGF-IR antibody is used in preparing a composition for the
CC treatment or prevention of the above-mentioned disorders. The present
CC sequence represents a human anti-IGF-IR antibody heavy chain amino acid
CC sequence, which is used in the exemplification of the present invention.
XX
SQ Sequence 470 AA;

Query Match 87.1%; Score 794; DB 8; Length 470;
Best Local Similarity 87.0%; Pred. No. 2.5e-59;
Matches 154; Conservative 8; Mismatches 11; Indels 4; Gaps 2;

Qy 1 GEGLVKPGGSLRLCAASGFTFSYSSNMWVRAQPGKLEWVSSISSSSYIYADSVKGR 60
Db 27 GGGVLPQGGSLRLCAASGFTFSYSSNMWVRAQPGKLEWVSSISSSSYIYADSVKGR 86

Qy 61 FTISRDNAKNSLYLQMSLRAEDTAVYYCARD-SSGWYEDYF---DYWGQGLTVTVSSAS 116
Db 87 FTISRDNSKNTLYLQMSLRAEDTAVYYCAKGYSGGWYVYVYVYVYVYVYVYVYVYVYV 146

Qy 117 TKGPSVFLPACSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 173
Db 147 TKGPSVFLPACSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 203

RESULT 6

ADD93783
ID ADD93783 standard; protein; 465 AA.
AC ADD93783;
XX
XX 29-JAN-2004 (first entry)
DT
XX Monoclonal antibody 20.13.3 heavy chain.
XX
KW Monoclonal antibody; antiasthmatic; antiallergic;
KW antiinflammatory; immunosuppressive; dermatological;
KW gastrointestinal-gen; antihelminthic; cytostatic; ophthalmological;
KW bronchodilator; interleukin-5; human; gene therapy.
OS Homo sapiens.

PH Key Location/Qualifiers
FT Peptide 1..19
FT Protein /note= "Signal peptide"
FT Protein /note= "Mature protein"
FT Region 20..138
FT Misc-difference 50..127
FT Region /note= "Region specifically described in Claim 1"
FT Region 50..54
FT Region /note= "CDR1"
FT Region 69..85
FT Region /note= "CDR2"
FT Region 118..127
FT Region /note= "CDR3"
FT Region 139..236
FT Region /note= "CH1 region"

FT Region 237..248
FT Region /note= "Hinge region"
FT Region 249..358
FT Region /note= "CH2 region"
FT Region 359..465
FT Region /note= "CH2 region"
XX WO2003085089-A2.
XX
XX 16-OCT-2003.
XX
XX 27-MAR-2003; 2003WO-US0009260.
XX
XX 29-MAR-2002; 2002US-0369044P.
XX (SCHE) SCHERING CORP.
XX (ABGE-) ABGENIX INC.
XX
XX Greenfeder S, Corvalan J;
XX
XX WPI; 2003-804302/75.
XX N-PSDB; ADD93782.
XX
XX New antibody or its antigen-binding fragment that specifically binds
XX interleukin-5, useful for diagnosing, treating or preventing a condition
XX associated with undesired interleukin-5 activity, e.g. asthma or allergic
XX rhinitis.
XX
XX Claim 1; Page 25; 75pp; English.

XX The present sequence is the protein sequence of the heavy chain of anti-
CC human interleukin-5 (IL-5) human monoclonal antibody (Mab) 20.13.3. To
CC obtain this IgG4 Mab, Xenomice (TM) were immunised with human IL-5.
CC Spleen and/or lymph nodes were then fused with myeloma P3-X63-Ag8 653 or
CC myeloma NSO-bcl2 cells, and hybridomas were screened by ELISA for the
CC presence of human IgG/kappa specific for IL-5. Nucleotides comprising the
CC present sequence, or nucleotides 1-707, 1102-1137, 1256-1585, 1683-2002,
CC 58-709, and 148-381 of it, are claimed and used in methods of the
CC invention. The invention relates to antibodies or their antigen-binding
CC fragments that specifically bind IL-5. Human anti-IL-5 antibodies are
CC provided, including chimeric, bispecific, derivatised, single chain
CC antibodies or portions of fusion proteins, and methods of making anti-IL-
CC 5 antibodies, pharmaceutical compositions comprising these antibodies and
CC methods of using the antibodies and compositions for diagnosis and
CC treatment. The invention also provides gene therapy methods using nucleic
CC acids encoding the heavy and/or light chain molecules that comprise the
CC human anti-IL-5 antibodies, and transgenic animals. The antibodies can be
CC used to prevent or inhibit a condition or disorder characterised by
CC undesired IL-5 activity, including asthma, asthma exacerbations, asthma
CC worsening episodes, chronic pneumonia, allergic rhinitis, perennial
CC allergic rhinitis, allergic bronchopulmonary aspergillosis,
CC hyperaerophilia, Churg-Strauss syndrome, atopic dermatitis, onchocercal
CC dermatitis, episodic angioedema, eosinophilic myalgia syndrome, coeliac
CC disease, eosinophilic gastroenteritis, helminth infections, Hodgkin's
CC disease, nasal polyps, Loeffler's syndrome, urticaria, hypereosinophilic
CC bronchitis, arteritis nodosa, sinusitis, chronic sinusitis, eosinophilic
CC oesophagitis, allergic eosinophilic oesophagitis, or allergic
CC conjunctivitis, by decreasing or inhibiting the infiltration of
CC eosinophils into affected tissue. The antibodies are also useful for
CC preventing or inhibiting an IL-5 mediated allergic response in a subject
CC or an IL-5 mediated event, such as eosinophil proliferation, maturation,
CC survival, activation, migration into the bloodstream, adhesion to
CC endothelium, infiltration into tissues, pulmonary oedema,
CC bronchoconstriction, airway hyperresponsiveness, pulmonary eosinophilia
CC or neutrophilia, cutaneous eosinophilia, or airway epithelial damage (all
CC claimed).

XX Sequence 465 AA;

Query Match 87.0%; Score 793; DB 7; Length 465;
Best Local Similarity 87.3%; Pred. No. 3e-59;
Matches 151; Conservative 9; Mismatches 11; Indels 2; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSMMVWVROAPGKGLWVSSISSSSYIYADSVKGR 60
DB 27 GGGIVQPGGSLRLSCAASGFTFSYSSMMVWVROAPGKGLWVSSISSSSYIYADSVKGR 86
QY 61 FTISRDNKNSLYLQMSLSRAEDTAVYVCARDSSGWYEDYFDYWGQGTFLVTVSSASTKGP 120
DB 87 FTISRDNKNSLYLQMSLSRAEDTAVYVCARDSSGWYEDYFDYWGQGTFLVTVSSASTKGP 144
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 173
DB 145 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 197

RESULT 7
ABR55342
ID ABR55342 standard; protein; 444 AA.
XX
AC ABR55342;
XX
DT 29-JUL-2003 (first entry)
XX
DE Amino acid sequence of a grafted VH chain for anti-KDR antibody.
XX
KW Antibody; kinase insert domain-containing receptor; KDR; antibody VRI65;
KW complementarity determining region; vascular endothelial growth factor;
KW CDR; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.
XX
OS Synthetic.
XX
XX WO2003031475-A2.
PN
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002WO-GB004619.
XX
PR 10-OCT-2001; 2001GB-00024317.
XX
XX (CELL-) CELTECH R & D LTD.
PA
XX Popplewell AG, Tickle SP, Zinkewich-Peotli K, Morrison RK;
PI
XX WPI; 2003-441133/41.
DR
XX
XX Novel antibody molecules having specificity for human kinase insert
PT domain-containing receptors, useful for treating inflammation, psoriasis,
PT rheumatoid arthritis, tumor growth and metastasis.
XX
XX Claim 16; Fig 21; 57pp; English.
XX
XX The specification describes an antibody molecule which has specificity
CC for human kinase insert domain-containing receptor (KDR). The antibody
CC comprises complementarity determining regions (CDRs) from the heavy and
CC light chain variable domains of the murine monoclonal antibody VRI65.
CC This antibody is specific for human KDR. The antibody of the invention
CC blocks vascular endothelial growth factor (VEGF) binding to KDR.
CC Antibodies of the invention are useful for treating a pathology in which
CC VEGF and/or KDR are implicated, and in the manufacture of a medicament
CC for the treatment of a pathology in which VEGF and/or KDR are implicated.
CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour
CC growth or metastasis. The present sequence represents a grafted VH chain,
CC comprising a VRI65 CDR regions and a human framework. It is used to
CC produce antibody molecules of the invention
XX
SQ Sequence 444 AA;

Query Match 86.7%; Score 791; DB 6; Length 444;
Best Local Similarity 87.9%; Pred. No. 4.2e-59;
Matches 152; Conservative 6; Mismatches 11; Indels 4; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSMMVWVROAPGKGLWVSSISSSSYIYADSVKGR 60
DB 8 GGGIVQPGGSLRLSCAASGFTFSYSSMMVWVROAPGKGLWVSSISSSSYIYADSVKGR 67

QY 61 FTISRDNKNSLYLQMSLSRAEDTAVYVCARDSSGWYEDYFDYWGQGTFLVTVSSASTKGP 120
DB 68 FTISRDNKNSLYLQMSLSRAEDTAVYVCARDSSGWYEDYFDYWGQGTFLVTVSSASTKGP 123
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 173
DB 124 SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 176

RESULT 8
ADL93666
ID ADL93666 standard; protein; 468 AA.
XX
AC ADL93666;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CD44-binding antibody heavy chain HAB-B8-heavy SEQ ID NO:161.
XX
KW human; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;
KW antiinflammatory; immunosuppressive; antiarthritis; antirheumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX
OS Homo sapiens.
XX
XX WO2004024750-A2.
PN
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029318.
XX
PR 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX
XX (DYAX-) DYAX CORP.
PI
XX Rondon IJ, Edge A, Baribault Kent R;
XX
XX WPI; 2004-270003/25.
DR
XX
XX New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX
XX Disclosure; SEQ ID NO 161; 128pp; English.
PS
XX The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CDR3 of the LC variable domain sequence. A protein of the invention has
CC cytotstatic, antiinflammatory, immunosuppressive, antiarthritis,
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a human CD44-binding
CC antibody heavy chain.
XX
SQ Sequence 468 AA;

Query Match 86.5%; Score 788.5; DB 8; Length 468;
Best Local Similarity 88.1%; Pred. No. 7.3e-59;
Matches 155; Conservative 5; Mismatches 11; Indels 5; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSSMMVWVROAPGKGLWVSSISSSSYIYADSVKGR 60

Db 27 GGGVLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVSSIGSPGGQTRYADSVYKGR 86
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCAR---DSSGWYEDYDYGQGLTLVTVSSAST 117
Db 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARDYDSSGI--SYFDYWGQGLTQVTVSSAST 144
Qy 118 KGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 173
Db 145 KGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 200

RESULT 9
ADL93669
ID ADL93669 standard; protein; 469 AA.
XX
AC ADL93669;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CD44-binding antibody heavy chain HAE-H-H10-heavy SEQ ID NO:164.
XX
KW human; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;
KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX
OS Homo sapiens.
XX
FN WO2004024750-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029318.
XX
PR 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Rondon IJ, Edge A, Baribault Kent R;
XX
DR WPI; 2004-270003/25.
XX
PT New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX
PS Disclosure; SEQ ID NO 164; 128pp; English.
XX
CC The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CD3 of the LC variable domain sequence. A protein of the invention has
CC cytotstatic, antiinflammatory, immunosuppressive, antiarthritic,
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a human CD44-binding
XX antibody heavy chain.
SQ Sequence 469 AA;

Query Match 86.1%; Score 785; DB 8; Length 469;
Best Local Similarity 87.0%; Pred. No. 1.5e-58;
Matches 154; Conservative 7; Mismatches 10; Indels 6; Gaps 2;

Qy 1 GEGVLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVSSISSSSIYYADSVYKGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKLEWVSSISGGGLTDYADSVYKGR 86
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWY---DYFDYWGQGLTLVTVSSAS 116
Db 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARD--GYDSSGSGYEGFDYWGQGLTLVTVSSAS 144
Qy 117 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 173
Db 145 TKGPSVFPFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 201

RESULT 10
ADL93662
ID ADL93662 standard; protein; 469 AA.
XX
AC ADL93662;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CD44-binding antibody heavy chain HAE-H10-heavy SEQ ID NO:157.
XX
KW human; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytotstatic;
KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX
OS Homo sapiens.
XX
FN WO2004024750-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029318.
XX
PR 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Rondon IJ, Edge A, Baribault Kent R;
XX
DR WPI; 2004-270003/25.
XX
PT New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX
PS Disclosure; SEQ ID NO 157; 128pp; English.
XX
CC The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CD3 of the LC variable domain sequence. A protein of the invention has
CC cytotstatic, antiinflammatory, immunosuppressive, antiarthritic,
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a human CD44-binding
XX antibody heavy chain.
SQ Sequence 469 AA;

Query Match 85.5%; Score 780; DB 8; Length 469;
Best Local Similarity 86.4%; Pred. No. 3.9e-58;

Matches 153; Conservative 8; Mismatches 10; Indels 6; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMWVRQAPGKGLWVSSISSSSSYIYADSVKGR 60
Db 27 GGLLVQPGGSLRLSCAASGFTFSYSSNMWVRQAPGKGLWVSSISSSSSYIYADSVKGR 86
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYVCARDSSGWYE---DYFDYWGQGTTLTVSSAS 116
Db 87 FTISRDNKNSLYLQMSLRAEDTAVYHCARD--GYDSSGYEGFDYWGQGTTLTVSSAS 144
Qy 117 TKGPSVPLPACSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
Db 145 TKGPSVPLPACSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 201

RESULT 11
ABG77162
ID ABG77162 standard; protein; 473 AA.
XX
AC ABG77162;
XX
DT 24-OCT-2002 (first entry)
XX
DE Germline protein sequence of anti-IGF-1R antibody DP-35(3-11)/D3-3/JH6.
XX
KW Insulin-like growth factor I receptor; antibody; human; cytostatic;
KW osteopathic; antiatherosclerotic; antiporiatic; IGF-1R; tumour;
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
KW acromegaly; gigantism; psoriasis; atherosclerosis.
XX
OS Homo sapiens.
XX
FN WO200253596-A2.
XX
PD 11-JUL-2002.
XX
PF 20-DEC-2001; 2001WO-US051113.
XX
PR 05-JAN-2001; 2001US-0259927P.
XX
PA (PFIZ) PFIZER INC.
PA (ABGE-) ABGENIX INC.
XX
PI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
DR WPI; 2002-575410/61.
XX
XX Novel humanized, chimeric monoclonal antibody that specifically binds to
PT insulin-like growth factor I (IGF-I) receptor useful for inhibiting
PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
XX
PS Disclosure; Fig 19D; 172pp; English.

This invention relates to a novel humanised, chimeric or human monoclonal antibody or its antigen binding portion that specifically binds to insulin-like growth factor I receptor (IGF-1R). The antibodies of the invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-1R and can inhibit in vivo tumour growth and IGF-1R tyrosine phosphorylation. The antibodies of the invention are useful for diagnosing the presence or location of an IGF-1R-expressing tumour in a subject. The antibody or its antigen-binding portion is also useful for treating cancer in a human. The method for this further involves an anti-neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The antibodies may also be useful for increasing IGF-1R activity and thus restoring IGF-1R activity in a condition characterised by low IGF-1R levels e.g. neuropathy, or osteoporosis. An antibody of the invention is also useful for inducing apoptosis of specific cells in a patient, and to treat non-cancerous states or disease, e.g. acromegaly, gigantism, psoriasis and atherosclerosis. Fully human anti-IGF-1R antibodies minimise the immunogenic and allergic responses intrinsic to mouse or mouse-derivatised monoclonal antibodies and thus increase the efficacy and safety of the administered antibodies. The present sequence represents an anti-insulin-like growth factor I receptor antibody of the

CC invention
XX
SQ Sequence 473 AA;
Query Match 85.4%; Score 778.5; DB 5; Length 473;
Best Local Similarity 86.1%; Pred. No. 5.3e-58;
Matches 155; Conservative 5; Mismatches 13; Indels 7; Gaps 2;
Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMWVRQAPGKGLWVSSISSSSSYIYADSVKGR 60
Db 27 GGLLVKPGGSLRLSCAASGFTFSYSSNMWVRQAPGKGLWVSSISSSSSYIYADSVKGR 86
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYVCAR----DSSGWYEDYF--DYWGQGTTLTVTS 113
Db 87 FTISRDNKNSLYLQMSLRAEDTAVYVCARVLEFLWLLYYYYYGMVWVGQGTTLTVTS 146
Qy 114 SASTKGPSVPLPACSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
Db 147 SASTKGPSVPLPACSRSTSESTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 206

RESULT 12
ADR28584
ID ADR28584 standard; protein; 473 AA.
XX
AC ADR28584;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human anti-IGF-1R antibody DP-35(3-11)/D3-3/JH6 protein SEQ ID NO:50.
XX
KW aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;
KW T-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;
KW neurodegenerative disorder; human;
KW anti-insulin-like growth factor I receptor antibody;
KW anti-IGF-1R antibody; cytostatic; immunosuppressive; endocrine;
KW vasotropic; neuroprotective; nootropic; antithyroid; vaccine;
KW gene therapy.
XX
OS Homo sapiens.
XX
FN WO2004071529-A2.
XX
PD 26-AUG-2004.
XX
PF 03-FEB-2004; 2004WO-IB000366.
XX
PR 13-FEB-2003; 2003US-0447353P.
XX
PA (PFIZ) PFIZER PROD INC.
XX
PI Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;
PI Cusmano JD, Guyot DJ, Page KL;
XX
XX WPI; 2004-625776/60.
DR
XX Treating or preventing aging or a disorder (e.g. multiple myeloma,
PT autoimmune disease or neurodegenerative disorder) in humans comprises
PT administering an amount of a human anti-insulin-like growth factor I
PT receptor antibody.
XX
PS Disclosure; SEQ ID NO 50; 105pp; English.

The present invention describes a method for treating or preventing aging or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus disorder, T-cell-mediated autoimmune disease, endocrinological disorder, ischaemia or neurodegenerative disorder) in a mammal. The method comprises administering to the mammal an amount of a human anti-insulin-like growth factor I receptor (IGF-1R) antibody. Also described is a pharmaceutical composition for treating or preventing the above-mentioned disorder in a mammal, comprising an amount of the human anti-IGF-1R antibody and a pharmaceutical carrier. The composition has cytostatic, immunosuppressive, endocrine, vasotropic, neuroprotective, nootropic and

CC antithyroid activities, and can be used in vaccines and in gene therapy.
CC The method and composition are useful for preventing or treating aging or
CC a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
CC ischaemia or neurodegenerative disorder) in mammals, such as humans. The
CC human IGF-IR antibody is used in preparing a composition for the
CC treatment or prevention of the above-mentioned disorders. The present
CC sequence represents a human anti-IGF-IR antibody heavy chain amino acid
CC sequence, which is used in the exemplification of the present invention.
XX
XX
SQ Sequence 473 AA;

Query Match 85.4%; Score 778.5; DB 8; Length 473;
Best Local Similarity 86.1%; Pred. No. 5.3e-58;
Matches 155; Conservative 5; Mismatches 13; Indels 7; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSYYIYADSVKGR 60
DB 27 GGLVLPFGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSYYIYADSVKGR 86
QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYYCAR----DSSGWYEDYF--DYWGQGTLLTVS 113
DB 87 FTISRDNKNSLYLQWNSLRAEDTAVYYCARVLRFLWLLYYIYGGNDYWGQGTLLTVS 146
QY 114 SASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173
DB 147 SASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 206

RESULT 13
ABR01511
ID ABR01511 standard; protein; 224 AA.
XX
AC ABR01511;
XX
DT 16-APR-2003 (first entry)
XX
DE Human anti-TIMP-1 antibody heavy chain #9.

XX Human; antibody: tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;
KW variable light chain; cytotatic; nephrotropic; cardiant; liver fibrosis;
KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
XX
OS Homo sapiens.

XX WO200286085-A2.
XX
XX 31-OCT-2002.
XX
XX 24-APR-2002; 2002WO-US012801.
XX
XX 24-APR-2001; 2001US-0285683P.
XX
XX (FARB) BAYER CORP.
XX (MORP-) MORPHOSYS AG.

XX Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
XX
XX WPI; 2003-129114/12.
XX N-PSDB; ABZ74782.

XX New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies,
PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
PT cancer.

XX Claim 20; Page 153-154; 228pp; English.

XX The invention relates to a novel purified preparation of a human
CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)

CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP
CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
CC variable light chain (VLC)DR3 region. An antibody preparation of the
CC invention has hepatotropic, cytotatic, nephrotropic and cardiant
CC activity. The human antibody is useful for decreasing an MMP-inhibiting
CC activity of a TIMP-1. It is especially useful for ameliorating the
CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The
CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
CC sequences shown in ABR01502-ABR01545 represent the heavy chain regions of
CC a human anti-TIMP-1 antibody of the invention
XX
XX Sequence 224 AA;

Query Match 85.3%; Score 777.5; DB 6; Length 224;
Best Local Similarity 86.7%; Pred. No. 2.7e-58;
Matches 150; Conservative 9; Mismatches 13; Indels 1; Gaps 1;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSYYIYADSVKGR 60
DB 8 GGLVLPFGGSLRLSCAASGFTFSYSNMVRQAPGKLEWVSSISSSSYYIYADSVKGR 67
QY 61 FTISRDNKNSLYLQWNSLRAEDTAVYYCARDSSGWYEDYFYWGQGTLLTVSSASTKGP 120
DB 68 FTISRDNKNSLYLQWNSLRAEDTAVYYCARDLT-YYPDLFDYWGQGTLLTVSSASTKGP 126
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173
DB 127 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 179

RESULT 14
ADJ32114
ID ADJ32114 standard; protein; 224 AA.

XX AC ADJ32114;
XX
XX 22-APR-2004 (first entry)
XX Human interferon-gamma antibody heavy chain amino acid sequence SeqID68.
DE antibody: antigen binding domain; interferon-gamma; INF-gamma;
KW antagonist antibody; antiinflammatory; immunosuppressive;
KW autoimmune disease; inflammatory condition; human; heavy chain.
XX
OS Homo sapiens.

XX US2003099647-A1.
XX
XX 29-MAY-2003.
XX
XX 05-OCT-2001; 2001US-00972656.
XX
XX 05-OCT-2001; 2001US-00972656.
XX
XX (DESH/) DESHPANDE R V.
XX (TSAI/) TSAI M.

XX Deshpande RV, Tsai M;
XX
XX WPI; 2003-696068/66.
XX N-PSDB; ADJ32113.
XX
XX New antibody or antigen binding domain, or its fragment, variant or
PT derivative, which binds to an interferon-gamma protein, useful for
PT preparing a composition for preventing or treating inflammatory or
PT autoimmune disorders.

XX Claim 10; SEQ ID NO 68; 113pp; English.

CC This invention relates to a novel antibody or antigen binding domain, or
 CC its fragment, variant or derivative, which binds to an interferon-gamma
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be
 CC useful for the development of compounds with an antiinflammatory or
 CC immunosuppressive activity through action as interferon-gamma agonists. A
 CC composition containing the antibody is useful for preventing or treating
 CC an autoimmune disease and an inflammatory condition. The present sequence
 CC is that of an antibody heavy chain of a human IFN-gamma antibody which
 CC may be part of the invention.

XX SQ Sequence 224 AA;

Query Match 85.2%; Score 777; DB 7; Length 224;
 Best Local Similarity 85.5%; Pred. No. 3e-58;
 Matches 148; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWSSISSSSSYYIYADSVKGR 60
 Db 8 GGLVQPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWSSISSSSSYYIYADSVKGR 67
 Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
 Db 68 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDYDYWGQGLTVTVSSASTKGP 127
 Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 173
 Db 128 SVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 180

RESULT 15

ABP71365
 ID ABP71365 standard; protein; 467 AA.

XX AC ABP71365;

XX DT 28-APR-2003 (first entry)

XX DE Anti-OPGL-1 antibody heavy chain.

XX KW Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;
 XX antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.

XX OS Mus musculus.

XX FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Region /note= "IgG2 signal peptide"
 FT Region 20..141
 FT Region /note= "variable region"
 FT Region 142..467
 FT Region /note= "constant region"

XX WO2003002713-A2.

XX PN 09-JAN-2003.

XX PD 25-JUN-2002; 2002WO-US020181.

XX PF 26-JUN-2001; 2001US-0301172P.

XX PR (ABGE-) ABGENIX INC.

XX PA (AMGE-) AMGEN INC.

XX PI Boyle WJ, Martin FH, Corvalan JR, Davis GC;

XX DR WPI; 2003-210262/20.

XX DR N-PSDB; ABZ59147.

XX PT New antibodies that interact with osteoprotegerin ligands, useful for
 PT treating osteopenic disorders, e.g. osteoporosis, bone loss from
 PT arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and
 PT osteonecrosis.

XX

PS Claim 1; Fig 2; 144pp; English.

XX The invention relates to antibodies that interact with osteoprotegerin
 CC ligands (OPGL). The antibody is useful for detecting the level of OPGL in
 CC a biological sample. The antibody, or the pharmaceutical composition
 CC comprising the antibody, is also useful for treating osteopenic disorder,
 CC an inflammatory condition with attendant bone loss, an autoimmune
 CC condition with attendant bone loss in a patient or rheumatoid arthritis
 CC in a patient. In particular, the antibody or composition is useful for
 CC treating bone diseases, e.g. osteoporosis, bone loss from arthritis,
 CC Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's
 CC syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, Menkes'
 CC syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or
 CC osteonecrosis. The present sequence represents an anti-OPGL-1 antibody
 CC heavy chain

XX SQ Sequence 467 AA;

Query Match 85.1%; Score 776.5; DB 6; Length 467;
 Best Local Similarity 84.8%; Pred. No. 7.7e-58;
 Matches 151; Conservative 7; Mismatches 11; Indels 9; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWSSISSSSSYYIYADSVKGR 60
 Db 27 GGLVQPGGSLRLSCAASGFTFSYSSNMVVRQAPGKGLVWSSISSSSSYYIYADSVKGR 86
 Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSS-----GWYEDYDYWGQGLTVTVSSA 115
 Db 87 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSS-----FDPWGQGLTVTVSSA 142
 Qy 116 STKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 173
 Db 143 STKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 200

Search completed: March 8, 2005, 06:17:20

Job time : 82.2075 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 91.8066 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-37

Perfect score: 912

Sequence: 1 GEGIVRPGGSLRLSCAASGF.....SWNSGALTSVGVHTPAVLQS 173

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/FCI_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCUUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	798.5	87.6	443	9	US-09-917-410-4
2	794	87.1	470	15	US-09-917-410-4
3	793	87.0	465	14	US-10-038-591-46
4	788.5	86.5	468	16	US-10-038-591-46
5	785	86.1	469	16	US-10-038-591-46
6	780	85.5	469	16	US-10-038-591-46
7	778.5	85.4	473	15	US-10-038-591-46
8	777.5	85.3	224	16	US-10-038-591-46
9	777	85.2	224	10	US-09-917-410-4
10	776.5	85.1	467	15	US-10-038-591-46
11	776	85.1	470	15	US-10-038-591-46
12	770.5	84.5	444	14	US-10-038-591-46
13	770.5	84.5	444	16	US-10-038-591-46

14	770.5	84.5	444	16	US-10-645-215-74
15	770	84.4	222	10	US-09-972-656-74
16	770	84.4	470	15	US-10-038-591-49
17	767	84.1	217	16	US-10-128-520-146
18	766.5	84.0	663	15	US-10-412-406-32
19	766.5	84.0	4852	15	US-10-412-406-33
20	765	83.9	463	16	US-10-663-244-160
21	764.5	83.8	222	16	US-10-128-520-152
22	764.5	83.8	462	16	US-10-663-244-165
23	763	83.7	217	16	US-10-128-520-141
24	762.5	83.6	466	16	US-10-663-244-162
25	760	83.3	221	16	US-10-128-520-171
26	759.5	83.3	220	16	US-10-128-520-154
27	759.5	83.3	220	16	US-10-128-520-156
28	759.5	83.3	464	16	US-10-663-244-156
29	758.5	83.2	218	16	US-10-128-520-144
30	758.5	83.2	367	15	US-10-045-674-453
31	758.5	83.2	368	11	US-09-837-306-196
32	756.5	82.9	222	16	US-10-128-520-145
33	756.5	82.9	445	14	US-10-320-231A-79
34	756	82.9	451	9	US-09-822-698A-26
35	755.5	82.8	464	16	US-10-663-244-158
36	754.5	82.7	462	16	US-10-663-244-155
37	753.5	82.6	460	16	US-10-663-244-159
38	753	82.6	217	16	US-10-128-520-140
39	753	82.6	217	16	US-10-128-520-142
40	753	82.6	451	14	US-10-153-382-17
41	752.5	82.5	446	15	US-10-408-901-38
42	750.5	82.3	224	16	US-10-128-520-150
43	750	82.2	449	9	US-09-736-371B-21
44	750	82.2	449	15	US-10-463-442-21
45	748.5	82.1	463	14	US-10-153-382-13

ALIGNMENTS

RESULT 1
US-09-917-410-4
; Sequence 4, Application US/09917410
; Patent No. US20020098183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
; CO, Man S.
; TITLE OF INVENTION: ANTI-L-SELECTIN ANTIBODIES FOR PREVENTION OF
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER
; EXTRACORPOREAL BLOOD CIRCULATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII, WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,410
; FILING DATE: 26-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020098183Alman D.
; REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 443

TYPE: amino acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-917-410-4

Query Match 87.6%; Score 798.5; DB 9; Length 443;
Best Local Similarity 89.0%; Pred. No. 3.6e-47;
Matches 154; Conservative 8; Mismatches 6; Indels 5; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLWVSSISSSSYIYADSVYKGR 60
Db 8 GGGVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVASISTGGS-TYTPDSVYKGR 66

Qy 61 FTISRDNKNSLYLQMNLSRAEDTAVYVCARDSSGWYEDFYDWGQGLTVTVSSASTKGP 120
Db 67 FTISRDNKNTLYLQMNLSRAEDTAVYVCARD---YDGYFDYWGQGLTVTVSSASTKGP 122

Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 173
Db 123 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 175

RESULT 2

US-10-038-591-46

Sequence 46, Application US/10038591

Publication No. US20040086503A1

GENERAL INFORMATION:

APPLICANT: Cohen, Bruce D.

APPLICANT: Beebe, Jean

APPLICANT: Miller, Penelope E.

APPLICANT: Moyer, James D.

APPLICANT: Corvalan, Jose R.

APPLICANT: Gallo, Michael

TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR

FILE REFERENCE: ABX-PF2

CURRENT APPLICATION NUMBER: US/10/038,591

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: 60/259,927

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 46

LENGTH: 470

TYPE: PRT

ORGANISM: Homo sapiens

US-10-038-591-46

Query Match 87.1%; Score 794; DB 15; Length 470;
Best Local Similarity 87.0%; Pred. No. 7.6e-47;
Matches 154; Conservative 8; Mismatches 11; Indels 4; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLWVSSISSSSYIYADSVYKGR 60
Db 27 GGGVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVASISGSGSYIYADSVYKGR 86

Qy 61 FTISRDNKNSLYLQMNLSRAEDTAVYVCARD-SSGWYEDFY---DWGQGLTVTVSSAS 116
Db 87 FTISRDNKNTLYLQMNLSRAEDTAVYVCARGYSSGWYIYGYGMDVWGQGLTVTVSSAS 146

Qy 117 TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 173
Db 147 TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 203

RESULT 3

US-10-401-344-2

Sequence 2, Application US/10401344

Publication No. US2003019404A1

GENERAL INFORMATION:

APPLICANT: Schering Corporation and Abgenix, Inc.

APPLICANT: Greenfeder, Scott

APPLICANT: Corvalan, Jose

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COMPOUNDS

FILE REFERENCE: L101564WI

CURRENT APPLICATION NUMBER: US/10/401,344

CURRENT FILING DATE: 2003-03-27

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2

LENGTH: 465

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: SIGNAL

LOCATION: (1)..(19)

OTHER INFORMATION:

FEATURE:

NAME/KEY: Variable Region

LOCATION: (20)..(138)

OTHER INFORMATION:

FEATURE:

NAME/KEY: CH1 Region

LOCATION: (139)..(236)

OTHER INFORMATION:

FEATURE:

NAME/KEY: Hinge Region

LOCATION: (237)..(248)

OTHER INFORMATION:

FEATURE:

NAME/KEY: CH2 Region

LOCATION: (249)..(358)

OTHER INFORMATION:

FEATURE:

NAME/KEY: CH3 Region

LOCATION: (359)..(465)

OTHER INFORMATION:

US-10-401-344-2

Query Match 87.0%; Score 793; DB 14; Length 465;

Best Local Similarity 87.3%; Pred. No. 8.9e-47;

Matches 151; Conservative 9; Mismatches 11; Indels 2; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLWVSSISSSSYIYADSVYKGR 60
Db 27 GGGVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSTISGSGSYIYADSVYKGR 86

Qy 61 FTISRDNKNSLYLQMNLSRAEDTAVYVCARDSSGWYEDFYDWGQGLTVTVSSASTKGP 120
Db 87 FTISRDNKNTLYLQMNLSRAEDTAVYVCARYNW--NYLHYWGQGLTVTVSSASTKGP 144

Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 173
Db 145 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQ 197

RESULT 4
US-10-663-244-161
Sequence 161, Application US/10663244
Publication No. US2004011093A1
GENERAL INFORMATION:
APPLICANT: Rondon, Isaac J.
APPLICANT: Edge, Albert
APPLICANT: Kent, Rachel Baribault
TITLE OF INVENTION: CD44 LIGANDS
FILE REFERENCE: 10280-063001
CURRENT APPLICATION NUMBER: US/10/663,244


```
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 161
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-161

Query Match      86.5%; Score 788.5; DB 16; Length 468;
Best Local Similarity 88.1%; Pred. No. 1.8e-46;
Matches 155; Conservative 5; Mismatches 11; Indels 5; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSISSSSYIYYADSVKGR 60
Db 27 GGLVQPGGSLRLSCAASGFTFSYMSWVRQAPGKGLWVSSIGPSGGQTRYADSVKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVVYCAR---DSSGWYEDYFDYWGQGLTVTVSSAST 117
Db 87 FTISRDNKNSLYLQMNLSRAEDTAVVYCARDYDSSGT--SYFDYWGQGLTVTVSSAST 144
QY 118 KGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
Db 145 KGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 200

RESULT 5
US-10-663-244-164
; Sequence 164, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-164

Query Match      86.1%; Score 785; DB 16; Length 469;
Best Local Similarity 87.0%; Pred. No. 3.2e-46;
Matches 154; Conservative 7; Mismatches 10; Indels 6; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSISSSSYIYYADSVKGR 60
Db 27 GGLVQPGGSLRLSCAASGFTFSYLSWVRQAPGKGLWVSSISYSGGLTDYADSVKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVVYCARDSSGWYB---DYFDYWGQGLTVTVSSAS 116
Db 87 FTISRDNKNSLYLQMNLSRAEDTAVVYCARD--GYDSSSGYEGFDYWGQGLTVTVSSAS 144
QY 117 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
Db 145 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 201

; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-164

Query Match      85.4%; Score 778.5; DB 15; Length 473;
Best Local Similarity 86.1%; Pred. No. 8.9e-46;
Matches 155; Conservative 5; Mismatches 13; Indels 7; Gaps 2;
```

```
RESULT 6
US-10-663-244-157
; Sequence 157, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 157
; LENGTH: 469
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-157

Query Match      85.5%; Score 780; DB 16; Length 469;
Best Local Similarity 86.4%; Pred. No. 7e-46;
Matches 153; Conservative 8; Mismatches 10; Indels 6; Gaps 2;

QY 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKGLWVSSISSSSYIYYADSVKGR 60
Db 27 GGLVQPGGSLRLSCAASGFTFSYLSWVRQAPGKGLWVSSISYSGGLTDYADSVKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVVYCARDSSGWYB---DYFDYWGQGLTVTVSSAS 116
Db 87 FTISRDNKNSLYLQMNLSRAEDTAVVYCARD--GYDSSSGYEGFDYWGQGLTVTVSSAS 144
QY 117 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
Db 145 TKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 201

RESULT 7
US-10-038-591-50
; Sequence 50, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-50

Query Match      85.4%; Score 778.5; DB 15; Length 473;
Best Local Similarity 86.1%; Pred. No. 8.9e-46;
Matches 155; Conservative 5; Mismatches 13; Indels 7; Gaps 2;
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Qy	1	GGGLVKPGSGLRLSCAASGFTFSSYSMMWVQAPCKGLEWVWSISSSSSYIYADSVKGR	60
Db	27	GGGLVKPGSGLRLSCAASGFTFSDYMSWIRQAPCKGLEWVWSISSSGSTIYIYADSVKGR	86
Qy	61	FTISRDNAKNSLYLQWNSLRADETAVVYCAR---DSSGWYEDYF--DWGGGTGLVTVWS	113
Db	87	FTISRDNAKNSLYLQWNSLRADETAVVYCARVLEFWLLYYYYYGMVWGGGTTVTVWS	146
Qy	114	SASTKGPSVFPLAPCSRSTSTSTAALGCLVKDYPPEPVTVSWNSGALTSGVHTTFFPAVLOS	173
Db	147	SASTKGPSVFPLAPCSRSTSTSTAALGCLVKDYPPEPVTVSWNSGALTSGVHTTFFPAVLOS	206

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RESULT 8
US-10-128-520-148
; Sequence 148, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 148
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-148

```

```

RESULT 9
US-09-972-656-68
; Sequence 68, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 68
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-68

Query Match      85.2%; Score 777; DB 10; Length 224;
Best Local Similarity 85.5%; Pred. No. 5.6e-46;

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	Matches	148;	Conservative	9;	Mismatches	16;	Indels	0;	Gaps	0
Qy	1	GGGLVPGGSLRLS	CAASGFTFSYSYNNWVRQAPKGLGWSSISSSSYIYADSVKGR	60						
Dd	8	GGGLVQGGSLRLS	CAASGFTFSYSYNSWRQAPKGLGWSAISGGGSTYYADSVKGR	67						
Qy	61	FTISRDNAKNSLYLQMN	SRAEDTAVYYCARDSSGWYEDFYWGQGTLVTVSSASTKGP	120						
Dd	68	FTISRDNKSNTLYLQMN	SRAEDTAVYYCAKDRGVGYSSLILDYWGQGTLVTVSSASTKGP	127						
Qy	121	SVTFPLAFCSRSTSESTAALGCLVKDYPPEPVTYSWNSGALTSGVHTFPAVLQS	173							
Dd	128	SVTFPLAPSSKSTSGTAALGCLVKDYEPPEPVTYSWNSGALTSGVHTFPVLQS	180							

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RESULT 10
US-10-180-648-2
; Sequence 2, Application US/10180648
; Publication No. US2004003353A1
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPG
; FILE REFERENCE: 06843.0049-00000
; CURRENT APPLICATION NUMBER: US/10/180.648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-2

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RESULT 11
US-10-038-591-45
; Sequence 45, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-45

Query Match      85.1%; Score 776; DB 15; Length 470;
Best Local Similarity 83.7%; Pred. No. 1.3e-45;
Matches 149; Conservative 10; Mismatches 13; Indels 6; Gaps 2;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSYIYADSVKGR 60
Db 27 GGELVQPGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSYIYADSVKGR 86
Qy 61 FTISRDNKNSLYLQMSLRADTAIVYCARDSSGWYEDYF-----DYWGQGLTVTVSSA 115
Db 87 FTISRDNKNSLYLQMSLRADTAIVYCARDSSGWYEDYF-----DYWGQGLTVTVSSA 145
Qy 116 STKGPSVPEPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
Db 146 STKGPSVPEPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 203

RESULT 12
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

Query Match      84.5%; Score 770.5; DB 14; Length 444;
Best Local Similarity 86.1%; Pred. No. 3e-45;
Matches 149; Conservative 5; Mismatches 12; Indels 7; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSYIYADSVKGR 60
Db 8 GGLVVKPGGSLRLSCAASGFTFSYDMSWVRQAPGKLEWVSTISSGSGYTYLDSIKGR 67
Qy 61 FTISRDNKNSLYLQMSLRADTAIVYCARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMSLRADTAIVYCARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
Db 121 SVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173

RESULT 13
US-10-150-475A-6
; Sequence 6, Application US/10150475A
; Publication No. US20030103985A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, G. et al.
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1211
; CURRENT APPLICATION NUMBER: US/10/150,475A
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: US 60/307,451
; PRIOR FILING DATE: 2001-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Humanised
; OTHER INFORMATION: Murine Antibody BIWA 4 Heavy Chain SEQ ID NO: 6
US-10-150-475A-6

Query Match      84.5%; Score 770.5; DB 14; Length 444;
Best Local Similarity 86.1%; Pred. No. 3e-45;
Matches 149; Conservative 5; Mismatches 12; Indels 7; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSYIYADSVKGR 60
Db 8 GGLVVKPGGSLRLSCAASGFTFSYDMSWVRQAPGKLEWVSTISSGSGYTYLDSIKGR 67
Qy 61 FTISRDNKNSLYLQMSLRADTAIVYCARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMSLRADTAIVYCARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
Db 121 SVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173

RESULT 14
US-10-645-215-6
; Sequence 6, Application US/10645215
; Publication No. US20040126379A1
; GENERAL INFORMATION:
; APPLICANT: Adolf, Gunther
; APPLICANT: Baum, Anke
; APPLICANT: Heider, Karl-Heinz
; TITLE OF INVENTION: Compositions and Methods for Treating Cancer using
; TITLE OF INVENTION: Cytotoxic CD44 Antibody Immunoconjugates and
; TITLE OF INVENTION: Chemotherapeutic Agents
; FILE REFERENCE: 1/1383
; CURRENT APPLICATION NUMBER: US/10/645,215
; CURRENT FILING DATE: 2003-08-21
; PRIOR APPLICATION NUMBER: EP 02 018 686.2
; PRIOR FILING DATE: August 21, 2002
; PRIOR APPLICATION NUMBER: US 60/405,956
; PRIOR FILING DATE: August 26, 2002
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-645-215-6

Query Match      84.5%; Score 770.5; DB 16; Length 444;
Best Local Similarity 86.1%; Pred. No. 3e-45;
Matches 149; Conservative 5; Mismatches 12; Indels 7; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSYIYADSVKGR 60
Db 8 GGLVVKPGGSLRLSCAASGFTFSYDMSWVRQAPGKLEWVSTISSGSGYTYLDSIKGR 67
Qy 61 FTISRDNKNSLYLQMSLRADTAIVYCARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
; TITLE OF INVENTION: Compositions and methods for treating cancer using
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; TITLE OF INVENTION: cytotoxic CD44 Antibody Immunoconjugates
; FILE REFERENCE: 1/1414
; CURRENT APPLICATION NUMBER: US/10/704,522
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: US 60/429,516
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: EP 02024881
; PRIOR FILING DATE: 2002-11-08
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 444
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Humanised Murine Antibody BIWA 4 Heavy Chain
US-10-704-522-6

Query Match      84.5%; Score 770.5; DB 16; Length 444;
Best Local Similarity 86.1%; Pred. No. 3e-45;
Matches 149; Conservative 5; Mismatches 12; Indels 7; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSMNWVRQAPGKLEWVSSISSSSYIYADSVKGR 60
Db 8 GGLVVKPGGSLRLSCAASGFTFSYDMSWVRQAPGKLEWVSTISSGSGYTYLDSIKGR 67
Qy 61 FTISRDNKNSLYLQMSLRADTAIVYCARDSSGWYEDYDYWGQGLTVTVSSASTKGP 120
; TITLE OF INVENTION: Compositions and methods for Treating Cancer using
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Db 68 FTISRDNKNSLYLQMNSLRAEDTAVYYCARQG-----LDYWGRTLVTVSSASTKGP 120
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173
Db 121 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173

RESULT 15
US-09-972-656-74
; Sequence 74, Application US/09972656
; Publication No. US20030099647A1
; GENERAL INFORMATION:
; APPLICANT: Deshpande, Rajendra
; APPLICANT: Tsai, Mei-Mei
; TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
; TITLE OF INVENTION: Neutralizing Activity
; FILE REFERENCE: A-799
; CURRENT APPLICATION NUMBER: US/09/972,656
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 135
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 74
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-656-74

Query Match 84.4%; Score 770; DB 10; Length 222;
Best Local Similarity 88.4%; Pred. No. 1.7e-45;
Matches 153; Conservative 4; Mismatches 14; Indels 2; Gaps 2;
Qy 1 GEGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSYIYADSVKGR 60
Db 8 GGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSYRYDADSVKGR 67
Qy 61 FTISRDNKNSLYLQMNSLRAEDTAVYYCARDSSGWYEDFYWGQGTLVTVSSASTKGP 120
Db 68 FTISRDNKNTLYLQMNSLRAEDTAVYCA-DQMGTTISGN-DYWGQGTLVTVSSASTKGP 125
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 173
Db 126 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 178

Search completed: March 8, 2005, 07:05:57
Job time : 92.8066 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 19.0225 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-37
Perfect score: 912
Sequence: 1 GEGLVKPGGSLRLSCAASG.....SWNSGALTSQVHTFPAVLQS 173

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	798.5	83.6	443	5	PCT-US96-13152-4
2	763	83.7	467	1	US-08-704-744-81
3	753	82.6	451	4	US-09-472-087-70
4	748.5	82.1	463	4	US-09-472-087-4
5	748.5	82.1	463	4	US-09-472-087-68
6	748	82.0	225	4	US-09-456-090A-56
7	748	82.0	225	4	US-09-456-090A-60
8	748	82.0	225	4	US-09-456-090A-92
9	748	82.0	225	4	US-09-453-234-56
10	748	82.0	225	4	US-09-453-234-60
11	748	82.0	225	4	US-09-453-234-92
12	747	81.9	225	4	US-09-456-090A-68
13	747	81.9	225	4	US-09-453-234-68
14	745	81.7	225	4	US-09-456-090A-106
15	745	81.7	225	4	US-09-453-234-106
16	742.5	81.4	463	4	US-09-472-087-1
17	742.5	81.4	463	4	US-09-472-087-63
18	742.5	81.4	463	4	US-09-472-087-64
19	742	81.4	225	4	US-09-456-090A-94
20	742	81.4	225	4	US-09-453-234-94
21	742	81.4	464	4	US-09-472-087-2
22	742	81.4	464	4	US-09-472-087-66
23	741	81.2	225	4	US-09-456-090A-108
24	741	81.2	225	4	US-09-453-234-108
25	738.5	81.0	248	4	US-09-315-926A-80
26	737	80.8	225	4	US-09-456-090A-110
27	737	80.8	225	4	US-09-453-234-110

28	735	80.6	225	4	US-09-456-090A-102	Sequence 102, App
29	735	80.6	225	4	US-09-453-234-102	Sequence 102, App
30	734.5	80.5	167	4	US-09-472-087-74	Sequence 74, Appl
31	734	80.5	470	4	US-09-859-053-32	Sequence 32, Appl
32	734	80.5	470	4	US-09-859-053-36	Sequence 36, Appl
33	732.5	80.3	174	4	US-09-472-087-12	Sequence 12, Appl
34	730	80.0	225	4	US-09-456-090A-70	Sequence 70, Appl
35	730	80.0	225	4	US-09-453-234-70	Sequence 70, Appl
36	728.5	79.9	171	4	US-09-472-087-83	Sequence 83, Appl
37	726.5	79.7	169	4	US-09-472-087-5	Sequence 5, Appl
38	726.5	79.7	169	4	US-09-472-087-13	Sequence 73, Appl
39	726	79.6	163	4	US-09-472-087-73	Sequence 13, Appl
40	726	79.6	163	4	US-09-472-087-84	Sequence 84, Appl
41	725	79.5	166	4	US-09-472-087-75	Sequence 75, Appl
42	724	79.4	225	4	US-09-456-090A-100	Sequence 100, App
43	724	79.4	225	4	US-09-453-234-100	Sequence 100, App
44	720	78.9	225	4	US-09-456-090A-58	Sequence 58, Appl
45	720	78.9	225	4	US-09-453-234-58	Sequence 58, Appl

ALIGNMENTS

RESULT 1
PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 698-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-4

Query Match 87.6%; Score 798.5; DB 5; Length 443;
Best Local Similarity 89.0%; Pred. No. 2.8e-63;
Matches 154; Conservative 8; Mismatches 6; Indels 5; Gaps 2;

[illegible]

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RESULT 2
US-08-704-744-81
; Sequence 81, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalie, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-704-744-81

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	Query Match	83.7%	Score 763;	DB 1;	Length 467;
	Best Local Similarity	84.4%;	Pred. No. 4.3e-60;		
	Matches 146;	Conservative	10;	Mismatches 17;	Indels 0; Gaps 0;
QY	1	GEGLVGGGLRLSLCAASGGTFFSSYMNWVRQAPKGLGWSSSSSSSYIYADSVKGR	60		
Db	27	GGGLVQGGSLRLSLCAASGGFSFRYMWTVRQAPKGLGWVASISGDNITYYDPSVRGR	86		
QY	61	FTISRDNAKNSLYLQWNSLRAEDTAVYYCARDSSGWEDYEDYWGQGLTVTVSSASTKGP	120		
Db	87	FTISRDPSKSTLYLQWNSLRAEDTAVYYCVRPDPYFSGHYEDFWGQGLTVTVSSASTKGP	146		

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Qy      121  SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 173
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Db      147  SVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQ 199

RESULT 3
US-09-472-087-70
; Sequence 70, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-70

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Query Match	82.6%;	Score 753;	DB 4;	Length 451;
Best Local Similarity	83.6%;	Pred. No. 3.2e-59;		
Matches 148;	Conservative 7;	Mismatches 18;	Indels 4;	Gaps 1
Qy	1	GGGLVPGGSLRLS	CAASGTFESYSNNV	WRQAPKGLG
		WSSYSSSSSYIY	ADSVKGR	60
Db	8	GGGVQGRSLR	LSCAASGTFESY	GMHWRQAPKGLG
		WSSYSSSSSYIY	ADSVKGR	67
Qy	61	FTISRDNAKNSLY	LQNMNSLR	AEADVYVCARDSSG
		WYEDYFDVWGQGT	FLTVVSSAS	116
Db	68	FTISRDNKNTLY	LQNMNSLR	AEADVYVCARDPRGATLY
		WYEDYFDVWGQGT	FLTVVSSAS	127
Qy	117	TKGPSVFPLP	APCSRSTSESTAAL	GCLVKDYPPPEPVTVSWNSG
		ALTSVHTTFAVL	QSQS	173
Db	128	TKGPSVFPLP	APCSRSTSESTAAL	GCLVKDYPPPEPVTVSWNSG
		ALTSVHTTFAVL	QSQS	184

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RESULT 4
US-09-472-087-4
; Sequence 4, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PP1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens

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US-09-472-087-4
Query Match      82.1%; Score 748.5; DB 4; Length 463;
Best Local Similarity 84.4%; Pred. No. 8.4e-59;
Matches 146; Conservative 7; Mismatches 17; Indels 3; Gaps 1;

QY 1 GEGLVKPGSRLSLCAASGFTFSSYSNMWVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
DB 27 GGGVVEPGRSLRLSLCTASGFTFSSYGMHWVRQAPGKGLEWAVIWDGSKNHYADSAKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120
DB 87 FTISRDNKNSLYLQMNLSRAEDTAVYYCAR---AGLLGYFDYWGQGLTVTVSSASTKGP 143
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTVSNWNSGALTSGVHTTTPAVLQS 173
DB 144 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTVSNWNSGALTSGVHTTTPAVLQS 196

RESULT 5
US-09-472-087-68
; Sequence 68, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, BILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOPFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 463
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-68

Query Match      82.1%; Score 748.5; DB 4; Length 463;
Best Local Similarity 84.4%; Pred. No. 8.4e-59;
Matches 146; Conservative 7; Mismatches 17; Indels 3; Gaps 1;

QY 1 GEGLVKPGSRLSLCAASGFTFSSYSNMWVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
DB 27 GGGVVEPGRSLRLSLCTASGFTFSSYGMHWVRQAPGKGLEWAVIWDGSKNHYADSAKGR 86
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120
DB 87 FTISRDNKNSLYLQMNLSRAEDTAVYYCAR---AGLLGYFDYWGQGLTVTVSSASTKGP 143
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTVSNWNSGALTSGVHTTTPAVLQS 173
DB 144 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTVSNWNSGALTSGVHTTTPAVLQS 196

RESULT 6
US-09-456-090A-56
; Sequence 56, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
```

```
US-09-456-090A-60
; Sequence 60, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: MI-5H
US-09-456-090A-60

Query Match      82.0%; Score 748; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 3.9e-59;
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

QY 1 GEGLVKPGSRLSLCAASGFTFSSYSNMWVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
DB 8 GGGVVPGRSLRLSLCAASGFTFSSYGMHWVRQAPGKGLEWVTLITYDGDNKYYADSVKGR 67
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120
DB 68 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDGIG---YFDYWGQGLTVTVSSASTKGP 123
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTVSNWNSGALTSGVHTTTPAVLQS 173
DB 124 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTVSNWNSGALTSGVHTTTPAVLQS 176

RESULT 7
US-09-456-090A-60
; Sequence 60, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: MI-5H
US-09-456-090A-60

Query Match      82.0%; Score 748; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 3.9e-59;
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

QY 1 GEGLVKPGSRLSLCAASGFTFSSYSNMWVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
DB 8 GGGVVPGRSLRLSLCAASGFTFSSYGMHWVRQAPGKGLEWVTLITYDGDNKYYADSVKGR 67
QY 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGLTVTVSSASTKGP 120
DB 68 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDGIG---YFDYWGQGLTVTVSSASTKGP 123
QY 121 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTVSNWNSGALTSGVHTTTPAVLQS 173
DB 124 SVFPLAPCSRSTSESTAALGCLVKDYPPEPTVTVSNWNSGALTSGVHTTTPAVLQS 176

RESULT 8
US-09-456-090A-92
; Sequence 92, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
```

```
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-11H
US-09-456-090A-92

Query Match      82.0%; Score 748; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 3.9e-59;
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSGMWVRQAPGKGLEWVSSISSSSIYYADSVKGR 60
Db 8 GGGVQVQPSRLSLCAASGFTFSYGHMWVRQAPGKGLEWVTLITYDGNKYYADSVKGR 67
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYDWGQGLTVTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMSLRAEDTAVYYCARDGIG----YFDYWGQGLTVTVSSASTKGP 123
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 176

RESULT 9
US-09-453-234-56
; Sequence 56, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-3H
US-09-453-234-56

Query Match      82.0%; Score 748; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 3.9e-59;
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSGMWVRQAPGKGLEWVSSISSSSIYYADSVKGR 60
Db 8 GGGVQVQPSRLSLCAASGFTFSYGHMWVRQAPGKGLEWVTLITYDGNKYYADSVKGR 67
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYDWGQGLTVTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMSLRAEDTAVYYCARDGIG----YFDYWGQGLTVTVSSASTKGP 123
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 176

RESULT 9
US-09-453-234-56
; Sequence 56, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-3H
US-09-453-234-56

Query Match      82.0%; Score 748; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 3.9e-59;
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSGMWVRQAPGKGLEWVSSISSSSIYYADSVKGR 60
Db 8 GGGVQVQPSRLSLCAASGFTFSYGHMWVRQAPGKGLEWVTLITYDGNKYYADSVKGR 67
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYDWGQGLTVTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMSLRAEDTAVYYCARDGIG----YFDYWGQGLTVTVSSASTKGP 123
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
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Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 176

RESULT 10
US-09-453-234-60
; Sequence 60, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-5H
US-09-453-234-60

Query Match      82.0%; Score 748; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 3.9e-59;
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSGMWVRQAPGKGLEWVSSISSSSIYYADSVKGR 60
Db 8 GGGVQVQPSRLSLCAASGFTFSYGHMWVRQAPGKGLEWVTLITYDGNKYYADSVKGR 67
Qy 61 FTISRDNKNSLYLQMSLRAEDTAVYYCARDSSGWYEDFYDWGQGLTVTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMSLRAEDTAVYYCARDGIG----YFDYWGQGLTVTVSSASTKGP 123
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 173
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 176

RESULT 11
US-09-453-234-92
; Sequence 92, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 92
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-11H
US-09-453-234-92

Query Match      82.0%; Score 748; DB 4; Length 225;
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```
Best Local Similarity 83.8%; Pred. No. 3.9e-59;
Matches 145; Conservative 8; Mismatches 16; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
Db 8 GGGVVQPGSLRLSCAASGFTFSYGNHVRQAPGKGLEWTLITYDGNKYIADSVKGR 67
Qy 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGTTLTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDGIG----YFDYWGQGTTLTVSSASTKGP 123
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQS 173
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQS 176

RESULT 12
US-09-456-090A-68
; Sequence 68, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-23H
US-09-456-090A-68

Query Match 81.9%; Score 747; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 4.7e-59;
Matches 145; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
Db 8 GGGVVQPGSLRLSCAASGFTFSYGNHVRQAPGKGLEWVAALWYDGSKTYNADSVKGR 67
Qy 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGTTLTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDGIG----YFDYWGQGTTLTVSSASTKGP 123
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQS 173
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQS 176

RESULT 13
US-09-453-234-68
; Sequence 68, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 68
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-23H
US-09-453-234-68

Query Match 81.9%; Score 747; DB 4; Length 225;
Best Local Similarity 83.8%; Pred. No. 4.7e-59;
Matches 145; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
Db 8 GGGVVQPGSLRLSCAASGFTFSYGNHVRQAPGKGLEWVAALWYDGSKTYNADSVKGR 67
Qy 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGTTLTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDGIG----YFDYWGQGTTLTVSSASTKGP 123
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQS 173
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQS 176

RESULT 14
US-09-456-090A-106
; Sequence 106, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-33H
US-09-456-090A-106

Query Match 81.7%; Score 745; DB 4; Length 225;
Best Local Similarity 83.2%; Pred. No. 7.1e-59;
Matches 144; Conservative 9; Mismatches 16; Indels 4; Gaps 1;

Qy 1 GEGLVKPGGSLRLSCAASGFTFSYSNMVRQAPGKGLEWVSSISSSSSYYIYADSVKGR 60
Db 8 GGGVVQPGSLRLSCAASGFTFSYGNHVRQAPGKGLEWTLITYDGNKYIADSVKGR 67
Qy 61 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDSSGWYEDYFDYWGQGTTLTVSSASTKGP 120
Db 68 FTISRDNKNSLYLQMNLSRAEDTAVYYCARDGIG----YFDYWGQGTTLTVSSASTKGP 123
Qy 121 SVFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQS 173
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTTTPAVLQS 176

RESULT 15
US-09-453-234-106
; Sequence 106, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
```

```

; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: GenPharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; CURRENT FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 106
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M2-33H
US-09-453-234-106

Query Match          81.7%;   Score 745;   DB 4;   Length 225;
Best Local Similarity 83.2%;   Pred. No. 7.le-59;
Matches 144;   Conservative 9;   Mismatches 16;   Indels 4;   Gaps 1;

QY 1 GEGLVKPGSLRLSCAASGFTFSYSSMNVRQAPGKGLEWVSSISSSSYIYADSVKGR 60
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 8 GGGVVQPGSLRLSCAASGFTFSYGMHVRQAPGKGLEWMLITYDGDNKKYADSVKGR 67
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 61 FTTSRDNKNSLYLQMSNLR AEDTAVYVCARDSSGWYEDFYDWGQGLTLVTSSASTKGP 120
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 68 FTTSRDNKNSLYLQMSNLR AEDTAVYVCARDGIG----YFDYWGQGLTLVTSSASTKGP 123
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 121 SVFPLAPCSRSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 173
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 124 SVFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSWNSGALTSGVHTTTPAVLQS 176
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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Search completed: March 8, 2005, 05:54:13
Job time : 20.0225 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 7.17801 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-38

Perfect score: 522

Sequence: 1 LDQLTQSPSSLSASVGRV.....EDFATYYCQQNSYPFTFGP 101

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79:*

1: Pirl.*

2: Pirl2.*

3: Pirl3.*

4: Pirl4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	90.6	129	2 S40369	Ig kappa chain - h
2	466	89.3	107	2 I69017	anti-HIV1 envelope
3	466	89.3	117	2 C21056	Ig kappa chain pre
4	459	87.9	108	1 KIHURN	Ig kappa chain V-I
5	454	87.0	125	2 S40333	Ig kappa chain V-J
6	454	87.0	132	2 S40334	Ig kappa chain - h
7	453	86.8	107	2 S36264	Ig lambda chain V
8	451.5	86.5	107	2 S47183	Ig kappa chain - h
9	451	86.4	117	2 B21056	Ig kappa chain pre
10	451	86.4	117	2 S46376	Ig kappa chain V-J
11	446	85.4	117	1 KIHUI1	Ig kappa chain pre
12	446	85.4	125	2 S40349	Ig kappa chain V-J
13	444	85.1	108	2 B49047	Ig kappa chain V r
14	441	84.5	108	2 S19674	Ig kappa chain V r
15	441	84.5	123	2 S40331	Ig kappa chain - h
16	439.5	84.2	124	2 S40336	Ig kappa chain V-J
17	439	84.1	117	2 S46371	Ig kappa chain V-J
18	437	83.7	95	2 PH0866	Ig kappa chain V r
19	437	83.7	117	2 S21527	Ig kappa chain pre
20	437	83.7	127	2 S40367	Ig kappa chain V-J
21	436.5	83.6	108	2 S34007	Ig kappa chain V r
22	436.5	83.6	108	2 S30521	Ig kappa chain V r
23	436	83.5	131	2 S40352	Ig kappa chain V-J
24	434	83.1	128	2 S46372	Ig light chain var
25	433.5	83.0	107	1 KIHUAR	Ig kappa chain V-I
26	433	83.0	108	2 S36277	Ig lambda chain V
27	433	83.0	125	2 S40353	Ig kappa chain V-J
28	433	83.0	127	2 S11240	Ig kappa chain V r
29	431	82.6	124	2 S40318	Ig kappa chain V r

30	430	82.4	95	2 PH0863	Ig kappa chain V r
31	430	82.4	107	2 S40366	Ig kappa chain V-J
32	430	82.4	129	2 S52789	Ig kappa chain V r
33	429	82.2	98	2 S41813	Ig kappa chain V r
34	429	82.2	117	2 S11700	Ig kappa chain pre
35	429	82.2	123	2 S40313	Ig kappa chain V-J
36	429	82.2	132	2 S38646	Ig kappa chain V r
37	428	82.0	117	1 KIHUI2	Ig kappa chain pre
38	427.5	81.9	107	2 S36275	Ig lambda chain V
39	427	81.8	108	1 KIHURE	Ig kappa chain V-I
40	427	81.8	117	2 S24206	Ig kappa chain V r
41	427	81.8	129	2 S52792	Ig kappa chain V r
42	427	81.8	129	2 S52793	Ig kappa chain V r
43	426	81.6	95	2 S45324	Ig kappa chain V r
44	426	81.6	105	2 S36266	Ig lambda chain V
45	426	81.6	108	1 KIHUMS	Ig kappa chain V-I

ALIGNMENTS

RESULT 1

S40369
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S40369
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891; PMID:8258341
A:Accession: S40369
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-129 <KLE>
A:Cross-references: EMBL:X72479; NID:g441426; PIDN:CA851147.1; PID:g441427
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:37-111/Domain: immunoglobulin homology <IMM>

Query Match 90.6%; Score 473; DB 2; Length 129;
Best Local Similarity 91.9%; Pred. No. 4.2e-34;
Matches 91; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy	2	DIQQTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRPKAPKSLIYAASSLSQGVPS	61
Db	22	DIQWTQSPSSLSASVGRVITTCRAHVISHNLVWFQKPKAPKSLIYAASSLSQGVPS	81
Qy	62	KFSGSGSGTFTLTITISSLOPEDFATYYCQQNSYPFTFG	100
Db	82	KFSGSGSGTFTLTITISSLOPEDFATYYCQQNSYPFTFG	120

RESULT 2

I69017
anti-HIV1 envelope protein gp120 V3 loop monoclonal antibody L chain V region - human (fr
C:Species: Homo sapiens (man)
C>Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jan-2000
C:Accession: I69017
R:Chin, L.T.; Duenas, M.; Levi, M.; Hinkula, J.; Wahren, B.; Borrebaeck, C.A.
Immunol. Lett. 44, 25-30, 1995
A:Title: Molecular characterization of a human anti-HIV 1 monoclonal antibody revealed a
A:Reference number: I54563; MUID:95237884; PMID:7721339
A:Accession: I69017
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-107 <RES>
A:Cross-references: GB:S77140; NID:g913352; PIDN:AA834102.1; PID:g913353
C:Genetics:
A:Gene: Ig V kappa
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-90/Domain: immunoglobulin homology <IMM>


```

Db      22 DIQTQSPSFLSASIGRVTITCRASQINSYLAWYQKPGKAPKLLIYVASTLSQGVPS 81
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      82 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 120
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
S36264
Ig lambda chain V region (clone alpha-CEA4-8A) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C:Accession: S36264
R:Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A:Title: Human anti-self antibodies with high specificity from phage display libraries.
A:Reference number: S36256; MUID:93178448; PMID:7679990
A:Accession: S36264
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-107 <GRI>
A:Cross-references: EMBL:Z18845; NID:g33426; PIDN:CAA79297.1; PID:g939919
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      86.8%; Score 453; DB 2; Length 107;
Best Local Similarity 87.9%; Pred. No. 1.9e-32;
Matches 87; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy      2 DIQTQSPSSLSASVGRVTITCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 EIVLTQSPSSLSASVGRVTITCRASQISSYLNWYQKPGKAPKLLIYAASSLSQGVPS 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 99
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
S47183
Ig kappa chain - human
C:Species: Homo sapiens (man)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47183
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A:Description: Cloning and analysis of Igm anti-thyroglobulin autoantibodies from patient
A:Reference number: S47181
A:Accession: S47183
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <MCI>
A:Cross-references: EMBL:X79785; NID:g506424; PIDN:CAA56181.1; PID:g506425
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-90/Domain: immunoglobulin homology <IMM>

Query Match      86.5%; Score 451.5; DB 2; Length 107;
Best Local Similarity 89.9%; Pred. No. 2.5e-32;
Matches 89; Conservative 4; Mismatches 5; Indels 1; Gaps 1;

Qy      2 DIQTQSPSSLSASVGRVTITCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 ETELTQSPSSLSASVGRVTITCRASGINSYLAWFQKPGKAPKSLIYAASSLSQGVPS 60
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYP-QFG 98
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9

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B21056
Ig kappa chain precursor V region (HK134) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 21-Jan-2000
C:Accession: B21056
R:Bentley, D.L.; Rabbitts, T.H.
Cell 32, 181-189, 1983
A:Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicate
A:Reference number: A21056; MUID:83129397; PMID:6402305
A:Accession: B21056
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <BEN>
A:Cross-references: GB:K01323; NID:g185995; PIDN:AAAS8931.1; PID:g185996
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

Query Match      86.4%; Score 451; DB 2; Length 117;
Best Local Similarity 91.6%; Pred. No. 3e-32;
Matches 87; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy      2 DIQTQSPSSLSASVGRVTITCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      23 DIQTQSPSSLSASVGRVTITCRASQISSYLAWYQKPGKAPKSLIYAASSLSQGVPS 82
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYP 96
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      83 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSYP 117
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
S46376
Ig kappa chain V-J region (T33-14) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 27-Jan-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S46376; S38649
R:Bensimon, C.; Chastagner, P.; Zouali, M.
EMBO J. 13, 2951-2962, 1994
A:Title: Human lupus anti-DNA autoantibodies undergo essentially primary V(chi) gene rear
A:Reference number: S46369; MUID:94313975; PMID:8039491
A:Accession: S46376
A:Molecule type: mRNA
A:Residues: 1-117 <BEN>
A:Cross-references: EMBL:Z27177; NID:g415969; PIDN:CAA81701.1; PID:g415970
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:25-99/Domain: immunoglobulin homology <IMM>

Query Match      86.4%; Score 451; DB 2; Length 117;
Best Local Similarity 86.0%; Pred. No. 3e-32;
Matches 86; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

Qy      2 DIQTQSPSSLSASVGRVTITCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      10 DIQTQSPSSVSASIGRVTITCRASQISSYLAWYQKPGKAPKLLIYAASSLSQGVPL 69
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 101
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      70 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSFPFG 109
      :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 11
K1HUI1
Ig kappa chain precursor V-1 region (HK101) - human
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1981 #sequence_revision 31-Mar-1981 #text_change 09-Jul-2004
C:Accession: A01881; A21056
R:Bentley, D.L.; Rabbitts, T.H.
Nature 288, 730-733, 1980
A:Title: Human immunoglobulin variable region genes - DNA sequences of two V-kappa genes
A:Reference number: A93241; MUID:81098966; PMID:6779204
A:Accession: A01881

```

A;Molecule type: DNA
A;Residues: 1-117 <BEN1>
A;Cross-references: UNIPROT:P01601; GB:V00558; GB:J00244; GB:J00246; NID:g33176; PIDN:CA
C;Note: the sequence was determined from the germline gene
R;Bentley, D.L.; Rabbitts, T.H.
Cell 32, 181-189, 1983
A;Title: Evolution of immunoglobulin V genes: evidence indicating that recently duplicated
A;Reference number: A21056; MUID:83129397; PMID:6402305
A;Accession: A21056
A;Molecule type: DNA
A;Residues: 1-117 <BEN2>
A;Cross-references: GB:K01322; NID:g185993; PIDN:AAA58930.1; PID:g185994
C;Genetics:
A;Gene: GDB:IGKV1
A;Cross-references: GDB:136264
A;Map position: 2p12-2p12
A;Introns: 19/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-117/Product: Ig kappa chain V-I region (HK101) #status predicted <MAT>
F;38-112/Domain: immunoglobulin homology <IMM>
F;45-110/Disulfide bonds: #status predicted

Query Match 85.4%; Score 446; DB 1; Length 117;
Best Local Similarity 90.5%; Pred. No. 8.2e-32; Indels 0; Gaps 0;
Matches 86; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQQTSPSSLSASVGRVVTITCRASODISYLAWFQORPGKAPKSLIYAASSLSQSGVPS 61
Db 23 DIQMTQSPSSLSASVGRVVTITCRAGISSWLAWYQKPKAPKSLIYAASSLSQSGVPS 82

Qy 62 KFSGSGSGTDFTLTISSQLQPEDFATYYCQYNVSP 96
Db 83 RFGSGSGTDFTLTISSQLQPEDFATYYCQYNVSP 117

RESULT 12
S40349
Ig kappa chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
C;Accession: S40349
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40349
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-125 <KLE>
A;Cross-references: EMBL:X72459; NID:g441386; PIDN:CAA51127.1; PID:g441387
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;33-107/Domain: immunoglobulin homology <IMM>

Query Match 85.4%; Score 446; DB 2; Length 125;
Best Local Similarity 87.8%; Pred. No. 8.7e-32; Indels 0; Gaps 0;
Matches 86; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 3 IQLTQSPSSLSASVGRVVTITCRASODISYLAWFQORPGKAPKSLIYAASSLSQSGVPSK 62
Db 19 IQLTQSPSSLSASVGRVVTITCRASQISSALAWYQKPKAPKLLIYDASSLESQVPSR 78

Qy 63 FSGSGSGTDFTLTISSQLQPEDFATYYCQYNVSPFTFG 100
Db 79 FSGSGSGTDFTLTISSQLQPEDFATYYCQYFNFTPLTFG 116

RESULT 13
B49047

Ig kappa chain V region (monoclonal striational autoantibody StrAB SA-1A) - human (fragme
C;Species: Homo sapiens (man)
C;Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: B49047
R;Victor, K.D.; Pascual, V.; Williams, C.L.; Lennon, V.A.; Capra, J.D.
Eur. J. Immunol. 22, 2231-2236, 1992
A;Title: Human monoclonal striational autoantibodies isolated from thymic B lymphocytes c
A;Reference number: A49047; MUID:92387224; PMID:1516616
A;Accession: B49047
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-108 <VIC>
A;Cross-references: UNIPROT:Q96SA9; UNIPROT:Q9UL77
A;Experimental source: thymic B lymphocytes
A;Note: sequence extracted from NCBI backbone (NCBIN:113208, NCBIP:113209)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 85.1%; Score 444; DB 2; Length 108;
Best Local Similarity 87.9%; Pred. No. 1.1e-31; Indels 0; Gaps 0;
Matches 87; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 DIQQTSPSSLSASVGRVVTITCRASODISYLAWFQORPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGRVVTITCRASQISSYLNWYQKPKAPKLLIYAASSLSQSGVPS 60

Qy 62 KFSGSGSGTDFTLTISSQLQPEDFATYYCQYNVSPFTFG 100
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQYSYTPFTFG 99

RESULT 14
S19674
Ig kappa chain V region (clone alpha-TEL9) - human
C;Species: Homo sapiens (man)
C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
C;Accession: S19674
R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J.
Mol. Biol. 222, 581-597, 1991
A;Title: By-passing immunization. Human antibodies from V-gene libraries displayed on ph
A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Accession: S19674
A;Molecule type: mRNA
A;Residues: 1-108 <MAR>
A;Cross-references: EMBL:X61642; NID:g37860; PIDN:CAA43823.1; PID:g1335386
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 441; DB 2; Length 108;
Best Local Similarity 85.9%; Pred. No. 2e-31; Indels 0; Gaps 0;
Matches 85; Conservative 7; Mismatches 7; Indels 0; Gaps 0;

Qy 2 DIQQTSPSSLSASVGRVVTITCRASODISYLAWFQORPGKAPKSLIYAASSLSQSGVPS 61
Db 1 EIVLTQSPSSLSASVGRVVTITCRASQISSYLNWYQKPKAPKLLIYAASSLSQSGVPS 60

Qy 62 KFSGSGSGTDFTLTISSQLQPEDFATYYCQYNVSPFTFG 100
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQQTNSPFTFG 99

RESULT 15
S40331
Ig kappa chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40331
R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40331

A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-123 <KLE>
A;Cross-references: EMBL:X72441; NID:g441350; PIDN:CAA51109.1; PID:g441351
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;32-106/Domain: immunoglobulin homology <IMM>

Query Match 84.5%; Score 441; DB 2; Length 123;
Best Local Similarity 87.9%; Pred. No. 2.3e-31;
Matches 87; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLASVSGDRVTITCRASODISYLAWFQORBGKPKSLIYAASSLQSGVPS 61
Db 17 DIQMTQSPSSLASVSGDRVTITCRASQSISSYLNWYQQKPKAPKLLIYAASSLQSGVPS 76

Qy 62 KFGSGSGTDFTLTITSSLPEDFATYYCQQVNSYPFTFG 100
Db 77 RFGSGSGTDFTLTITSSLPEDFATYYCQQSYSTPRTFG 115

Search completed: March 8, 2005, 06:39:30
Job time : 7.22801 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 37.7184 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-38

Perfect score: 522

Sequence: 1 LDIGLTQSPSLASVGVDRV.....EDFATYCCQNSVPTFGP 101

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	468	89.7	236	2	Q7Z3Y4	Q7Z3Y4 homo sapien
2	462	88.5	236	2	Q6GMX8	Q6GMX8 homo sapien
3	459	87.9	108	1	KV1V_HUMAN	P0430 homo sapien
4	457	87.5	108	2	Q9UL70	Q9UL70 homo sapien
5	452	86.6	236	2	Q6GMX9	Q6GMX9 homo sapien
6	446	85.4	117	1	KV1I_HUMAN	P01601 homo sapien
7	438	83.9	236	2	Q6PIH7	Q6PIH7 homo sapien
8	433.5	83.0	107	1	KVID_HUMAN	P01596 homo sapien
9	432	82.8	108	2	Q9UL77	Q9UL77 homo sapien
10	430	82.4	244	2	Q6SZC8	Q6SZC8 homo sapien
11	429	82.2	108	1	KV1Y_HUMAN	P80362 homo sapien
12	428	82.0	117	1	KV1J_HUMAN	P01602 homo sapien
13	427.5	81.9	107	2	Q6SA9	Q6SA9 homo sapien
14	427	81.8	108	1	KVIO_HUMAN	P01607 homo sapien
15	427	81.8	236	2	Q6GMW1	Q6GMW1 homo sapien
16	426	81.6	108	1	KV1S_HUMAN	P01611 homo sapien
17	425	81.4	108	1	KV1H_HUMAN	P01600 homo sapien
18	425	81.4	108	1	KV1P_HUMAN	P01608 homo sapien
19	422	80.8	240	2	Q6SZC9	Q6SZC9 homo sapien
20	421	80.7	108	1	KV1L_HUMAN	P01604 homo sapien
21	421	80.7	108	1	KV1R_HUMAN	P01610 homo sapien
22	420	80.5	236	2	Q6GMX0	Q6GMX0 homo sapien
23	419	80.3	108	1	KV1E_HUMAN	P01597 homo sapien
24	419	80.3	108	1	KV1G_HUMAN	P01599 homo sapien
25	417	79.9	129	1	KV1W_HUMAN	P04431 homo sapien
26	416.5	79.8	107	2	Q9UL81	Q9UL81 homo sapien
27	415	79.5	108	1	KV1B_HUMAN	P01594 homo sapien
28	415	79.5	108	1	KV1F_HUMAN	P01598 homo sapien
29	415	79.5	236	2	Q6PIT5	Q6PIT5 homo sapien
30	414	79.3	234	2	Q7Z473	Q7Z473 homo sapien
31	413	79.1	108	2	Q9UL79	Q9UL79 homo sapien

32	412	78.9	108	1	KV1M_HUMAN	P01605 homo sapien
33	406	77.8	108	1	KV1Q_HUMAN	P01609 homo sapien
34	403	77.2	129	1	KV1X_HUMAN	P04432 homo sapien
35	402	77.0	108	1	KV1A_HUMAN	P01593 homo sapien
36	402	77.0	108	1	KV1N_HUMAN	P01606 homo sapien
37	400	76.6	108	1	KV1K_HUMAN	P01603 homo sapien
38	399	76.4	116	2	Q96PF6	Q96PF6 homo sapien
39	396	75.9	236	2	Q6PIH4	Q6PIH4 homo sapien
40	395	75.7	108	1	KV1C_HUMAN	P01595 homo sapien
41	379.5	72.7	109	1	KV1T_HUMAN	P01612 homo sapien
42	372	71.3	108	2	Q9UL83	Q9UL83 homo sapien
43	372	71.3	112	1	KV1U_HUMAN	P01613 homo sapien
44	368	70.5	236	2	Q7TS98	Q7TS98 mus musculus
45	367	70.3	128	1	KV5E_MOUSE	P01637 mus musculus

ALIGNMENTS

RESULT 1

Q7Z3Y4 PRELIMINARY; PRT; 236 AA.

AC Q7Z3Y4; DT 01-OCT-2003 (Tremblrel. 25, Created)

DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)

DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal Muscle;

RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

FAhey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,

Jones S.J., Marra M.A.;

"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]

RP SEQUENCE FROM N.A.

RC TISSUE=Skeletal Muscle;

RX Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.

RA Strausberg R.;

DR EMBL; BC005332; AA0405332.1; -.

DR HSSP; P01834; 1HEZ.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig cl.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF07654; Cl-set; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.

KW Hypothetical protein_

SEQUENCE 236 AA; 25702 MW; 7FBF4ED23084BC6 CRC64;


```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035044; AAD56280.1; --
DR PIR; PH0863; PH0863.
DR HSP; P01607; LBWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 108
FT NON TER 108
SQ SEQUENCE 108 AA; 11633 MW; B7BEDC3E41FCA37 CRC64;

Query Match 87.5%; Score 457; DB 2; Length 108;
Best Local Similarity 88.0%; Pred. No. 7,6e-40;
Matches 88; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQQTQSPSSLSASVGRVITTCRASQDISIYLAWFOQPKAPKSLIYAASSLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGISNYLAWYQKPKVPSLIYAASSLSQGVPS 60
Qy 62 KFGSGSGTDFTLTISSLOPEDFATYCCQVNSYPFTFG 101
Db 61 RFSGSGSGTDFTLTISSLOPEDVATYCCQVNSAPRTFG 100

RESULT 5
O6GMX9 PRELIMINARY; PRT; 236 AA.
AC Q6GMX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villaon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Heiton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
```

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RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; --
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25924 MW; PDE2093DC560CF7 CRC64;

Query Match 86.6%; Score 452; DB 2; Length 236;
Best Local Similarity 86.9%; Pred. No. 6e-39;
Matches 86; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQQTQSPSSLSASVGRVITTCRASQDISIYLAWFOQPKAPKSLIYAASSLSQGVPS 61
Db 23 DIQMTQSPSSLSASVGRVITTCRASQNSVRLAWYQQRPEKAPKSLIYATSSLHSGVPS 82
Qy 62 KFGSGSGTDFTLTISSLOPEDFATYCCQVNSYPFTFG 100
Db 83 RFSGSGSGTDFTLTISSLOPEDFATYCCQVNTYPLTFG 121

RESULT 6
KV11 HUMAN STANDARD; PRT; 117 AA.
AC P01601;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region HK101 precursor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RT kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=83129397; PubMed=6402305; DOI=10.1016/0092-8674(83)90508-1;
RA Bentley D.L., Rabbitts T.H.;
RT "Evolution of immunoglobulin V genes: evidence indicating that
RT recently duplicated human V kappa sequences have diverged by gene
RT conversion.";
RL Cell 32:181-189(1983).
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01322; AAA58930.1; --
DR EMBL; K01324; AAA58932.1; --
DR EMBL; V00558; CAA23824.1; --
DR PIR; A01881; KIHU11.
DR HSP; P01607; LBWW.
```

DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 >117 Ig kappa chain V-I region HK101.
 FT DOMAIN 23 45 Framework-1.
 FT DOMAIN 46 56 Complementarity-determining-1.
 FT DOMAIN 57 71 Framework-2.
 FT DOMAIN 72 78 Complementarity-determining-2.
 FT DOMAIN 79 110 Framework-3.
 FT DOMAIN 111 >117 Complementarity-determining-3.
 FT DISULFID 45 110 By similarity.
 FT NON TER 117 117
 SQ SEQUENCE 117 AA; 12799 MW; D7D0FF3718CEF587 CRC64;
 Query Match 85.4%; Score 446; DB 1; Length 117;
 Best Local Similarity 90.5%; Pred. No. 1.2e-38;
 Matches 86; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
 QY 2 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQGVPS 61
 DB 23 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQGVPS 82
 QY 62 KFGSGSGTDFTLTISLQPEDFATYCCQYNSYP 96
 DB 83 RFGSGSGTDFTLTISLQPEDFATYCCQYNSYP 117
 RESULT 7
 ID Q6PIH7 PRELIMINARY; PRT; 236 AA.
 AC Q6PIH7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan T., Moore T., Max S.I., Wang J., Haieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uesdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smailus D.B., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;

RA Strausberg R.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC034141; AAH34141.1; -.
 DR HSP; P01607; IAR2
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF07654; Cl-set; 1.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IGV; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
 Query Match 83.9%; Score 438; DB 2; Length 236;
 Best Local Similarity 86.9%; Pred. No. 1.7e-37;
 Matches 86; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 2 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQGVPS 61
 DB 23 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQGVPS 82
 QY 62 KFGSGSGTDFTLTISLQPEDFATYCCQYNSYPPTFG 100
 DB 83 RFGSGSGTDFTLTISLQPEDFATYCCQYNSYPPTFG 121
 RESULT 8
 ID KVID_HUMAN STANDARD; PRT; 107 AA.
 AC P01596;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig kappa chain V-I region CAR.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE
 RX MEDLINE=75075135; PubMed=4216454;
 RA Milstein C.P., Deverson E.V.;
 RT "Primary structure of kappa light chain from a human myeloma
 protein".
 RL Eur. J. Biochem. 49:377-391 (1974).
 CC -I- MISCELLANEOUS: The C region of this chain has the INV (1,2)
 marker.
 CC -I- MISCELLANEOUS: This chain was isolated from a myeloma protein.
 DR HSP; P80362; IWL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 KW Direct protein sequencing; Glycoprotein; Immunoglobulin V region.
 FT CARBOHYD 28 28 N-linked (GlcNAc...).
 FT NON TER 107 107
 SQ SEQUENCE 107 AA; 11703 MW; E1BF0DF9844C3346 CRC64;
 Query Match 83.0%; Score 433.5; DB 1; Length 107;
 Best Local Similarity 81.0%; Pred. No. 2.1e-37;
 Matches 81; Conservative 14; Mismatches 4; Indels 1; Gaps 1;
 QY 2 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQGVPS 61

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Db 1 DIQWTQSPSTLSASVGRVAVTTCRASQNISSWLAWYQKPKAPKLVLYKSSSLESQVPS 60
Qy 62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 101
Db 61 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 99

RESULT 9
Q9UL77 PRELIMINARY; PRT; 108 AA.
AC Q9UL77
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin light chain variable region
DE (Fragment)
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kallis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035037; AAD56273.1; -.
DR PIR; B49047; B49047.
DR PIR; S34083; S34083.
DR HSSP; P01607; 1BWW.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 108
FT NON TER 108
SQ SEQUENCE 108 AA; 11738 MW; C06681716C4D16F3 CRC64;

Query Match 82.8%; Score 432; DB 2; Length 108;
Best Local Similarity 85.9%; Pred. No. 3.1e-37;
Matches 85; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Qy 2 DIQWTQSPSSLSASVGRVAVTTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQWTQSPSSLSASVGRVAVTTCRASQSISSYLAWYQKPKAPNLLIYAASSLSQSGVPS 60

Qy 62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
Db 61 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSYTSWTFG 99

RESULT 10
Q65ZC8 PRELIMINARY; PRT; 244 AA.
AC Q65ZC8
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
GN Name=scFv;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.S., Wing M.G., Winter G.;
RA "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
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DR EMBL; Y13057; CAA73500.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IGV; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 244
FT NON TER 244
SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;

Query Match 82.4%; Score 430; DB 2; Length 244;
Best Local Similarity 80.8%; Pred. No. 1.2e-36;
Matches 80; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

Qy 2 DIQWTQSPSSLSASVGRVAVTTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db 137 DIQWTQSPSTLSASIGDRVITTCRASSGIYHVAWYQKPKAPKFLIYKASSLASGAPS 196

Qy 62 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPFTFG 100
Db 197 RFGSGSGTDTFTLTISLQPEDFATYYCQQNSYPLTFG 235

RESULT 11
KVLY HUMAN STANDARD; PRT; 108 AA.
ID KVLY HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7993911;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers.";
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the VL-
RT related fragment of the human kappa Bence Jones protein Wat.";
RL J. Mol. Biol. 147:185-193(1981).
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1WTL; X-ray; A/B=1-108.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure; Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DOMAIN 108 107
```

```
FT DISULFID 23 88 By similarity.
FT CONFLICT 30 31 TN -> SD (in Ref. 2).
FT STRAND 4 7
FT STRAND 10 13
FT TURN 15 16
FT STRAND 19 25
FT TURN 30 31
FT STRAND 33 38
FT TURN 40 41
FT STRAND 45 49
FT TURN 50 52
FT STRAND 53 54
FT TURN 56 57
FT STRAND 60 61
FT TURN 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 98 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 82.2%; Score 429; DB 1; Length 108;
Best Local Similarity 81.8%; Pred. No. 6.3e-37;
Matches 81; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFQQRPGKAPKSLIYAASLSQGVPS 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQWTSQSPSSLSASVGRVITTCRASQDISIYLAWFQQRPGKAPKSLIYAASLSQGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KFGSGSGTDFTLTISSLPQEDPATYCCQVNSYPTFG 100
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFSGSGSGTDFTLTISSLPQEDPATYCCQVNSYPTFG 99
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 12
KV1J HUMAN
ID "KV1J_HUMAN STANDARD; PRT; 117 AA.
AC P01602;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig kappa chain V-I region HK102 precursor (Fragment).
GN Name=IGKV1-5;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=81098966; PubMed=6779204;
RA Bentley D.L., Rabbitts T.H.;
RT "Human immunoglobulin variable region genes -- DNA sequences of two V
RL kappa genes and a pseudogene.";
RL Nature 288:730-733(1980).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; J00245; AAA59087.1; -.
DR EMBL; Z00001; CAA77292.1; -.
DR PIR; A01882; KIHUL2.
DR HSP; P01607; LEWV.
DR Genew; HGNC:5741; IGKV1-5.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
```

```
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 >117 Ig kappa chain V-I region HK102.
FT DOMAIN 23 45 Framework-1.
FT DOMAIN 46 56 Complementarity-determining-1.
FT DOMAIN 57 71 Framework-2.
FT DOMAIN 72 78 Complementarity-determining-2.
FT DOMAIN 79 110 Framework-3.
FT DOMAIN 111 >117 Complementarity-determining-3.
FT DISULFID 45 110 By similarity.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12768 MW; AD1DF3A40AFA1A9B CRC64;

Query Match 82.0%; Score 428; DB 1; Length 117;
Best Local Similarity 86.2%; Pred. No. 8.8e-37;
Matches 81; Conservative 9; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFQQRPGKAPKSLIYAASLSQGVPS 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 23 DIQWTSQSPSSLSASVGRVITTCRASQDISIYLAWFQQRPGKAPKSLIYAASLSQGVPS 82
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Qy 62 KFGSGSGTDFTLTISSLPQEDPATYCCQVNSY 95
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 83 RFSGSGSGTDFTLTISSLPQEDPATYCCQVNSY 116
   :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 13
Q96SA9
ID Q96SA9 PRELIMINARY; PRT; 107 AA.
AC Q96SA9;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-mysin immunoglobulin kappa light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mysin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96396; AAB68785.1; -.
DR PIR; B49047; B49047.
DR PIR; PH0867; PH0867.
DR PIR; S16840; S16840.
DR PIR; S1977; S1977.
DR PIR; S34083; S34083.
DR PIR; S34086; S34086.
DR HSP; P01607; LEWV.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG_LIKE; 1.
FT NON TER 1 1
FT NON TER 107 107
SQ SEQUENCE 107 AA; 11520 MW; 4BB43E9C5B577F16 CRC64;

Query Match 81.9%; Score 427.5; DB 2; Length 107;
Best Local Similarity 87.0%; Pred. No. 8.9e-37;
Matches 87; Conservative 4; Mismatches 6; Indels 3; Gaps 2;
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Qy 2 DIOLTPSSLSASVGDRTVITCRASODISYILAWFOORPKAPKSLIYAASSLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGDRTVITCRASODISYILAWFOORPKAPKSLIYAASSLSQGVPS 60
Qy 62 KFGSGSGTDTFTLTISLQPEDFATYYCQQVNSY-PFTFG 100
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 RFSGSGSGTDTFTLTISLQPEDFATYYCQQVNSY-PFTFG 98
|||

RESULT 14
KV10 HUMAN STANDARD; PRT; 108 AA.
AC P01607;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Ig kappa chain V-I region Rei.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RE SEQUENCE.
RX MEDLINE=76023758; PubMed=809329;
RA Palm W., Hilschmann N.;
RT "The primary structure of a crystalline monoclonal immunoglobulin
RT kappa-type L-chain, subgroup I (Bence-Jones protein Rei); isolation
RT and characterization of the tryptic peptides; the complete amino acid
RT sequence of the protein; a contribution to the elucidation of the
RT three-dimensional structure of antibodies, in particular their
RT combining site.";
RL Hoppe-Seyler's Z. Physiol. Chem. 356:167-191(1975).
RN [2]
RX X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
MEDLINE=76039968; PubMed=1182131;
RA Epp O., Lattman E.E., Schiffer M., Huber R., Palm W.;
RT "The molecular structure of a dimer composed of the variable portions
RT of the Bence-Jones protein Rei refined at 2.0-A resolution.";
RL Biochemistry 14:4943-4952(1975).
CC -1- MISCELLANEOUS: The C region of this chain has the INV (1,2)
CC marker.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91663; KIHURE.
DR PDB; 1AR2; X-ray; @=1-107.
DR PDB; 1BWW; X-ray; A/B=1-107.
DR PDB; 1REI; X-ray; A/B=1-107.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR Pfam; PF00047; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW 3D-structure, Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin v region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT STRAND 19 25
FT STRAND 30 31
FT STRAND 33 38
FT STRAND 40 41
FT STRAND 45 49
FT STRAND 50 52
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FT STRAND 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT HELIX 80 82
FT STRAND 84 90
FT STRAND 97 98
FT STRAND 102 106
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11902 MW; 9E8143E1188BCE2A CRC64;

Query Match 81.8%; Score 427; DB 1; Length 108;
Best Local Similarity 81.8%; Pred. No. 1e-36;
Matches 81; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 2 DIOLTPSSLSASVGDRTVITCRASODISYILAWFOORPKAPKSLIYAASSLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGDRTVITCRASODISYILAWFOORPKAPKSLIYAASSLSQGVPS 60
Qy 62 KFGSGSGTDTFTLTISLQPEDFATYYCQQVNSY-PFTFG 100
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 RFSGSGSGTDTFTLTISLQPEDFATYYCQQVNSY-PFTFG 99
|||

RESULT 15
Q6GMW1 PRELIMINARY; PRT; 236 AA.
AC O6GMW1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RE SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
```

DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFEGA087AFAC437 CRC64;

Query Match 81.8%; Score 427; DB 2; Length 236;
Best Local Similarity 85.7%; Pred. No. 2.4e-36;
Matches 84; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

QY 3 IQLTQSPSSLSASVGDRTTTCRASQDISIVLAWFOORPGKPKSLIYAASSLSQSGVPSK 62
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 24 IQMTQSPSSLSASVGDRTTTCRASQGISNDLGLWYQOKPKAPKLLIYAASSLSQSGVPSR 83
||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 63 FSGSGSGTDFTLTISSSQPEDFATYYCQYNSYPFTFG 100
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 FSGSGSGTDFTLTISSSQPEDFATYYCLQDYNYPWTFG 121
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Search completed: March 8, 2005, 06:35:56
Job time : 38.7184 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 46.8263 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-38
Perfect score: 522
Sequence: 1.LDQLTQSPSLASVGDV.....EDFATYYCQQNSVPTFGP 101

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A.Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	522	100.0	101	2	AAY34316 IgG antib
2	515	98.7	164	2	AAY34317 IgG antib
3	482	92.3	127	6	AAB37206 Human AB-
4	479	91.8	127	6	AAB37204 Human AB-
5	476	91.2	224	4	AAB75040 TRO005 Hu
6	474	90.8	107	4	AAB82890 Anti-huma
7	473	90.6	241	5	AAB90948 Insulin/i
8	471	90.2	107	4	AAB72880 Human ant
9	471	90.2	107	8	ADO36490 Human ant
10	471	90.2	107	8	ADO36502 Human ant
11	471	90.2	107	8	ADO36494 Human ant
12	471	90.2	108	1	ADP81246 Anti-pneu
13	471	90.2	111	1	ADP81870 Anti-pneu
14	468	89.7	109	2	AAR40956 Human ger
15	466	89.3	95	6	ABO27128 Human ger
16	466	89.3	95	7	ADF10068 VEGF anti
17	466	89.3	95	7	ADF10170 Antibody
18	466	89.3	95	7	ADF09963 Antibody
19	466	89.3	95	7	ADJ080248 V kappa ge
20	466	89.3	95	8	ADO07317 Human ant
21	466	89.3	107	4	AAB72882 Human ant
22	466	89.3	107	6	ABR54919 Light cha
23	466	89.3	109	2	AAR47041 Sequence
24	465	89.1	107	4	AAB62087 Human V1
25	465	89.1	107	4	AAB60400 Consensus

26	465	89.1	107	4	AAB61585 Human var
27	465	89.1	107	8	ADE71454 Human ant
28	465	89.1	107	8	ADJ88008 Human var
29	465	89.1	107	8	ADN12054 Variable
30	465	89.1	107	8	ADP43328 Human mon
31	465	89.1	108	2	AAW70622 Human con
32	465	89.1	108	3	AAW82345 Human con
33	465	89.1	108	5	AAU76522 Anti-Inte
34	465	89.1	108	5	ADP61191 Human ant
35	465	89.1	108	7	ADF11407 18B2 anti
36	465	89.1	108	8	ADG38991 Human con
37	465	89.1	108	8	ADR03366 Human sub
38	465	89.1	108	8	ADP79572 Human kap
39	465	89.1	109	5	AU74544 Human sub
40	465	89.1	110	5	AAE28149 Human con
41	465	89.1	214	7	ADF11431 18B2 anti
42	464	88.9	107	4	AAB67511 Light cha
43	464	88.9	109	2	AAR30764 Consensus
44	464	88.9	236	3	AAY96297 Human IGF
45	464	88.9	299	4	AAG63637 Amino aci

ALIGNMENTS

RESULT 1
AAY34316
ID AAY34316 standard; protein; 101 AA.
XX AC AAY34316;
XX DT 19-NOV-1999 (first entry)
XX DE IGG antibody 2.1.1 kappa chain sequence.
XX KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX OS Homo sapiens.
XX PN WO9945031-A2.
XX FD 10-SEP-1999.
XX PF 03-MAR-1999; 99WO-US004583.
XX PR 03-MAR-1998; 98US-00034607.
XX PR 03-FEB-1999; 99US-00244253.
XX PA (ABGE-) ABGENIX INC.
XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX DR WPI; 1999-540816/45.
XX DR N-PSDB; AAZ20417.
XX PT New monoclonal antibody, used for treating e.g. graft versus host
XX PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX CC Claim 61; Fig 31; 245pp; English.
XX CC This sequence represents the kappa chain of an antibody of the invention.
XX CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
XX CC complement and a variable region that binds to the epitope on CD147 bound
XX CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
XX CC can selectively kill activated T-cells, activated B-cells or resting or
XX CC activated monocytes. The products and methods can be used for treating
XX CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
XX CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
XX CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
SQ Sequence 101 AA;
Query Match 100.0%; Score 522; DB 2; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.6e-32;
Matches 101; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LDIQLTQSPSSLSASVGDRTVITICRASQDISIYLAWFQORPGKAPKSLIYAASSLSQSGVP 60
DB 1 LDIQLTQSPSSLSASVGDRTVITICRASQDISIYLAWFQORPGKAPKSLIYAASSLSQSGVP 60
QY 61 SKFSGSGSGTDFLTITISLQPEDFATYCCQYNSYPFTFGP 101
DB 61 SKFSGSGSGTDFLTITISLQPEDFATYCCQYNSYPFTFGP 101
RESULT 2
AAV34317
ID AAV34317 standard; protein; 164 AA.
XX
AC AAV34317;
XX
DT 19-NOV-1999 (first entry)
XX
DE Igg antibody 2.6.1 kappa chain sequence.
XX
KW Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
FN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
WPI; 1999-540816/45.
DR N-PSDB; AAZ20418.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 61; Fig 33; 245pp; English.
XX
CC This sequence represents the kappa chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IgM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX
SQ Sequence 164 AA;
Query Match 98.7%; Score 515; DB 2; Length 164;
Best Local Similarity 99.0%; Pred. No. 8.3e-32;

Matches 100; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LDIQLTQSPSSLSASVGDRTVITICRASQDISIYLAWFQORPGKAPKSLIYAASSLSQSGVP 60
DB 4 LDIQLTQSPSSLSASVGDRTVITICRASQDISIYLAWFQORPGKAPKSLIYAASSLSQSGVP 63
QY 61 SKFSGSGSGTDFLTITISLQPEDFATYCCQYNSYPFTFGP 101
DB 64 SKFSGSGSGTDFLTITISLQPEDFATYCCQYNSYPFTFGP 104
RESULT 3
AAE37206
ID AAE37206 standard; protein; 127 AA.
XX
AC AAE37206;
XX
DT 07-AUG-2003 (first entry)
XX
DE Human AB-PGI-XGI-051 PSMA antibody light chain variable region (VH).
XX
KW Human; Prostate specific membrane antigen; carcinoma; sarcoma; cancer;
KW PSMA; melanoma; therapy; N-acetylated alpha-linked acidic dipeptidase;
KW folate hydrolase; dipeptidyl dipeptidase IV; gamma-glutamyl hydrolase;
KW NAALADase; antibody; light chain variable region; VH.
XX
OS Homo sapiens.
XX
FN WO2003034903-A2.
XX
PD 01-MAY-2003.
XX
PF 23-OCT-2002; 2002WO-US033944.
XX
PR 23-OCT-2001; 2001US-0335215P.
PR 07-MAR-2002; 2002US-0362747P.
PR 20-SEP-2002; 2002US-0412618P.
XX
PA (PSMA-) PSMA DEV CO LLC.
XX
PI Maddon PJ, Donovan GP, Olson WC, Schuelke N, Gardner J, Ma D;
XX
WPI; 2003-403281/38.
DR N-PSDB; AAD56221.
XX
PT Novel isolated antibody which binds to epitope on prostate specific
PT membrane antigen, and competitively inhibits binding of second antibody
PT to its target epitope on the antigen, useful for treating prostate
PT cancer.
XX
PS Claim 26; Page 233; 238pp; English.
XX
CC The invention relates to an antibody or its antigen-binding fragment
CC which specifically binds to epitope on prostate specific membrane antigen
CC (PSMA), and competitively inhibits the specific binding of a second
CC antibody to its target epitope on PSMA. The invention is useful for
CC diagnosing, treating or preventing PSMA-mediated disease such as prostate
CC cancer or non-prostate cancer bladder chosen from cancer including
CC transitional cell carcinoma, pancreatic cancer including pancreatic duct
CC carcinoma, lung cancer including non-small cell lung carcinoma, kidney
CC cancer including conventional renal cell carcinoma, sarcoma including
CC soft tissue sarcoma, breast cancer including breast carcinoma, brain
CC cancer including glioblastoma multiforme, neuroendocrine carcinoma, colon
CC cancer including colonic carcinoma, testicular cancer including
CC testicular embryonal carcinoma, or melanoma including malignant melanoma.
CC The invention is useful also for inhibiting or enhancing folate hydrolase
CC activity of a folate hydrolase polypeptide, N-acetylated alpha-linked
CC acidic dipeptidase (NAALADase) activity of a NAALADase polypeptide,
CC dipeptidyl dipeptidase IV activity of a dipeptidyl dipeptidase IV
CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-glutamyl
CC hydrolase polypeptide. The present sequence is human PSMA antibody light
CC chain variable region (VH)
XX

CC polypeptide, gamma-glutamyl hydrolase activity of a gamma-glutamyl
CC hydrolase polypeptide. The present sequence is human PSMA antibody light
CC chain variable region (VH)
XX
SQ Sequence 127 AA;

Query Match 91.8%; Score 479; DB 6; Length 127;
Best Local Similarity 92.9%; Pred. No. 3.6e-29;
Matches 92; Conservative 4; Mismatches 3; Indels 0; Gaps 0

QY 2 DIQLTSPSSLSASVGDVRVTTICRASQDISIYLAWFOORCKAPKSLIYRASSLSQSGVPS 61
DB 21 DIQLTSPSSLSASVGDVRVTTICRASQDISIYLAWFOORCKAPKSLIYRASSLSQSGVPS 80
QY 62 KFSGSGSGDTFTLTITSSLSQPEDFATYYCQYNSYPFTFG 100
DB 81 KFSGSGSGDTFTLTITSSLSQPEDFATYYCQYNSYPFTFG 119

RESULT 5
AAB75040
ID AAB75040 standard; protein; 224 AA.
AC
AC AAB75040;
XX
XX 19-JUL-2001 (first entry)
XX
XX TRO005 HuMab kappa chain protein sequence 3E2K.
XX
XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW human antibody phage display library; immunisation; transgenic animal.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX
XX WO200125492-A1.
PN
XX
XX 12-APR-2001.
XX
XX 02-OCT-2000; 2000WO-US027237.
XX
XX 02-OCT-1999; 99US-0157415P.
PR
XX 01-DEC-1999; 99US-00453234.
PR
XX
XX (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
PA
XX
XX Buechler J, Valkirs G, Gray J, Lonberg N;
PI
XX
XX WPI; 2001-335567/35.
XX
XX
XX Producing a human antibody phage display library comprises providing a
PT transgenic animal whose genome comprises human immunoglobulin genes and
PT isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
XX
XX Example 37; Page 121-122; 16ipp; English.

The present invention describes a method (M1) for producing a human
CC antibody phage display library (I), comprising: (1) providing a nonhuman
CC transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC (2) isolating nucleic acids encoding human antibody chains (III) from
CC lymphatic cells; and (3) forming a library of display packages whose
CC members comprise a nucleic acid encoding (III) which is displayed from
CC the package. The method is used for producing a human antibody display
CC library, e.g., a Fab phage display library. The display method may be
CC used to screen nucleic acids encoding antibody chains obtained from
CC immunised nonhuman transgenic animals, and from this a population of
CC antibodies may be prepared. Production of a human monoclonal antibodies
CC display library using this method means there is no need to immunise
CC humans with antigens, and the difficulties faced with immortalising B
CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
XX represent sequences used in the exemplification of the present invention


```

XX PT New human monoclonal antibody to heparanase, for use in treating or
XX PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
XX PT erythematosis, allograft rejection, atherosclerosis, and Alzheimer's
XX PT disease.
XX PS Claim 47; SEQ ID NO 4; 108pp; English.
XX CC The present invention describes an isolated human monoclonal antibody
XX CC which binds to and inhibits activity of human heparanase. Human anti-
XX CC heparanase antibodies of the present invention have cytostatic,
XX CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
XX CC dermatological, antiarteriosclerotic, neuroprotective and neurotropic
XX CC activities, and can be used as heparanase antagonists. The antibody,
XX CC methods and compositions of the present invention are useful in treating
XX CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
XX CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
XX CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
XX CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
XX CC erythematosis, allograft rejection, vascular restenosis, atherosclerosis,
XX CC and Alzheimer's disease. The present sequence represents a human anti-
XX CC heparanase 2H8 Vk amino acid sequence, which is used in the
XX CC exemplification of the present invention.
XX SQ Sequence 107 AA;
Query Match 90.2%; Score 471; DB 8; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.2e-28;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DIQQTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGISSLAWYQQKPEKAPKSLIYAASSLSQSGVPS 60
Qy 62 KFSGSGSGTDTLTITISLQPEDFATYYCQYNVPYTFG 100
Db 61 RFGSGSGTDTLTITISLQPEDFATYYCQYNVPYTFG 99
RESULT 10
AD036502
ID AD036502 standard; protein; 107 AA.
AC AD036502;
XX AC
XX DT 12-AUG-2004 (first entry)
XX DE Human anti-heparanase 5G10 Vk amino acid sequence SEQ ID NO:16.
XX KW human; monoclonal antibody; heparanase; heparanase inhibitor;
XX KW anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
XX KW antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
XX KW neuroprotective; neurotropic; heparanase antagonist; cancer; tumour;
XX KW melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
XX KW bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
XX KW mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
XX KW autoimmune disease; arthritis; asthma; lupus erythematosis;
XX KW allograft rejection; vascular restenosis; atherosclerosis;
XX KW Alzheimer's disease.
XX OS Homo sapiens.
XX OS
XX PN WO2004043989-A2.
XX PD 27-MAY-2004.
XX PF 05-NOV-2003; 2003WO-US035464.
XX PR 07-NOV-2002; 2002US-0424803P.
XX PA (MEDA-) MEDAREX INC.
XX PA (CELL-) CELLTech R & D.
XX

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PI Huang H, Holmes S, Mason S;
XX WPI; 2004-411694/38.
XX DR N-PSDB; ADO36501.
XX PT New human monoclonal antibody to heparanase, for use in treating or
XX PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
XX PT erythematosis, allograft rejection, atherosclerosis, and Alzheimer's
XX PT disease.
XX PS Claim 47; SEQ ID NO 16; 108pp; English.
XX CC The present invention describes an isolated human monoclonal antibody
XX CC which binds to and inhibits activity of human heparanase. Human anti-
XX CC heparanase antibodies of the present invention have cytostatic,
XX CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
XX CC dermatological, antiarteriosclerotic, neuroprotective and neurotropic
XX CC activities, and can be used as heparanase antagonists. The antibody,
XX CC methods and compositions of the present invention are useful in treating
XX CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
XX CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
XX CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
XX CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
XX CC erythematosis, allograft rejection, vascular restenosis, atherosclerosis,
XX CC and Alzheimer's disease. The present sequence represents a human anti-
XX CC heparanase 5G10 Vk amino acid sequence, which is used in the
XX CC exemplification of the present invention.
XX SQ Sequence 107 AA;
Query Match 90.2%; Score 471; DB 8; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.2e-28;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DIQQTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGRVITTCRASQGISSLAWYQQKPEKAPKSLIYAASSLSQSGVPS 60
Qy 62 KFSGSGSGTDTLTITISLQPEDFATYYCQYNVPYTFG 100
Db 61 RFGSGSGTDTLTITISLQPEDFATYYCQYNVPYTFG 99
RESULT 11
AD036494
ID AD036494 standard; protein; 107 AA.
XX AC AD036494;
XX AC
XX DT 12-AUG-2004 (first entry)
XX DE Human anti-heparanase 2D9 Vk amino acid sequence SEQ ID NO:8.
XX KW human; monoclonal antibody; heparanase; heparanase inhibitor;
XX KW anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
XX KW antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
XX KW neuroprotective; neurotropic; heparanase antagonist; cancer; tumour;
XX KW melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
XX KW bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
XX KW mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
XX KW autoimmune disease; arthritis; asthma; lupus erythematosis;
XX KW allograft rejection; vascular restenosis; atherosclerosis;
XX KW Alzheimer's disease.
XX OS Homo sapiens.
XX OS
XX PN WO2004043989-A2.
XX PD 27-MAY-2004.
XX PF 05-NOV-2003; 2003WO-US035464.
XX PR 07-NOV-2002; 2002US-0424803P.

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XX PA (MEDA-) MEDAREX INC.
XX PA (CELL-) CELLTech R & D.
XX PI Huang H, Holmes S, Mason S;
XX XX WPI; 2004-411694/38.
XX DR N-PSDB; ADO36493.
XX XX
XX PT New human monoclonal antibody to heparanase, for use in treating or
XX PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
XX PT erythematous, allograft rejection, atherosclerosis, and Alzheimer's
XX PT disease.
XX PS Claim 11; SEQ ID NO 8; 108pp; English.
XX CC
XX CC The present invention describes an isolated human monoclonal antibody
XX CC which binds to and inhibits activity of human heparanase. Human anti-
XX CC heparanase antibodies of the present invention have cytostatic,
XX CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
XX CC dermatological, antiarteriosclerotic, neuroprotective and nootropic
XX CC activities, and can be used as heparanase antagonists. The antibody,
XX CC methods and compositions of the present invention are useful in treating
XX CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
XX CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
XX CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
XX CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
XX CC erythematous, allograft rejection, vascular restenosis, atherosclerosis,
XX CC and Alzheimer's disease. The present sequence represents a human anti-
XX CC heparanase 2D9 V $\kappa$  amino acid sequence, which is used in the
XX CC exemplification of the present invention.
XX SQ Sequence 107 AA;

Query Match 90.2%; Score 471; DB 8; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.2e-28;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQRPKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQRPKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFSGSGGTDTLTITSSLOPEDFATYTCQQVNSYPPTFG 100
Db 61 KFSGSGGTDTLTITSSLOPEDFATYTCQQVNSYPPTFG 99

RESULT 12
AAP81246
ID AAP81246 standard; protein; 108 AA.
XX AC AAP81246;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 07-JAN-1991 (first entry)
XX XX
XX DE Anti-pseudomonas aeruginosa human type antibody L-chain contg. constant
XX DE region of kappa and lambda types.
XX KW Pseudomonas aeruginosa F4; Pseudomonas aeruginosa HI; immunotherapy.
XX OS Homo sapiens.
XX XX
XX FN JP63152984-A.
XX PD 25-JUN-1988.
XX PF 20-MAR-1986; 86JP-00064183.
XX XX
XX PR 18-AUG-1986; 86JP-00191687.
XX PR 20-MAR-1987; 87JP-00064183.
XX PA (WAKT ) WAKUNAGA SEIYAKU KK.

The Ab can also be used for immunologic control of infection caused by
Ps aeruginosa. The antibody is made effective against various classes or
subclasses of resistant Ps.aeruginosa by recombining corres. DNA L-chain
contg. versatile coding region. (Updated on 25-MAR-2003 to correct PF
disclosure; Fig 6 Page 612; 12pp; Japanese.

The Ab can also be used for immunologic control of infection caused by
Ps aeruginosa. The antibody is made effective against various classes or
subclasses of resistant Ps.aeruginosa by recombining corres. DNA L-chain
contg. versatile coding region. (Updated on 25-MAR-2003 to correct PF

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XX WPI; 1988-216877/31.
XX DR N-PSDB; AAN81636.
XX XX
XX PT Anti-Pseudomonas aeruginosa type antibody L-chain coding DNA - contains
XX PT constant kappa and lambda type regions, and versatile region recognising
XX PT ps.aeruginosa F4 and HI types.
XX PS Claim 8; Page 602; 12pp; Japanese.
XX XX
XX CC It also contains a variable region recognising Ps.aeruginosa F4 and HI
XX CC types. The Ab can be used for immunologic control of infection caused by
XX CC Ps.aeruginosa. The antibody is made effective against various classes or
XX CC subclasses of resistant Ps.aeruginosa by recombining corres. DNA L-chain
XX CC contg. versatile coding region. (Updated on 25-MAR-2003 to correct PF
XX CC field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
XX CC 2003 to correct PA field.)
XX SQ Sequence 108 AA;

Query Match 90.2%; Score 471; DB 1; Length 108;
Best Local Similarity 92.9%; Pred. No. 1.3e-28;
Matches 92; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQRPKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQRPKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFSGSGGTDTLTITSSLOPEDFATYTCQQVNSYPPTFG 100
Db 61 KFSGSGGTDTLTITSSLOPEDFATYTCQQVNSYPPTFG 99

RESULT 13
AAP81870
ID AAP81870 standard; protein; 111 AA.
XX AC AAP81870;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 05-JAN-1991 (first entry)
XX XX
XX DE Anti-pseudomonas aeruginosa human type antibody L-chain contg. constant
XX DE region of kappa and lambda types.
XX KW Pseudomonas aeruginosa F4; Pseudomonas aeruginosa HI; immunotherapy.
XX OS Homo sapiens.
XX XX
XX FN JP63152984-A.
XX PD 25-JUN-1988.
XX PF 20-MAR-1986; 86JP-00064183.
XX XX
XX PR 18-AUG-1986; 86JP-00191687.
XX PR 20-MAR-1987; 87JP-00064183.
XX PA (WAKT ) WAKUNAGA SEIYAKU KK.

WPI; 1988-216877/31.
XX DR N-PSDB; AAN81636.
XX XX
XX PT Anti-Pseudomonas aeruginosa type antibody L-chain coding DNA - contains
XX PT constant kappa and lambda type regions, and versatile region recognising
XX PT ps.aeruginosa F4 and HI types.
XX PS Disclosure; Fig 6 Page 612; 12pp; Japanese.
XX XX
XX CC The Ab can also be used for immunologic control of infection caused by
XX CC Ps aeruginosa. The antibody is made effective against various classes or
XX CC subclasses of resistant Ps.aeruginosa by recombining corres. DNA L-chain
XX CC contg. versatile coding region. (Updated on 25-MAR-2003 to correct PF

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CC field.) (Updated on 25-MAR-2003 to correct PR field.) (Updated on 25-MAR-
CC 2003 to correct PA field.)
XX
SQ Sequence 111 AA;

Query Match      90.2%; Score 471; DB 1; Length 111;
Best Local Similarity 92.9%; Pred. No. 1.3e-28;
Matches 92; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 DIQLTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQGVPS 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 4 DIQWTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQPGKAPKSLIQAASSLSQGVPS 63
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KFGSGSGTDFTLTISLSQPEDFATYCCQYNSYPFTFG 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 64 KFGSGSGTDFTLTISLSQPEDFATYCCQYNYPRFTFG 102
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 14
AAR40956
ID AAR40956 standard; protein; 109 AA.
XX
AC AAR40956;
XX
DT 25-MAR-2003 (revised)
DT 25-FEB-1994 (first entry)
XX
DE Human germ-line gene HK137 antibody light (kappa) chain.
XX
KW humanised antibody; human germ-line; light chain; variable region;
KW framework region; reshaped antibody; CDR-grafted antibody;
KW complementarity determining region; immuno silent.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 1..23
FT /label= FR1
FT /note= "framework region"
FT Region 24..34
FT /label= CDR1
FT Region 35..49
FT /label= FR2
FT /note= "framework region"
FT Region 50..56
FT /label= CDR2
FT Region 57..88
FT /label= FR3
FT /note= "framework region"
FT Region 89..97
FT /label= CDR3
FT Region 98..109
FT /label= FR4
FT /note= "framework region"
XX
PN WO9317105-A1.
XX
PD 02-SEP-1993.
XX
PF 19-FEB-1993; 93WO-GB000363.
XX
PR 19-FEB-1992; 92GB-00003459.
XX
PA (SCOT-) SCOTGEN LTD.
XX
PI Winter GP, Carr FJ, Harris WJ;
XX
DR WPI; 1993-288411/36.
XX
PT New altered antibodies with reduced immune responses - have germ-line
PT aminoacid residues replacing somatically mutated residues.
XX
PS Example 3; Fig 4b; 53pp; English.
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XX A humanised antibody comprised CDRs originally from a mouse MAb RSV19
CC specific for Respiratory Syncytial Virus transplanted onto heavy and
CC light chain V region domains derived from NEM and RE1 myeloma proteins,
CC respectively. The framework regions of this CDR-grafted antibody were
CC converted to the germ-line equivalent. For conversion of the K-chain, the
CC germ-line light chain VK137 (AAR40956) was used. Germ-line framework
CC regions are those present in immature B cells, i.e. prior to any somatic
CC mutation which takes place during maturation. Unlike mutations in the
CC CDRs, any mutation in framework regions does not affect affinity for an
CC antigen and is therefore essentially random. The mutation may, however,
CC cause the "self" antibody to be recognised as "foreign" and conversion to
CC the unmutated germ-line sequence renders the framework regions "immuno
CC silent". (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 109 AA;

Query Match      89.7%; Score 469; DB 2; Length 109;
Best Local Similarity 91.9%; Pred. No. 2.1e-28;
Matches 91; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 DIQLTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQGVPS 61
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 DIQWTQSPSSLSASVGDRTVITCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQGVPS 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 62 KFGSGSGTDFTLTISLSQPEDFATYCCQYNSYPFTFG 100
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 RFGSGSGTDFTLTISLSQPEDFATYCCQYNSYRLTFG 99
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 15
ABO27128
ID ABO27128 standard; protein; 95 AA.
XX
AC ABO27128;
XX
DT 10-SEP-2003 (first entry)
DE Human germline light chain variable region gene segment #8.
XX
KW Human; light chain variable region; VK; humanised antibody;
KW chimeric antibody; complementarity determining region; CDR;
KW canonical CDR structure type.
XX
OS Homo sapiens.
XX
PN US2003039649-A1.
XX
PD 27-FEB-2003.
XX
PF 12-JUL-2002; 2002US-00194975.
XX
PR 12-JUL-2001; 2001US-0305111P.
XX
PA (FOOT/) FOOTE J.
XX
PI Foote J;
XX
DR WPI; 2003-492151/46.
XX
PT Making humanized antibody for converting antibody, by making chimeric
PT antibodies containing complementarity determining region from non-human
PT antibody and appropriate framework sequences of human antibodies.
XX
PS Example 1; Fig 2; 31pp; English.
XX
CC The invention describes a method of making a humanised antibody,
CC comprising making chimeric antibodies containing a complementarity
CC determining region (CDR) from a non-human antibody and appropriate
CC framework sequences (I) of human antibodies. (I) is selected by using
CC canonical CDR structure types of non-human antibody in comparison to
CC germline canonical CDR structure types of human antibodies as the basis
CC for selection, for humanisation. The method is useful for making a
```


CC humanised antibody or a converted antibody. The method is applicable for
CC converting a subject antibody sequence of any subject species to a less
CC immunogenic form suitable for use in an object species. The method is
CC reliable for identifying suitable human framework sequences to support
CC non-human CDR regions and to provide humanised antibodies that retain
CC high antigen binding with low immunogenicity in humans, without the need
CC for direct comparison of framework sequences, without the need for
CC determining critically important amino acid residues in the framework,
CC and without the need for multiple iteration and construction to obtain
CC humanised antibodies with suitable therapeutic properties. The antibody
CC has high affinity and low immunogenicity without need for comparing
CC framework sequences between non-human and human antibodies. This sequence
CC represents a human light chain variable region gene segment used in the
CC creation of humanised antibodies
XX
SQ Sequence 95 AA;

Query Match 89.3%; Score 466; DB 6; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.7e-28;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 2 DIQLTQSPSSLASVGDRTTITCRASQDISIYLAWFQQRPGKAPKSLIYAASSLQSGVPS 61
Db 1 DIQMTQSPSSLASVGDRTTITCRASQGISNYLAWFQQRPGKAPKSLIYAASSLQSGVPS 60
Qy 62 KFGSGSGTDFTLTISSLPEDFATYYCQYNYP 96
Db 61 RFGSGSGTDFTLTISSLPEDFATYYCQYNYP 95

Search completed: March 8, 2005, 06:17:23
Job time : 49.8263 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 53.5981 Seconds ;
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-38

Perfect score: 522
Sequence: 1 LDILQTGPSLSASVGRV.....EDFATYCCQYNSVPTFGP 101

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*
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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	482	92.3	127	15	US-10-395-894-25
2	482	92.3	127	16	US-10-395-894-25
3	479	91.8	127	15	US-10-395-894-21
4	479	91.8	127	16	US-10-395-894-21
5	474	90.8	127	15	US-10-221-529-4
6	471	90.2	107	16	US-10-703-714-4
7	471	90.2	107	16	US-10-703-714-8
8	471	90.2	107	16	US-10-703-714-16
9	467	89.5	108	17	US-10-783-311-126
10	466	89.3	95	14	US-10-194-975-61
11	466	89.3	95	15	US-10-308-817-8
12	466	89.3	95	15	US-10-453-698-8
13	466	89.3	95	16	US-10-379-392-68
					Sequence 25, Appl
					Sequence 25, Appl
					Sequence 21, Appl
					Sequence 21, Appl
					Sequence 4, Appl
					Sequence 4, Appl
					Sequence 8, Appl
					Sequence 16, Appl
					Sequence 126, Appl
					Sequence 61, Appl
					Sequence 8, Appl
					Sequence 68, Appl

14	466	89.3	107	15	US-10-251-085B-145	Sequence 145, App
15	466	89.3	107	16	US-10-737-252-145	Sequence 145, App
16	465	89.1	107	14	US-10-268-501-5	Sequence 5, Appl
17	465	89.1	107	15	US-10-608-626-5	Sequence 5, Appl
18	465	89.1	107	15	US-10-600-152-14	Sequence 14, Appl
19	465	89.1	107	16	US-10-619-754-5	Sequence 5, Appl
20	465	89.1	108	9	US-09-056-160B-12	Sequence 12, Appl
21	465	89.1	108	10	US-09-320-262A-8	Sequence 8, Appl
22	465	89.1	108	10	US-09-795-798-3	Sequence 3, Appl
23	465	89.1	108	14	US-10-234-671-12	Sequence 12, Appl
24	465	89.1	108	15	US-10-408-901-20	Sequence 20, Appl
25	465	89.1	108	16	US-10-912-994-8	Sequence 8, Appl
26	465	89.1	109	9	US-09-811-123-6	Sequence 6, Appl
27	465	89.1	110	14	US-10-044-896-4	Sequence 4, Appl
28	465	89.1	214	15	US-10-408-901-44	Sequence 44, Appl
29	464	88.9	107	9	US-09-948-939-13	Sequence 13, Appl
30	463	88.7	214	14	US-10-153-382-19	Sequence 19, Appl
31	461	88.3	107	15	US-10-309-762-62	Sequence 62, Appl
32	461	88.3	107	15	US-10-309-762-164	Sequence 164, App
33	461	88.3	107	17	US-10-638-265-76	Sequence 76, Appl
34	460	88.1	107	10	US-09-851-614-2	Sequence 2, Appl
35	460	88.1	107	14	US-10-035-637-2	Sequence 2, Appl
36	460	88.1	107	14	US-10-073-644C-4	Sequence 4, Appl
37	460	88.1	108	17	US-10-725-962-40	Sequence 40, Appl
38	460	88.1	111	14	US-10-203-754A-18	Sequence 18, Appl
39	459	87.9	291	15	US-10-406-830-10	Sequence 10, Appl
40	458	87.7	116	17	US-10-783-311-174	Sequence 174, App
41	458	87.7	128	15	US-10-389-221-12	Sequence 12, Appl
42	457	87.5	107	15	US-10-309-762-61	Sequence 61, Appl
43	457	87.5	107	15	US-10-309-762-64	Sequence 64, Appl
44	457	87.5	107	15	US-10-309-762-88	Sequence 88, Appl
45	457	87.5	126	16	US-10-469-125-8	Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-10-395-894-25
; Sequence 25, Application US/10395894
; Publication No. US20040033229A1
; GENERAL INFORMATION:
; APPLICANT: MADON, Paul J.
; APPLICANT: DONOVAN, Gerald P.
; APPLICANT: OLSON, William C.
; APPLICANT: SCHLKE, No. US20040033229Albert
; APPLICANT: GARDNER, Jason
; APPLICANT: MA Dangehe
; TITLE OF INVENTION: PSMA ANTIBODIES AND PROTEIN MULTIMERS
; FILE REFERENCE: P00741.70005.US
; CURRENT APPLICATION NUMBER: US/10/395,894
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: PCT/US02/33944
; PRIOR FILING DATE: 2002-10-23
; PRIOR APPLICATION NUMBER: US 60/335,215
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: US 60/362,747
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 60/412,618
; PRIOR FILING DATE: 2002-09-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25
; LENGTH: 127
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-395-894-25

Query Match 92.3%; Score 482; DB 15; Length 127;
Best Local Similarity 93.9%; Pred. No. 1.4e-34;
Matches 93; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQQTGPSLSASVGRVTTTCRASQDISIYLAWFQORPGKAPKSLIYAASSLSQGVPS 61


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; Sequence 4, Application US/10221529
; Publication No. US20040038293A1
; GENERAL INFORMATION:
; APPLICANT: NOVARTIS AG
; TITLE OF INVENTION: ANTIBODIES TO HUMAN CD154
; FILE REFERENCE: 4-31266A
; CURRENT APPLICATION NUMBER: US/10/221,529
; CURRENT FILING DATE: 2003-05-22
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-221-529-4

Query Match      90.8%; Score 474; DB 15; Length 107;
Best Local Similarity 91.9%; Pred. No. 5.8e-34;
Matches 91; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGDRTVTTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 100
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 99

RESULT 6
US-10-703-714-4
; Sequence 4, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Haichun
; APPLICANT: Holmes, Steven
; APPLICANT: Mason, Sean
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
; FILE REFERENCE: MXI-294
; CURRENT APPLICATION NUMBER: US/10/703,714
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/424803
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-703-714-4

Query Match      90.2%; Score 471; DB 16; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.1e-33;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGDRTVTTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 100
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 99

RESULT 7
US-10-703-714-8
; Sequence 8, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Haichun
; APPLICANT: Holmes, Steven
; APPLICANT: Mason, Sean
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
; FILE REFERENCE: MXI-294
; CURRENT APPLICATION NUMBER: US/10/703,714
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/424803
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-703-714-8

Query Match      90.2%; Score 471; DB 16; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.1e-33;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGDRTVTTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 100
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 99

RESULT 8
US-10-703-714-16
; Sequence 16, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Haichun
; APPLICANT: Holmes, Steven
; APPLICANT: Mason, Sean
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
; FILE REFERENCE: MXI-294
; CURRENT APPLICATION NUMBER: US/10/703,714
; CURRENT FILING DATE: 2003-11-07
; PRIOR APPLICATION NUMBER: 60/424803
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 64
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-703-714-16

Query Match      90.2%; Score 471; DB 16; Length 107;
Best Local Similarity 90.9%; Pred. No. 1.1e-33;
Matches 90; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGDRTVTTCRASQGISWLAWYQOKPEKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 100
Db 61 RFGSGSGTDFTLTISSQLQPEDFATYYCQYNSYPFTFG 99

RESULT 9
US-10-783-311-126
; Sequence 126, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
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; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
; FEATURE:
; OTHER INFORMATION: Light Chain amino acid sequence
; US-10-783-311-126

Query Match      89.5%; Score 467; DB 17; Length 108;
Best Local Similarity 89.9%; Pred. No. 2.4e-33;
Matches 89; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy  2 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQGVPS 61
Db  2 DIQMTQSPSSFSASTGDRVITTCRASQGISYSLAWYQQKPKAPKLLIYAASTLSQGVPS 61

Qy  62 KFGSGSGTDTLTITSSLPQEDFATYYCQQYNSYPFTFG 100
Db  62 KFGSGSGTDTLTITSSLPQEDFATYYCQQYNSYPFTFG 100

RESULT 10
US-10-194-975-61
; Sequence 61, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: Foote, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; PRIOR FILING DATE: 2002-10-10
; PRIOR APPLICATION NUMBER: US 60/305,111
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-194-975-61

Query Match      89.3%; Score 466; DB 14; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.5e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy  2 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQGVPS 61
Db  1 DIQMTQSPSSLSASVGRVITTCRASQGISNYLAWFOQKPGKAPKSLIYAASSLSQGVPS 60

Qy  62 KFGSGSGTDTLTITSSLPQEDFATYYCQQYNSYP 96
Db  61 RFSGSGSGTDTLTITSSLPQEDFATYYCQQYNSYP 95

RESULT 11
US-10-308-817-8
; Sequence 8, Application US/10308817
; Publication No. US20030219861A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; APPLICANT: Wu, Dayang
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 1087-37
; CURRENT APPLICATION NUMBER: US/10/308,817
; CURRENT FILING DATE: 2002-12-03
; NUMBER OF SEQ ID NOS: 195
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
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; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
; US-10-308-817-8

Query Match      89.3%; Score 466; DB 15; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.5e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy  2 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQGVPS 61
Db  1 DIQMTQSPSSLSASVGRVITTCRASQGISNYLAWFOQKPGKAPKSLIYAASSLSQGVPS 60

Qy  62 KFGSGSGTDTLTITSSLPQEDFATYYCQQYNSYP 96
Db  61 RFSGSGSGTDTLTITSSLPQEDFATYYCQQYNSYP 95

RESULT 12
US-10-453-698-8
; Sequence 8, Application US/10453698
; Publication No. US20040038308A1
; GENERAL INFORMATION:
; APPLICANT: Rother, Russell
; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 95
; TYPE: PRT
; ORGANISM: human
; US-10-453-698-8

Query Match      89.3%; Score 466; DB 15; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.5e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy  2 DIQQTSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQGVPS 61
Db  1 DIQMTQSPSSLSASVGRVITTCRASQGISNYLAWFOQKPGKAPKSLIYAASSLSQGVPS 60

Qy  62 KFGSGSGTDTLTITSSLPQEDFATYYCQQYNSYP 96
Db  61 RFSGSGSGTDTLTITSSLPQEDFATYYCQQYNSYP 95

RESULT 13
US-10-379-392-68
; Sequence 68, Application US/10379392
; Publication No. US20040110226A1
; GENERAL INFORMATION:
; APPLICANT: Lazar, Gregory Alan
; APPLICANT: Desjarlais, John Rudolf
; APPLICANT: Marshall, Shannon Alicia
; APPLICANT: Dahiyat, Bassil I.
; TITLE OF INVENTION: ANTIBODY OPTIMIZATION
; FILE REFERENCE: A-71386-3 463077-236
; CURRENT APPLICATION NUMBER: US/10/379,392
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/360,843
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 60/384,197
; PRIOR FILING DATE: 2002-05-29
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 68
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-379-392-68
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Query Match      89.3%; Score 466; DB 16; Length 95;
Best Local Similarity 94.7%; Pred. No. 2.5e-33;
Matches 90; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGDRTVTTCRASQGISNYLWFOQPGKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFSGSGSGTDTFTLTISLQPEDFATYYCQYNSYP 96
Db 61 RFSGSGSGTDTFTLTISLQPEDFATYYCQYNSYP 95

RESULT 14
US-10-251-085B-145
; Sequence 145, Application US/10251085B
; Publication No. US20040072164A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21
; CURRENT APPLICATION NUMBER: US/10/251,085B
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 107
; TYPE: PRT
; ORGANISM: human
US-10-251-085B-145

Query Match      89.3%; Score 466; DB 15; Length 107;
Best Local Similarity 89.9%; Pred. No. 2.9e-33;
Matches 89; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQLTQSPSSLSASVGDRTVTTCRASQDISIYLWFOQPGKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFSGSGSGTDTFTLTISLQPEDFATYYCQYNSYPFTFG 100
Db 61 RFSGSGSGTDTFTLTISLQPEDFATYYCQYKNYPLTFG 99

RESULT 15
US-10-737-252-145
; Sequence 145, Application US/10737252
; Publication No. US20040175736A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Renshaw, Mark
; APPLICANT: Lin, Ying-Chi
; APPLICANT: Maruyama, Toshiaki
; TITLE OF INVENTION: ENGINEERED TEMPLATES AND THEIR USE IN SINGLE PRIMER AMPLIFICATION
; FILE REFERENCE: 1087-21 CIP
; CURRENT APPLICATION NUMBER: US/10/737,252
; CURRENT FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/251,085
; PRIOR FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: US 60/323,455
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 145
; LENGTH: 107
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; TYPE: PRT
; ORGANISM: human
US-10-737-252-145

Query Match      89.3%; Score 466; DB 16; Length 107;
Best Local Similarity 89.9%; Pred. No. 2.9e-33;
Matches 89; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGDRTVTTCRASQDISIYLAWFOQPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQLTQSPSSLSASVGDRTVTTCRASQDISIYLWFOQPGKAPKSLIYAASSLSQSGVPS 60

Qy 62 KFSGSGSGTDTFTLTISLQPEDFATYYCQYNSYPFTFG 100
Db 61 RFSGSGSGTDTFTLTISLQPEDFATYYCQYKNYPLTFG 99

Search completed: March 8, 2005, 07:05:57
Job time : 53.5981 secs
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 11.1056 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-38
Perfect score: 522
Sequence: 1 LDQLTQSPSSLSASVGRV.....EDFATYYCQQNSVPTFTGP 101

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	473	90.6	109	2	US-07-934-373C-3
2	473	90.6	109	3	US-08-437-642B-3
3	473	90.6	109	4	US-08-146-206C-3
4	473	90.6	109	4	US-09-705-686-3
5	473	90.6	109	4	US-09-705-392A-3
6	473	90.6	109	4	US-09-705-398-3
7	473	90.6	109	5	PCT-US93-07832-3
8	465	89.1	107	2	US-07-934-373C-18
9	465	89.1	107	3	US-08-437-642B-18
10	465	89.1	107	4	US-08-146-206C-18
11	465	89.1	107	4	US-09-648-067A-14
12	465	89.1	107	4	US-09-705-686-18
13	465	89.1	107	4	US-09-705-392A-18
14	465	89.1	107	4	US-09-705-398-18
15	465	89.1	107	5	PCT-US93-07832-18
16	465	89.1	108	3	US-08-974-899-3
17	465	89.1	108	4	US-09-795-798-3
18	463	88.7	214	4	US-09-472-087-71
19	452	86.6	108	3	US-09-025-769B-14
20	452	86.6	108	4	US-09-490-070A-14
21	452	86.6	108	4	US-09-490-153-14
22	452	86.6	108	4	US-09-490-324-14
23	451	86.4	108	2	US-08-378-939-32
24	451	86.4	108	2	US-08-378-939-34
25	451	86.4	108	3	US-08-974-899-2
26	451	86.4	108	4	US-08-795-798-2
27	451	86.4	109	3	US-09-157-370-3

Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 48, Appli
Sequence 313, App
Sequence 30, Appl
Sequence 40, Appl
Sequence 28, Appl
Sequence 43, Appl
Sequence 28, Appl
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Sequence 28, Appl
Sequence 43, Appl
Sequence 28, Appl
Sequence 43, Appl
Sequence 43, Appl

ALIGNMENTS

RESULT 1
US-07-934-373C-3
; Sequence 3, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-07-934-373C-3

Query Match 90.6%; Score 473; DB 2; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DIQLTQSPSSLSASVGRVTITCRASODISIYLANFQORPGKAPKSLIYAASSLSQGVPS 61

Db 1 DIQWTSFSSLSASVGRVITTCRASQDVSSYLAWYQQKPKAPKLLIYAASSLSGVPs 60
Qy 62 KFGSGSGTDTLTITISSLPQEDFATYYCQYNSVPFTFG 100
Db 61 RFGSGSGTDTLTITISSLPQEDFATYYCQYNSLPYTFG 99

RESULT 2

US-08-437-642B-3
; Sequence 3, Application US/08437642B
; Patent No. 6054297
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-437-642B-3
Query Match 90.6%; Score 473; DB 3; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DIQWTSFSSLSASVGRVITTCRASQDVSSYLAWYQQKPKAPKLLIYAASSLSGVPs 61
Db 1 DIQWTSFSSLSASVGRVITTCRASQDVSSYLAWYQQKPKAPKLLIYAASSLSGVPs 60
Qy 62 KFGSGSGTDTLTITISSLPQEDFATYYCQYNSVPFTFG 100
Db 61 RFGSGSGTDTLTITISSLPQEDFATYYCQYNSLPYTFG 99

RESULT 3

US-08-146-206C-3
; Sequence 3, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear

US-08-146-206C-3
Query Match 90.6%; Score 473; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;
Qy 2 DIQWTSFSSLSASVGRVITTCRASQDVSSYLAWYQQKPKAPKLLIYAASSLSGVPs 61
Db 1 DIQWTSFSSLSASVGRVITTCRASQDVSSYLAWYQQKPKAPKLLIYAASSLSGVPs 60
Qy 62 KFGSGSGTDTLTITISSLPQEDFATYYCQYNSVPFTFG 100
Db 61 RFGSGSGTDTLTITISSLPQEDFATYYCQYNSLPYTFG 99

RESULT 4

US-09-705-686-3
; Sequence 3, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,686
FILING DATE: 02-NOV-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-686-3

Query Match 90.6%; Score 473; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVVTITCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGRVVTITCRASQDVSSYLAWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 62 KFGSGSGTDFTLTISSLPQEDFATYYCQYNSYPFTFG 100
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQYNSLPYFTFG 99

RESULT 5

US-09-705-392A-3
Sequence 3, Application US/09705392A
Patent No. 6719971
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,392A
FILING DATE: 02-NOV-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-392A-3

Query Match 90.6%; Score 473; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVVTITCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGRVVTITCRASQDVSSYLAWYQKPGKAPKLLIYAASSLSQSGVPS 60

Qy 62 KFGSGSGTDFTLTISSLPQEDFATYYCQYNSYPFTFG 100
Db 61 RFGSGSGTDFTLTISSLPQEDFATYYCQYNSLPYFTFG 99

RESULT 6

US-09-705-398-3
Sequence 3, Application US/09705398
Patent No. 6800738
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/705,398
FILING DATE: 02-NOV-1993
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P1D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9881
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 109 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-705-398-3

Query Match 90.6%; Score 473; DB 4; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVTTTCRASQDISIYLAWFOORFGKAPKSLIYAASSLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGRVTTTCRASQDVSSYLAWYQOKFGKAPKLLIYAASSLSQGVPS 60
Qy 62 KFSGSGSGTDTLTITSSLPQEDFATYYCQYNSVPPTFG 100
Db 61 RFGSGSGTDTLTITSSLPQEDFATYYCQYNSLPYTFG 99

RESULT 7

PCT-US93-07832-3
; Sequence 3, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT

; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 109 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

PCT-US93-07832-3

Query Match 90.6%; Score 473; DB 5; Length 109;
Best Local Similarity 89.9%; Pred. No. 1.7e-35;
Matches 89; Conservative 7; Mismatches 3; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVTTTCRASQDISIYLAWFOORFGKAPKSLIYAASSLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGRVTTTCRASQDVSSYLAWYQOKFGKAPKLLIYAASSLSQGVPS 60

Qy 62 KFSGSGSGTDTLTITSSLPQEDFATYYCQYNSVPPTFG 100

Db 61 RFGSGSGTDTLTITSSLPQEDFATYYCQYNSLPYTFG 99

RESULT 8

US-07-934-373C-18
; Sequence 18, Application US/07934373C
; Patent No. 5821337

; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/934,373C
; FILING DATE: 21-Aug-1992
; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272

; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994

; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid

; TOPOLOGY: Linear

US-07-934-373C-18

Query Match 89.1%; Score 465; DB 2; Length 107;
Best Local Similarity 89.9%; Pred. No. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVTTTCRASQDISIYLAWFOORFGKAPKSLIYAASSLSQGVPS 61
Db 1 DIQMTQSPSSLSASVGRVTTTCRASQDISIYLAWYQOKFGKAPKLLIYAASSLSQGVPS 60

Qy 62 KFSGSGSGTDTLTITSSLPQEDFATYYCQYNSVPPTFG 100

Db 61 RFGSGSGTDTLTITSSLPQEDFATYYCQYNSLPYTFG 99

RESULT 9

US-08-437-642B-18
; Sequence 18, Application US/08437642B
; Patent No. 6054297

; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter

; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/437,642B
; FILING DATE: 09-May-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P2C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-437-642B-18

Query Match      89.1%; Score 465; DB 3; Length 107;
Best Local Similarity 89.9%; Pred. No. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db  1 DIQMTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 60

Qy  62 KFGSGSGTDTFTLTISSLQPEDFATYYCQQVNSYPFTFG 100
Db  61 RFGSGSGTDTFTLTISSLQPEDFATYYCQQVNSLPWTFG 99

RESULT 10
US-08-146-206C-18
; Sequence 18, Application US/08146206C
; Patent No. 6407213
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,206C
; FILING DATE: 17-No. 6407213-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
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; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-146-206C-18

Query Match      89.1%; Score 465; DB 4; Length 107;
Best Local Similarity 89.9%; Pred. No. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db  1 DIQMTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 60

Qy  62 KFGSGSGTDTFTLTISSLQPEDFATYYCQQVNSYPFTFG 100
Db  61 RFGSGSGTDTFTLTISSLQPEDFATYYCQQVNSLPWTFG 99

RESULT 11
US-09-648-067A-14
; Sequence 14, Application US/09648067A
; Patent No. 6627196
; GENERAL INFORMATION:
; APPLICANT: Baughman, Sharon A.
; APPLICANT: Shak Steven
; TITLE OF INVENTION: Dosages for Treatment with Anti-ErbB2 Antibodies
; FILE REFERENCE: P1775R1
; CURRENT APPLICATION NUMBER: US/09/648,067A
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,018
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/213,822
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 15
; SEQ ID NO 14
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VL consensus sequence
; US-09-648-067A-14

Query Match      89.1%; Score 465; DB 4; Length 107;
Best Local Similarity 89.9%; Pred. No. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy  2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 61
Db  1 DIQMTQSPSSLSASVGRVITTCRASQDISIYLAWFOORPGKAPKSLIYAASSLSQSGVPS 60

Qy  62 KFGSGSGTDTFTLTISSLQPEDFATYYCQQVNSYPFTFG 100
Db  61 RFGSGSGTDTFTLTISSLQPEDFATYYCQQVNSLPWTFG 99

RESULT 12
US-09-705-686-18
; Sequence 18, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
```

;;
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Genentech, Inc.
;; STREET: 1 DNA Way
;; CITY: South San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94080
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
;; BEST LOCAL SIMILARITY 89.1%; Score 465; DB 4; Length 107;
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: WinPatIn (Genentech)
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/705,686
;; FILING DATE: 02-Nov-1993
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/146206
;; FILING DATE: 17-NOV-1993
;; APPLICATION NUMBER: 07/715272
;; FILING DATE: 14-JUN-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 40,378
;; REFERENCE/DOCKET NUMBER: P0709P1D3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1994
;; TELEFAX: 650/952-9881
;;
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-686-18

Query Match 89.1%; Score 465; DB 4; Length 107;
Best Local Similarity 89.9%; Pred.No. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRFKAPKSLIYAASSLSQGVPS 61
Db 1 DIQWTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRFKAPKSLIYAASSLSQGVPS 60
Qy 62 KFGSGSGTDTLTLTISLQPEDFATYYCQYNSLPWTFG 100
Db 61 RFGSGSGTDTLTLTISLQPEDFATYYCQYNSLPWTFG 99

RESULT 13
US-09-705-392A-18
; Sequence 18, Application US/09705392A
; Patent No. 6719371
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,392A
; FILING DATE: 02-Nov-1993

;;
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/146206
;; FILING DATE: 17-NOV-1993
;; APPLICATION NUMBER: 07/715272
;; FILING DATE: 14-JUN-1991
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Lee, Wendy M.
;; REGISTRATION NUMBER: 40,378
;; REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 650/225-1994
;; TELEFAX: 650/952-9881
;;
;; INFORMATION FOR SEQ ID NO: 18:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 107 amino acids
;; TYPE: Amino Acid
;; TOPOLOGY: Linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-392A-18

Query Match 89.1%; Score 465; DB 4; Length 107;
Best Local Similarity 89.9%; Pred.No. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
Qy 2 DIQLTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRFKAPKSLIYAASSLSQGVPS 61
Db 1 DIQWTQSPSSLSASVGRVITTCRASQDISIYLAWFOQRFKAPKSLIYAASSLSQGVPS 60
Qy 62 KFGSGSGTDTLTLTISLQPEDFATYYCQYNSLPWTFG 100
Db 61 RFGSGSGTDTLTLTISLQPEDFATYYCQYNSLPWTFG 99

RESULT 14
US-09-705-398-18
; Sequence 18, Application US/09705398
; Patent No. 6800738
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705,398
; FILING DATE: 02-Nov-1993
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-705-398-18

Query Match 89.1%; Score 465; DB 4; Length 107;
Best Local Similarity 89.9%; Pred. NO. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVTTTCRASQDISIYLAWFOQPGKAPKSLIYAAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGRVTTTCRASQDISIYNLAWYQKPKAPKLLIYAAASSLESQVPS 60

Qy 62 KPSGSGSGTDFTLTITSSIQPEDFATYYCQQYNSLPWTFG 100
Db 61 RFGSGSGTDFTLTITSSIQPEDFATYYCQQYNSLPWTFG 99

RESULT 15

PCT-US93-07832-18
; Sequence 18, Application PC/TUS9307832
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: Immunoglobulin Variants
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07832
; FILING DATE: 19930820
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/05126
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/934373
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 709P2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 107 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
PCT-US93-07832-18

Query Match 89.1%; Score 465; DB 5; Length 107;
Best Local Similarity 89.9%; Pred. NO. 8.5e-35;
Matches 89; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

Qy 2 DIQLTQSPSSLSASVGRVTTTCRASQDISIYLAWFOQPGKAPKSLIYAAASSLSQSGVPS 61
Db 1 DIQMTQSPSSLSASVGRVTTTCRASQDISIYNLAWYQKPKAPKLLIYAAASSLESQVPS 60

Qy 62 KPSGSGSGTDFTLTITSSIQPEDFATYYCQQYNSLPWTFG 100
Db 61 RFGSGSGTDFTLTITSSIQPEDFATYYCQQYNSLPWTFG 99

Search completed: March 8, 2005, 05:54:14
Job time : 12.1056 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 11.3 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-39

Perfect score: 856

Sequence: 1 LTCFSGFSLITRGVGVDMW.....PVTVMNSGALTSQVHTFQL 159

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR.79.*

2: PIR1.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488.5	57.1	124	2 A49002	Ig heavy chain V r
2	480.5	56.1	472	2 S31459	Ig gamma-1 chain -
3	474	55.4	220	2 A49444	Ig gamma-1 heavy c
4	450.5	52.6	241	2 S69131	Ig heavy chain (DO
5	449.5	52.5	374	2 S69339	Ig heavy chain V r
6	447.5	52.3	470	2 S22080	Ig heavy chain pre
7	442	51.6	231	2 PC4155	Ig gamma-2b chain
8	433	50.6	138	2 S31513	Ig heavy chain - h
9	411	48.0	119	2 S18555	Ig heavy chain V r
10	410.5	48.0	220	2 S68211	Ig heavy chain (Ma
11	410.5	48.0	444	2 PC4436	monoclonal antibod
12	393	45.9	121	1 GIHUHE	Ig heavy chain V-I
13	392	45.8	121	2 A36005	Ig heavy chain V r
14	389	45.4	213	2 S68213	Ig heavy chain (Ma
15	388	45.3	125	1 MEHUMC	Ig heavy chain V-I
16	383.5	44.8	548	2 S38864	Ig epsilon chain C
17	377	44.0	221	2 S49220	Ig gamma-1 chain -
18	371.5	43.4	118	2 S18556	Ig heavy chain V r
19	371	43.3	246	2 S38950	Ig gamma chain - m
20	371	43.3	446	2 S40295	Ig gamma-2a chain
21	362.5	42.3	469	2 S37483	Ig gamma-2a chain
22	357.5	41.8	122	2 S11740	Ig heavy chain pre
23	356.5	41.6	254	2 B31790	Ig heavy chain V r
24	355.5	41.5	231	2 B23746	Ig Fab region IV-J
25	351.5	41.1	474	1 G2MS11	Ig gamma-2b chain
26	350.5	40.9	475	2 S01321	Ig gamma-2b chain
27	348.5	40.7	143	2 PF0174	Ig heavy chain pre
28	348.5	40.7	214	2 PC4202	monoclonal antibod
29	347.5	40.6	113	2 S26465	Ig heavy chain V r

30 345.5 40.4 147 1 G2HUCS Ig heavy chain pre
31 342 40.0 96 2 S26323 Ig heavy chain V r
32 340 39.7 549 2 S04845 Ig heavy chain pre
33 339.5 39.7 568 2 A34891 Ig heavy chain pre
34 338 39.5 143 2 S23624 Ig heavy chain V r
35 337 39.4 107 2 A49442 Ig heavy chain V r
36 336 39.3 96 2 S26924 Ig heavy chain V r
37 332.5 38.8 120 1 GIHUCO Ig heavy chain V-I
38 330 38.6 592 2 S25705 Ig mu chain - shee
39 323.5 37.8 116 2 S26328 Ig heavy chain V r
40 318 37.1 119 1 GIHUDW Ig heavy chain V-I
41 316 36.9 96 2 S26922 Ig heavy chain V r
42 316 36.9 509 2 S17597 Ig delta chain (WI
43 314 36.7 121 2 S09959 Ig heavy chain V r
44 313.5 36.6 380 2 S12839 Ig heavy chain pre
45 313 36.6 149 2 S30752 Ig heavy chain pre

ALIGNMENTS

RESULT 1

A49002

Ig heavy chain V region, rheumatoid factor RF antibody - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999

C/Accession: A49002

R/Stuber, F.; Lee, S.K.; Bridges Jr., S.L.; Koopman, W.J.; Schroeder, H.W.J.; Gaskin, F.;

Arthritis Rheum. 35, 900-904, 1992

A/Title: A rheumatoid factor from a normal individual encoded by VH2 and V kappa II gene

A/Reference number: A49002; MUID:92352481; PMID:1322670

A/Accession: A49002

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-124 <STU>

A/Cross-references: GB:M0808; NID:G185515; PIDN:AA52989.1; PID:G567176

A/Experimental source: EBV-transformed lymphoblastoid cell line SSH23

A/Note: sequence extracted from NCBI backbone (NCBIN:110261, NCBIP:110262)

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

F;15-99/Domain: immunoglobulin homology <IMM>

Query Match 57.1%; Score 488.5; DB 2; Length 124;

Best Local Similarity 88.6%; Pred. No. 2.9e-34;

Matches 93; Conservative 3; Mismatches 8; Indels 1; Gaps 1;

Qy 1 LTCFSGFSLITRGVGVDMWIRQPPGKALWIALIYWNDDKRYSPSLKSLRLTITKDTSKNQ 60

Db 20 LTCFSGFSLTSGVGWIRQPPGKALEWIALIYWNDDRRYSPSLKSLRLTITKDTSKNQ 79

Qy 61 VLTLTNTMDPVDATYYCAHHFFDSSGYY-PFDSWGQGLTVSVSS 104

Db 80 VLTLTNTMDPVDATYYCAHWTVDSSGYLGFQYWGQGLTVTVSS 124

RESULT 2

S31459

Ig gamma-1 chain - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999

C/Accession: S31459

R/Patri, S.; Nau, F.

submitted to the EMBL Data Library, December 1992

A/Reference number: S31459

A/Accession: S31459

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-472 <PAT>

A/Cross-references: EMBL:X69797

C/Superfamily: immunoglobulin C region; immunoglobulin homology

C/Keywords: immunoglobulin

F;277-346/Domain: immunoglobulin homology <IMM>

```
Query Match          56.1%; Score 480.5; DB 2; Length 472;
Best Local Similarity 59.4%; Pred. No. 5.9e-33;
Matches 95; Conservative 17; Mismatches 43; Indels 5; Gaps 2;

QY 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
37 VTCTISGFSL--NNYGVDMIRQPPGKALEWLGSGGYDEDIDYFVLKSLRLSIYKDTSKSQ 94
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 VVLTMTNMDPVDATATYCAHHFFDSS--GYPPDSMGQGTIVSVSSASTKGPSVRLPLAP 117
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
95 VSLTSLTMTTDTATYTCARVDVSSHAFAFAYASTDFWPGLLISVLASASTTPPKRVPLTS 154
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 118 CSRSTSESTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF 157
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
155 CCGDTSSIVTLGCLVSSYMPPEPVTVWNSGALTSGVHTF 194
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
A49444
IG gamma-1 heavy chain (New) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999
C;Accession: A49444
R;Saul, F.A.; Poljak, R.J.
Proteins 14, 363-371, 1992
A;Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A res
A;Reference number: A49444; MUID:93066153; PMID:1438175
A;Accession: A49444
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-220 <SAU>
A;Note: this sequence modified after extraction from NCBI backbone
A;Note: this sequence report includes corrections based on crystal structure refinement
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;137-202/Domain: immunoglobulin homology <IMM>

Query Match          55.4%; Score 474; DB 2; Length 220;
Best Local Similarity 57.4%; Pred. No. 9e-33;
Matches 93; Conservative 19; Mismatches 34; Indels 16; Gaps 3;

QY 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 55
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 LTCTVSGTSF-----DDYVTVWVRQPPGKLEWIGVFTGTTLLDPSLRGRVTMLVN 72
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 56 TSKNQVLTMTNMDPVDATATYCAHHFFDSSGYPPFDSMGQGTIVSVSSASTKGPSVRLPL 115
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
73 TSKNQFSLRSLSVTAADTAVYTCARNLIAGG-----IDWQGGSLVTVSSASTKGPSVRLPL 128
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 116 APCSRSTSESTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF 157
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
129 APSKSTSGGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF 170
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 4
S69131
IG heavy chain (DOT) - human (fragment)
N;Alternate names: anti-riboflavin IGG Fd fragment
C;Species: Homo sapiens (man)
C;Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C;Accession: S69131
R;Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A;Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A;Reference number: S69130; MUID:95255298; PMID:7737190
A;Accession: S69131
A;Molecule type: protein
A;Residues: 1-241 <STO>
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: blocked amino end; heterotrimer; immunoglobulin; pyroglutamic acid
F;1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAR>
F;140-205/Domain: immunoglobulin homology <IMM>
F;1/Modified site: pyroglutamic carboxylic acid (Gln) #status experimental
```

```
Query Match          52.6%; Score 450.5; DB 2; Length 241;
Best Local Similarity 57.3%; Pred. No. 9.4e-31;
Matches 90; Conservative 17; Mismatches 47; Indels 3; Gaps 2;

QY 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 ISCKASGYAF--ENYIHWVRQAPGLGLEWMGIFNPVAGAVSEKFRDLRLVMSDTSANT 77
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 VVLTMTNMDPVDATATYCAHHFFDSSGYPPFDSMGQGTIVSVSSASTKGPSVRLPLAPCSR 120
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
78 VSMQLRNLRSDDDTGRVFCARVSYDFS--QYGMVWVGQGTIVSVSSASTKGPSVRLPLAPCSR 136
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 STSESTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF 157
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
137 STSESTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF 173
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
S69339
IG heavy chain V region precursor - human
C;Species: Homo sapiens (man)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 01-Dec-2000
C;Accession: S69339; S72664
R;Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69339
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-374 <KHA>
A;Cross-references: EMBL:X81695
R;Khamilichi, A.A.
submitted to the EMBL Data Library, September 1994
A;Reference number: S72664
A;Accession: S72664
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-140, 'C', 142-374 <KH2>
A;Cross-references: EMBL:X81695
C;Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match          52.5%; Score 449.5; DB 2; Length 374;
Best Local Similarity 56.5%; Pred. No. 1.8e-30;
Matches 95; Conservative 13; Mismatches 35; Indels 25; Gaps 4;

QY 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALIIYWNDDKRYSPSLKSLRLTIYKDTSKNQ 60
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
39 LTCTFGSFLSKSGVGVDMIRQPPGQALEWLALIFWDDDKRYSPSLRLTIYKDTSKNQ 98
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 VVLTMTNMDPVDATATYCAHHFFDSSGY---YPPDSMGQGTIVSVSSASTK----- 108
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
99 VVLTMTNMDPADTATYYCG---YSVEGYGGYGRFHSWGQGTIVTSSEPSKCDKTHTCPP 155
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 109 -----GPSVRLAPCSRST--SESTAALGCLVKDYFPEPVTVSNW 146
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
156 CPABELLGGFSVFLFPKPKDTLMISETPEVTCVVVDVSHEDPEVKEN 203
   :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
S22080
IG heavy chain precursor (B/MT. 4A.17.H5.A5) - bovine
N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
C;Species: Bos primigenius taurus (cattle)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S22080; S06610; A31303
R;Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A;Reference number: S22080
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
```

```

RESULT 8
S31513
Ig heavy chain - human
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S31513
R;Chastagner, P.; Demaison, C.; Theze, J.; Zouali, M.
submitted to the EMBL Data Library, December 1992
A;Description: Dominance of clonotypic patterns and variable gene usage of anti-DNA auto
A;Reference number: S31509
A;Accession: S31513
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-138 <CHA>
A;Cross-references: EMBL:X69861; NID:G33084; PIDN:CAA49495.1; PID:G33085
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;30-114/Domain: immunoglobulin homology <IMM>

Query Match 50.6%; Score 433; DB 2; Length 138;
Best Local Similarity 80.6%; Pred. No. 1.5e-29;
Matches 83; Conservative 6; Mismatches 14; Indels 0; Gaps 0;

QY 1 LTCFSGFSLITRGVGDWIRQPGKALQWLALIYWDDKRYSPSLKSLRTITTKDTSKNQ 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 35 LTCFSGFSLSLTSRGVGVGWIRQPGKLTLEWALIYWDDDKRYSPSLKSLRTITTKDTSQN 94
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 VLVTMTNMDPVDATYYCAHHFPDSSGGYYPFDSWGQGLTVSVS 103
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 95 VLVTMTNMDPVDATYYCAHHPGIAVTGNGFDYWGQGLTVTVS 137
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 9
S18555
Ig heavy chain V region precursor (VII-5) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 13-Jan-1995 #sequence_revision 06-Jun-1997 #text_change 21-Jul-2000
C:Accession: S18555
R;Shin, E.K.; Matsuda, F.; Nagaoka, H.; Fukita, Y.; Imai, T.; Yokoyama, K.; Soeda, E.; H
EMBO J. 10, 3641-3645, 1991
A;Title: Physical map of the 3' region of the human immunoglobulin heavy chain locus: cl
A;Reference number: S18551; MUID:92037524; PMID:1935893
A;Accession: S18555
A;Molecule type: DNA
A;Residues: 1-119 <SHI>
A;Cross-references: EMBL:X62111; NID:G37839; PIDN:CAA44021.1; PID:G3980125
C;Genetics:
A;introns: 16/1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-119/Product: Ig heavy chain V region (VII-5) #status predicted <MAT>
F;34-118/Domain: immunoglobulin homology <IMM>

Query Match 48.0%; Score 411; DB 2; Length 119;
Best Local Similarity 95.0%; Pred. No. 9.1e-28;
Matches 76; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 LTCFSGFSLITRGVGDWIRQPGKALQWLALIYWDDKRYSPSLKSLRTITTKDTSKNQ 60
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 39 LTCFSGFSLSLTSRGVGVGWIRQPGKALEWALIYWDDDKRYSPSLKSLRTITTKDTSKNQ 98
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 VLVTMTNMDPVDATYYCAH 80
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 99 VLVTMTNMDPVDATYYCAH 118
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 10
S68211
Ig heavy chain (Mab13-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000

```

```
C;Accession: S68211
C;/rakagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A;Reference number: S68211; MUID:96085223; PMID:7498516
A;Accession: S68211
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-220 <TK>
A;Cross-references: EMBL:D29669; NID:g473958; PIDN:BAA06140.1; PID:g473959
A;Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequence
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;136-200/Domain: immunoglobulin homology <IMM>
```

Query Match	48.0%; Score 410.5; DB 2; Length 220;
Best Local Similarity	51.2%; Pred. No. 2e-27;
Matches	82; Conservative 22; Mismatches 47; Indels 9; Gaps 3;

```
Qy      1  LTCFSGFSILTRGVGDWIRQPCKALQWLALIYWNDDK---RYSPLKSRLTITIKDTS 57
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|
Db     16  LSLCTSGETF--SNRYMHWRQLPPGKRLEIAVITVKSDNYGAKYAESVRGRFTISRDDS 73
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|

Qy     58  KNQVVLTMVNMDPVDATYTYCAHHFPDSSGGYPYPPDSNGCGTLVSVSASTKGPSVFPLAP 117
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|
Db     74  KSVYLQMNRLREEDATYYCCR-----TPWYAMDCWGQGTSLIVSSAKTTPPSVYFLAP 129
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|

Qy    118  CSRSTSESTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTF 157
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|
Db    130  GSAAQTNSMYTLGLCLVKGYFPEPVTVTWNSGSLSSGVHTF 169
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|
```

RESULT 11

PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)

C;Species: Mus musculus (house mouse)
C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C;Accession: PC4436

A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A;Reference number: JC5810; MUID:98063277; PMID:9398605
A;Accession: PC4436
A;Molecule type: protein
A;Residues: 1-444 <AKA>
C;Comment: This catalytic antibody has peroxidase oxidase activity. It is directed again
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;251-320/Domain: immunoglobulin homology <IMM>
F;22/Disulfide bonds: interchain (to 98) #status predicted
F;99/Disulfide bonds: interchain (to 109) #status predicted

Query Match	48.0%; Score 410.5; DB 2; Length 444;
Best Local Similarity	51.2%; Pred. No. 4.2e-27;
Matches	82; Conservative 22; Mismatches 47; Indels 9; Gaps 3;

```
Qy      1  LTCFSGFSILTRGVGDWIRQPCKALQWLALIYWNDDK---RYSPLKSRLTITIKDTS 57
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|
Db     20  LSLCTSGETF--SNRYMHWRQLPPGKRLEIAVITVKSDNYGAKYAESVRGRFTISRDDS 77
       :|::|||:::|||||:~::~|::|::|::|::|::|::|::|::|::|::|

Qy     58  KNQVVLTMVNMDPVDATYTYCAHHFPDSSGGYPYPPDSNGCGTLVSVSASTKGPSVFPLAP 117
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|
Db     78  KSVYLQMNRLREEDATYYCCR-----TPWYAMDCWGQGTSLIVSSAKTTPPSVYFLAP 133
       :|::|||:::|||||:~::~|::|::|::|::|::|::|::|::|::|::|

Qy    118  CSRSTSESTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTF 157
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|
Db    134  GSAAQTNSMYTLGLCLVKGYFPEPVTVTWNSGSLSSGVHTF 173
       :|::|||:::|||||:|::|::|::|::|::|::|::|::|::|::|::|::|
```

RESULT 12

G1HUHE
Ig heavy chain V-II region (He) - human

C;Species: Homo sapiens (man)
C;Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 09-Jul-2004
C;Accession: A02093

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GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 59.3785 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-39
Perfect score: 856
Sequence: 1 LTCFSGSLITRGVGDWI.....PVTVMNSGALTSQVHTFQL 159

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	518	60.5	476	2 Q6GMX1	Q6gm1 homo sapien
2	516	60.3	476	2 Q6MZK7	Q6mzx7 homo sapien
3	513.5	60.0	465	2 Q6GMX6	Q6gm6 homo sapien
4	506.5	59.2	473	2 Q8TC63	Q8tc63 homo sapien
5	496	57.9	493	2 Q68CN4	Q68cn4 homo sapien
6	494.5	57.8	473	2 Q6P055	Q6p055 homo sapien
7	493.5	57.7	544	2 Q6PJ95	Q6pj95 homo sapien
8	493	57.6	417	2 Q6N093	Q6n093 homo sapien
9	489	57.1	472	2 Q6N089	Q6n089 homo sapien
10	484	56.5	470	2 Q6PJ44	Q6pja4 homo sapien
11	482	56.3	464	2 Q6MZU6	Q6mzu6 homo sapien
12	476	55.6	482	2 Q7Z351	Q7z351 homo sapien
13	474	55.4	480	2 Q6N094	Q6n094 homo sapien
14	471.5	55.1	465	2 Q6P6C4	Q6p6c4 homo sapien
15	471	55.0	466	2 Q6IN78	Q6in78 homo sapien
16	470	54.9	478	2 Q6PI81	Q6pi81 homo sapien
17	466	54.4	521	2 Q8N4Y9	Q8n4y9 homo sapien
18	465.5	54.4	473	2 Q6MZV7	Q6mzv7 homo sapien
19	463.5	54.1	475	2 Q6MZQ6	Q6mqz6 homo sapien
20	458.5	53.6	518	2 Q6N030	Q6n030 homo sapien
21	454.5	53.1	475	2 Q6N095	Q6n095 homo sapien
22	452	52.8	466	2 Q6N096	Q6n096 homo sapien
23	452	52.8	470	2 Q7Z5W1	Q7z5w1 homo sapien
24	450.5	52.6	481	2 Q6N097	Q6n097 homo sapien
25	440.5	51.5	469	2 Q7Z7P5	Q7z7p5 homo sapien
26	436.5	51.0	208	2 Q6ZP87	Q6zpb7 homo sapien
27	434	50.7	121	2 Q9UL96	Q9ul96 homo sapien
28	433.5	50.6	475	2 Q6GMW7	Q6gmw7 homo sapien
29	431	50.4	480	2 Q6PJ21	Q6pji1 homo sapien
30	409.5	47.8	471	2 Q66K04	Q66k04 mus musculus
31	393	45.9	121	1 HV2E_HUMAN	P01818 homo sapien

32	388.5	45.4	465	2	Q6PJB2	Q6pjb2 mus musculus
33	388	45.3	125	1	HV2D_HUMAN	P01817 homo sapien
34	385	45.0	458	2	Q65ZQ1	Q65zq1 homo sapien
35	383	44.7	464	2	Q6PIP8	Q6pip8 mus musculus
36	379.5	44.3	463	2	Q99LC4	Q99lc4 mus musculus
37	376	43.9	492	2	Q7Z374	Q7z374 homo sapien
38	375.5	43.9	473	2	Q91Z05	Q91z05 mus musculus
39	370	43.2	470	2	Q7TMK1	Q7tmk1 mus musculus
40	370	43.2	605	2	Q6GN83	Q6gn83 xenopus lae
41	368	43.0	472	2	Q6PJA7	Q6pja7 mus musculus
42	364.5	42.6	496	2	Q96KX8	Q96kx8 homo sapien
43	356	41.6	473	2	Q9D8L4	Q9d8l4 mus musculus
44	355	41.5	585	2	Q6GPX4	Q6gpx4 xenopus lae
45	351	41.0	484	2	Q6PF95	Q6pf95 mus musculus

ALIGNMENTS

RESULT 1
Q6GMX1 PRELIMINARY; PRT; 476 AA.
AC Q6GMX1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalka U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073773; AAH73773.1; -;
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig ci.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.

RESULT 4

```
Q8TC63 ID Q8TC63 PRELIMINARY; PRT; 473 AA.
AC Q8TC63
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG4 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heide F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalski A., Smalhus D.B., Schnerch A., Schein J.B.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC025985; AA025985.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00196; COPPER_BLUE; UNKNOWN_1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
```

```
Query Match 59.2%; Score 506.5; DB 2; Length 473;
Best Local Similarity 63.3%; Pred. No. 5.6e-41;
Matches 100; Conservative 17; Mismatches 36; Indels 5; Gaps 2;

Qy 1 LTCTFGSLITRGVGVDTATYTC-CAHFFDSSGYPFDSWGQGLVSVSSASTKGPSVPLAPCS 60
Db 46 LTCTVSGDSVASSSYNGWVRQPPKGLGIGTINFGNMYSPSLRSRVMTSDMSNS 105
Qy 61 VLMTMTNMDPVDATYTC-AHFFDSSGYPFDSWGQGLVSVSSASTKGPSVPLAPCS 119
Db 106 FYLKLDVTAADTAVYCAAGHVMGFAH----WGQGLVSVSPASTKGPSVPLAPCS 161
Qy 120 RSTSESTAALGCLVKDYFPEPTVSMNSGALTSVHTF 157
Db 162 RSTSESTAALGCLVKDYFPEPTVSMNSGALTSVHTF 199
```

RESULT 5

```
Q68CN4 ID Q68CN4 PRELIMINARY; PRT; 493 AA.
AC Q68CN4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp686E23209 (Fragment).
GN Name=DKFZp686E23209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Rectum tumor;
RG The German cDNA Consortium;
RA Bloeker H., Boecker M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749861; CAH18705.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DR KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 493 AA; 54117 MW; A1E4F5ED3FABAB40 CRC64;
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Query Match 57.9%; Score 496; DB 2; Length 493;
Best Local Similarity 60.9%; Pred. No. 6.3e-40;
Matches 98; Conservative 17; Mismatches 40; Indels 6; Gaps 3;

Qy 1 LTCTFGSLITRGVGVDTATYTC-CAHFFDSSGYPFDSWGQGLVSVSSASTKGPSVPLA 59
Db 62 LSCAAGFDFT--YAMHWVRQSPRLVAVISYEGGKHQVADSVKGRATIRDSNKK 119
Qy 60 QVVLMTNMDPVDATYTC-CAHFFDSSGYPFDSWGQGLVSVSSASTKGPSVPLA 116
Db 120 TVSLQLSLSTEDTGVVYCCARDPLPLSSWHTNVALDVWGQGTAVIVSSASTKGPSVPLA 179
Qy 117 PCSRSTSESTAALGCLVKDYFPEPTVSMNSGALTSVHTF 157
Db 180 PCSRSTSESTAALGCLVKDYFPEPTVSMNSGALTSVHTF 220
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RESULT 6

```
Q6P055 ID Q6P055 PRELIMINARY; PRT; 473 AA.
AC Q6P055
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
```

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettanan M., Madan A.C., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeslee R., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
RL EMBL: BC019046; AAH19046.1; -;
DR HSSP; P01861; 1AQQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
DW Hypothetical protein.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;

[illegible]

RESULT	8
Q6N093	
ID	Q6N093
AC	PRELIMINARY;
PRT	417 AA.
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	HYPOTHETICAL protein DKFZp68104196 (Pragmat).
GN	Name=DKFZp68104196;
OS	homo sapiens (Human);
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
NCBI_TaxID	=9606;
[1]	SEQUENCE FROM N.A.
RN	RP
RC	TISSUE=Human esophagus tumor;
RG	The German Human cDNA Consortium;

RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640623; CAB45777.1; -;
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;

Query Match 57.6%; Score 493; DB 2; Length 417;
 Best Local Similarity 57.9%; Pred. NO. 1e-39;
 Matches 95; Conservative 15; Mismatches 26; Indels 4; Gaps 2;

QY 19 WIRPPGKALQWLALI-YWDDKRYSPSLKSLRLTITKDTSKNOVLTNNMDPVDVTATYY 77
 Db 8 WVRQAPGKLEWAVIAIYDGTQYADSVRGFTVSRDNSANTLFLEMLSRPDTAVYY 67
 QY 78 CAHFFDSSGGYVPFDSQGLVSVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYF 137
 Db 68 CAK---AHSGTSKDPWQGGTLVTVSSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYF 124

QY 138 PEPVTVSNMGALTSQGVHTF 157
 Db 125 PEPVTVSNMGALTSQGVHTF 144

RESULT 9

Q6N089 PRELIMINARY; PRT; 472 AA.
 ID Q6N089
 AC Q6N089
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686P15220.
 GN Name=DKFZp686P15220;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human rectum tumor;
 RG The German Human CDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640627; CAB45781.1; -;
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 57.1%; Score 489; DB 2; Length 472;
 Best Local Similarity 59.5%; Pred. No. 2.9e-39;
 Matches 97; Conservative 18; Mismatches 36; Indels 12; Gaps 4;
 QY 1 LTRFSGSLITRGVGVWDWIRQPPGKALQWLALYWNDDK-RYSPSLKSLRLTITKDTSKN 59
 Db 39 LSCAASGFTF--DDYAHWHVROAPGKLEWVSGISWNSGSYAYADSVKGRFTISRDGNK 96
 QY 60 QVLTMTNMDPVDVTATYYC-----AHFFDSSGGYVPFDSQGLVSVSSASTKGPSVFP 114
 Db 97 SLYLQWNSLRAEDTALYVCAKEIGHNFY----YGMVDVWQGGTLVTVSSASTKGPSVFP 152
 QY 115 LAPCSRSTSESTAALGCLVKDYFPPEPVTVSNMGALTSQGVHTF 157
 Db 153 LAPSSKSTSGGTAALGCLVKDYFPPEPVTVSNMGALTSQGVHTF 195

RESULT 10

Q6PJN4 PRELIMINARY; PRT; 470 AA.
 ID Q6PJN4
 AC Q6PJN4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uscdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalusi U., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC018747; AAH18747.1; -;
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig.cl.
 DR InterPro; IPR003006; Ig.MHC.
 DR InterPro; IPR003596; Ig.v.
 DR Pfam; PF07654; Cl-set; 3.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; IGC1; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 KW Hypothetical protein.
 SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; PDDB9348ADC37E6D CRC64;

Query Match 55.1%; Score 471.5; DB 2; Length 465;
Best Local Similarity 60.8%; Pred. No. 1.5e-37;
Matches 96; Conservative 16; Mismatches 41; Indels 5; Gaps 3

QY 1 LCTFSGFSLLTRGVGVYDWIRQPPGKALQWLALIVYNDKKEYS-PSLKSRLTITKDTSGN 59
DB 39 LSCAASGF--FFSEYWMWVRQAPGKLEWVANIKDDGSATYHLDSVGRFTISRDNARN 96
QY 60 QVVLVTMTNPDVDTATYCAHFHFDSSGGYYPFDSSWGQGLTVSVSSASTKGPSVFFPLAPCS 119
DB 97 TLYLQNSLRVEDTAMTYCAREIPGRCFYDF--WGHTLTVSVSSASTKGPSVFFPLAPCS 154
QY 120 RSTSESTAALGCLVKDYFPPEPVTVMNSGALTSGVHTF 157
DB 155 RSTSESTAALGCLVKDYFPPEPVTVMNSGALTSGVHTF 192

RESULT 15
Q6IN78 PRELIMINARY; PRT; 466 AA.
ID AC Q6IN78
AC Q6IN78
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX MEDLINE=223388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.C., Rubin G.M., Hong L.,
RA Sapotnick M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards D., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Schmutz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RL [2]
RS SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC072419; AAH72419.1; -;
RL HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.

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DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGc1; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDEB1076E CRC64;

Query Match 55.0%; Score 471; DB 2; Length 466;
Best Local Similarity 59.1%; Pred. No. 1.6e-37;
Matches 94; Conservative 20; Mismatches 35; Indels 10; Gaps 3;

Qy 1 LTCFTSGFSLITRGVGVWDIRQPPGKALQWLALIYWDDKRYSPSLKSLRLTITKDTSKNQ 60
   ||||| : : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| : |||||
Db 39 LSCAASGLTVSSN--YMHVVRQAPGKGLEWVSVLYIGGATYYADSVKGRFTISRDNKNT 96

Qy 61 VVLTMTNMDPVDATYYCAHHFFDSSGVY--PFDSWGQGTIVSVSSASTKGPSVFPLAPC 118
   : || : || : || : || : || : || : || : || : || : || : || : || : ||
Db 97 LYLQMNLSRAEDTAVYYCAR-----GNYVVPAPWGQGTIVTVSSASTKGPSVFPLAPS 150

Qy 119 SRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTF 157
   : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 151 SKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTF 189
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Search completed: March 8, 2005, 06:35:57
Job time : 60.3785 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 73.7167 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-39
Perfect score: 856
Sequence: 1 LTCTFSGFSLITRGVDWI.....PVTVWNSGALTSCVHTFQL 159

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	856	100.0	159	2	Aay34307 Igg antib
2	766	89.5	149	2	Aay34305 Igg antib
3	700.5	81.8	517	6	Abu08019 Monoclonal
4	700.5	81.8	518	7	Adf65782 Human ant
5	700.5	81.8	518	8	Adj92518 Human SOJ
6	678.5	79.3	448	8	Adf71916 Hu3G8VH-2
7	670	78.3	453	6	Abp58287 Humanised
8	670	78.3	472	6	Abp58289 Humanised
9	664.5	77.6	448	8	Adf71908 Hu3G8VH-1
10	664.5	77.6	448	8	Adf71912 Hu3G8VH-5
11	664	77.6	228	7	Adj32130 Human int
12	644.5	75.3	450	5	Abp66596 Human RSV
13	644.5	75.3	450	5	Abp66594 Human RSV
14	644.5	75.3	450	5	Abp66598 Human RSV
15	644.5	75.3	450	5	Abp66564 Human RSV
16	644.5	75.3	450	5	Abp66592 Human RSV
17	644.5	75.3	450	5	Abp66600 Human RSV
18	644.5	75.3	450	6	Abu69427 Respirato
19	644.5	75.3	450	6	Abu69455 Respirato
20	644.5	75.3	450	6	Abu69459 Respirato
21	644.5	75.3	450	6	Abu69457 Respirato
22	644.5	75.3	450	6	Abu69463 Respirato
23	644.5	75.3	450	6	Abu69461 Respirato
24	644.5	75.3	450	7	Ade35952 SYNAGIS a
25	644.5	75.3	450	7	Ade35956 SYNAGIS a

26	644.5	75.3	450	7	Ade35958	SYNAGIS a
27	644.5	75.3	450	7	Ade35954	SYNAGIS a
28	644.5	75.3	450	7	Ade35922	SYNAGIS a
29	644.5	75.3	450	7	Ade35950	SYNAGIS a
30	643.5	75.2	450	5	Abp66562	Human RSV
31	643.5	75.2	450	6	Abu69425	Respirato
32	643.5	75.2	450	7	Ade35920	SYNAGIS a
33	641.5	74.9	434	7	Ade35960	SYNAGIS a
34	641.5	74.9	450	5	Abp66590	Human RSV
35	641.5	74.9	450	5	Abp66588	Human RSV
36	641.5	74.9	450	5	Abp66602	Human RSV
37	641.5	74.9	450	5	Abp66586	Human RSV
38	641.5	74.9	450	6	Abu69451	Respirato
39	641.5	74.9	450	6	Abu69453	Respirato
40	641.5	74.9	450	6	Abu69465	Respirato
41	641.5	74.9	450	6	Abu69449	Respirato
42	641.5	74.9	450	7	Ade35948	SYNAGIS a
43	641.5	74.9	450	7	Ade35946	SYNAGIS a
44	641.5	74.9	450	7	Ade35944	SYNAGIS a
45	640.5	74.8	450	4	AAE10517	Humanised

ALIGNMENTS

RESULT 1
AAY34307
ID AAY34307 standard; protein; 159 AA.
XX
AC AAY34307;
XX
DT 19-NOV-1999 (first entry)
XX
DE Igg antibody 2.3.2 heavy chain sequence.
XX
KW Antibody: CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
PN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034507.
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
DR WPI; 1999-540816/45.
XX
N-PSDB; AAZ20408.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 60; Fig 32; 245pp; English.
XX
CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the Igm MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
XX (e.g. lupus), and inflammatory diseases (e.g. arthritis)
SQ Sequence 159 AA;
Query Match 100.0%; Score 856; DB 2; Length 159;
Best Local Similarity 100.0%; Pred. No. 5.1e-70;
Matches 159; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LTCTFSGSLITRGVGVDMIRQPPGKALQWLALYWNDDKRYSPSLKSLRITITKDTSKNQ 60
Db 1 LTCTFSGSLITRGVGVDMIRQPPGKALQWLALYWNDDKRYSPSLKSLRITITKDTSKNQ 60
Qy 61 VVLTMTNMDPVDATYTCYCAHHFFDSSGYYPFDSWGQGTLSVSSASTKGPSVFLAPCSR 120
Db 61 VVLTMTNMDPVDATYTCYCAHHFFDSSGYYPFDSWGQGTLSVSSASTKGPSVFLAPCSR 120
Qy 121 STSESTAALGCLVKDYFPEPVTWNSGALTSVHTFQL 159
Db 121 STSESTAALGCLVKDYFPEPVTWNSGALTSVHTFQL 159
RESULT 2
AAV34305
ID AAV34305 standard; protein; 149 AA.
XX
AC AAV34305;
XX
DT 19-NOV-1999 (first entry)
XX
DE Igg antibody 2.4.4 heavy chain sequence.
XX
KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
PN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RP, Yang X;
XX
DR WPI; 1999-540816/45.
DR N-PSDB; AAZ20406.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancers, autoimmune diseases and inflammatory diseases.
XX
PS Claim 60; Fig 30; 245pp; English.
XX
CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (Mab) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IGM Mab ABX-CBL, providing that the antibody is not CBL1. The Mab
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood
CC (e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC (e.g. lupus), and inflammatory diseases (e.g. arthritis)

SQ Sequence 149 AA;
Query Match 89.5%; Score 766; DB 2; Length 149;
Best Local Similarity 100.0%; Pred. No. 7.6e-62;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LTCTFSGSLITRGVGVDMIRQPPGKALQWLALYWNDDKRYSPSLKSLRITITKDTSKNQ 60
Db 8 LTCTFSGSLITRGVGVDMIRQPPGKALQWLALYWNDDKRYSPSLKSLRITITKDTSKNQ 67
Qy 61 VVLTMTNMDPVDATYTCYCAHHFFDSSGYYPFDSWGQGTLSVSSASTKGPSVFLAPCSR 120
Db 68 VVLTMTNMDPVDATYTCYCAHHFFDSSGYYPFDSWGQGTLSVSSASTKGPSVFLAPCSR 127
Qy 121 STSESTAALGCLVKDYFPEPVT 142
Db 128 STSESTAALGCLVKDYFPEPVT 149
RESULT 3
ABU08019
ID ABU08019 standard; protein; 517 AA.
XX
AC ABU08019;
XX
DT 10-MAY-2003 (first entry)
XX
DE Monoclonal rabies virus antibody heavy chain, clone JB.1.
XX
KW Human; antibody; constant region; monoclonal antibody 57; Mab 57;
KW variable region; Rabies; neurological disease; infection;
KW central nervous system; rabies virus; Lyssavirus; Rhabdoviridae;
KW pathogen; vaccine; virucide; heavy chain.
XX
OS Homo sapiens.
XX
PN WO2003016501-A2.
XX
PD 27-FEB-2003.
XX
PF 21-AUG-2002; 2002WO-US026584.
XX
PR 21-AUG-2001; 2001US-0314023P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Hooper DC, Dietzschold B;
XX
DR WPI; 2003-278566/27.
DR N-PSDB; ABX12861.
XX
PT New recombinant antibody comprising a constant region of Mab 57 linked to
PT a non-Mab 57 variable region, useful for treating an individual exposed
PT to a pathogen, e.g. rabies infection.
XX
PS Claim 1; Page 35; 38pp; English.
XX
CC The invention discloses a recombinant antibody comprising a constant
CC region of monoclonal antibody (Mab) 57 linked to a non-Mab 57 variable
CC region. Rabies is an acute, neurological disease caused by infection of
CC the central nervous system with the rabies virus, a member of the
CC Lyssavirus genus of the family Rhabdoviridae. Also disclosed are methods
CC for producing an isolated recombinant antibody by culturing a host cell,
CC containing a recombinant expression vector comprising the nucleic acid
CC molecule encoding the antibody, and isolating the recombinant antibody
CC expressed and treating an individual exposed to a pathogen by
CC administering to the individual the recombinant antibody. The recombinant
CC antibodies are useful for preventing (vaccine) and treating an individual
CC exposed to a pathogen, e.g. rabies infection. They are also useful for
CC the qualitative and quantitative determination of the rabies virus. The
CC sequences presented are the antibody protein fragments, the nucleic acids
CC encoding them or the PCR primers used to construct the recombinant
CC expression vector

XX SQ Sequence 517 AA;
Query Match 81.8%; Score 700.5; DB 6; Length 517;
Best Local Similarity 84.2%; Pred. No. 3e-55;
Matches 133; Conservative 9; Mismatches 13; Indels 3; Gaps 2;
Qy 1 LTCFSGSLTRGVGVWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 39 LTCFSGFSLSTSGVGWIRQPGKALEWVTLIYWDKRYSPSLENRVIRKDTSKNQ 98
Qy 61 VLTWNTNDPVDATYYCAHFFDSSGYYP-FDSWGQGLTVSVSSASTKGPSVFLAPCS 119
Db 99 VALTMTNDPDLDTGTYTCAHROHISS--FPWFDSWGQGLTVSVSSASTKGPSVFLAPCS 156
Qy 120 RSTSESTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF 157
Db 157 RSTSGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF 194
RESULT 4
ADP65782
ID ADP65782 standard; protein; 518 AA.
XX AC ADP65782;
XX DT 12-FEB-2004 (first entry)
XX DE Human anti-rabies MAb JB.1 antibody heavy chain.
XX KW Immunoglobulin; Ig; heavy chain; light chain; human;
XX KW monoclonal rabies virus neutralising antibody; rabies virus protein;
XX KW neuronal tissue; antirabies; MAb JB.1.
XX OS Homo sapiens.
XX PN US2003157112-A1.
XX PD 21-AUG-2003.
XX PF 21-AUG-2002; 2002US-00225108.
XX PR 16-MAY-2000; 2000US-0204518P.
XX PR 04-MAY-2001; 2001US-00848832.
XX PR 21-AUG-2001; 2001US-0314023P.
XX PA (HOOP/) HOOPER D C.
XX PA (DIET/) DIETZSCHOLD B.
XX PI Hooper DC, Dietzschold B;
XX DR WPI; 2003-777974/73.
XX DR N-PSDB; ADP65781.
XX PT New isolated nucleic acid molecule encoding a sequence that neutralizes
XX PT an antibody that binds to rabies virus protein, useful for diagnosing,
XX PT preventing or treating infection of pathogens that target neuronal
XX PT tissues, e.g. rabies.
XX PS Claim 2; SEQ ID NO 10; 22pp; English.
XX CC The present invention relates to the isolation of immunoglobulin (Ig)
XX CC heavy and light chains of human monoclonal rabies virus neutralising
XX CC antibody, and the polynucleotide sequences encoding them. The antibody
XX CC specifically binds to a rabies virus protein. Also disclosed is a fused
XX CC gene encoding a chimeric immunoglobulin light or heavy chain comprising a
XX CC first DNA sequence encoding an immunoglobulin light or heavy chain
XX CC variable region of a monoclonal rabies virus neutralising antibody
XX CC produced by a heterohybridoma cell line and a second DNA sequence
XX CC encoding a human light or heavy chain constant region, and methods of
XX CC producing a recombinant antibody. The polynucleotide sequences,
XX CC antibodies and methods are useful for diagnosing, preventing or treating
XX CC an infection of pathogens that target neuronal tissues, particularly

CC rabies. The present sequence represents human anti-rabies MAb JB.1
CC antibody heavy chain.
XX SQ Sequence 518 AA;
Query Match 81.8%; Score 700.5; DB 7; Length 518;
Best Local Similarity 84.2%; Pred. No. 3e-55;
Matches 133; Conservative 9; Mismatches 13; Indels 3; Gaps 2;
Qy 1 LTCFSGFSLTRGVGVWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 39 LTCFSGFSLSTSGVGWIRQPGKALEWVTLIYWDKRYSPSLENRVIRKDTSKNQ 98
Qy 61 VLTWNTNDPVDATYYCAHFFDSSGYYP-FDSWGQGLTVSVSSASTKGPSVFLAPCS 119
Db 99 VALTMTNDPDLDTGTYTCAHROHISS--FPWFDSWGQGLTVSVSSASTKGPSVFLAPCS 156
Qy 120 RSTSESTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF 157
Db 157 RSTSGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF 194
RESULT 5
ADJ92518
ID ADJ92518 standard; protein; 518 AA.
XX AC ADJ92518;
XX DT 06-MAY-2004 (first entry)
XX DE Human SOJB monoclonal antibody heavy chain protein.
XX KW Rabies virus infection; pharmaceutical; vaccine; gene therapy; virucide;
XX KW human; SOJB monoclonal antibody.
XX OS Homo sapiens.
XX PN US2004013672-A1.
XX PD 22-JAN-2004.
XX PF 13-JUN-2003; 2003US-00461148.
XX PR 16-MAY-2000; 2000US-0204518P.
XX PR 04-MAY-2001; 2001US-00848832.
XX PR 21-AUG-2001; 2001US-0314023P.
XX PR 21-AUG-2002; 2002US-00225108.
XX PA (UYJE-) UNIV JEFFERSON THOMAS.
XX PI Hooper DC, Dietzschold B;
XX DR WPI; 2004-108190/11.
XX DR N-PSDB; ADJ92517.
XX PT New pharmaceutical composition comprising at least two recombinant rabies
XX PT virus-neutralizing human antibodies, useful for treating or preventing
XX PT rabies virus infection.
XX PS Claim 1; SEQ ID NO 4; 28pp; English.
XX CC The present invention relates to a method of treating or preventing a
XX CC rabies virus infection in a subject. The invention also relates to novel
XX CC pharmaceutical composition comprising a carrier and at least two
XX CC recombinant rabies virus-neutralising human antibodies, where the
XX CC antibody comprises an antibody comprising an antibody light chain or its
XX CC homologue and an antibody heavy chain or its homologue. The
XX CC pharmaceutical composition is useful for treating or preventing rabies
XX CC virus infection. The invention is also useful as vaccine and in gene
XX CC therapy. The pharmaceutical composition is useful for treating or
XX CC preventing rabies virus infection. The present sequence is rabies virus-
XX CC neutralising human SOJB monoclonal antibody heavy chain protein used in
XX CC the invention.

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XX SQ Sequence 518 AA;
Query Match      81.8%; Score 700.5; DB 8; Length 518;
Best Local Similarity 84.2%; Pred. No. 3e-55;
Matches 133; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

Qy 1 LCTCFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 60
Db 39 LCTCFSGSLSTSGVGVWIRQPPGKALEWTLIYWNDDKRYSPSLKSLRVTIRKDTSKNQ 98
Qy 61 VVLTMNMDPVDATYYCAHHFFDSSGYYP-FDSWGQGTLYVSSASTKGPSVFPPLAPCS 119
Db 99 VALTMNMDPLDTGYTCAHRQHISS--FPWFDSWGQGTLYVSSASTKGPSVFPPLAPCS 156
Qy 120 RSTSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTF 157
Db 157 RSTSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTF 194

RESULT 6
ADF71916
ID ADF71916 standard; protein; 448 AA.
XX AC ADF71916;
XX DT 26-FEB-2004 (first entry)
XX DE HuJG8VH-22G1Ag amino acid sequence SEQ ID NO:115.
XX KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX OS Synthetic.
XX OS Mus sp.
XX OS Homo sapiens.
XX PN WO2003101485-A1.
XX PD 11-DEC-2003.
XX PF 29-MAY-2003; 2003MO-US017111.
XX PR 30-MAY-2002; 2002US-0384689P.
XX PR 10-JAN-2003; 2003US-0439320P.
XX PA (MACR-) MACROGENICS INC.
XX PI Johnson LS, Huang L, Li H, Tuailon N;
XX WI; 2004-042985/04.
XX PT Novel anti-CD16A antibody comprising complementarity determining regions
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
PT lacks effector function, useful for treating deleterious immune response.
XX PS Disclosure; SEQ ID NO 115; 103pp; English.
XX CC The present invention describes an anti-CD16A antibody (I) comprising a
CC VH domain comprising complementarity determining regions (CDRs) derived
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A

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CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an FC region derived from a human IgG heavy chain, where the FC region
CC lacks effector function or is modified to reduce binding to an FC
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
CC utropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIG) therapy e.g., allergic asthma. The present sequence
CC is used in the exemplification of the present invention.
XX SQ Sequence 448 AA;

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Query Match      79.3%; Score 678.5; DB 8; Length 448;
Best Local Similarity 83.4%; Pred. No. 2.6e-53;
Matches 131; Conservative 9; Mismatches 12; Indels 5; Gaps 2;

Qy 1 LCTCFSGSLITRGVGVWIRQPPGKALQWLALYWNDDKRYSPSLKSLRTITKDTSKNQ 60
Db 20 LCTCFSGSLSTSGVGVWIRQPPGKALEWTLIYWNDDKRYSPSLKSLRTISKDTSKNQ 79
Qy 61 VVLTMNMDPVDATYYCAHHFFDSSGYYPFDSWGQGTLYVSSASTKGPSVFPPLAPCSR 120
Db 80 VVLTMNMDPVDATYYCAR---INPAYFAY--WGQGTLYVSSASTKGPSVFPPLAPSK 134
Qy 121 STSESTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTF 157
Db 135 STSGGTAALGCLVKDYFPEPTVTVSWNSGALTSGVHTF 171

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RESULT 7
ABP58287
ID ABP58287 standard; protein; 453 AA.
XX AC ABP58287;
XX DT 23-OCT-2003 (revised)
XX DT 31-MAR-2003 (first entry)
XX DE Humanised 10D5 antibody heavy chain.
XX KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Chimeric.
XX PH Key Location/Qualifiers
XX FT Region 1..123
XX FT /note= "light chain variable region"
XX FT Region 31..135
XX FT /note= "CDR1"
XX FT Region 52..167
XX FT /note= "CDR2"
XX FT Region 100..112
XX FT /note= "CDR3"
XX PN WO200288307-A2.
XX

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PD 07-NOV-2002.
XX
PF 26-APR-2002; 2002WO-US011854.
XX
PR 30-APR-2001; 2001US-0287653P.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Hinton PR, Vasquez M;
XX
DR WPI; 2003-183836/18.
XX
PT New humanized 10D5 antibody, useful for the manufacture of a medicament
PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
PT disease or cerebral amyloid angiopathy.
XX
PS Claim 5; Page 10-12; 52pp; English.
XX
CC The present sequence is the protein sequence of the heavy chain of a
CC humanised antibody of the present invention. In the variable portion, the
CC complementarity determining regions (CDRs) originate from murine
CC monoclonal antibody 10D5 and the framework region originates from human
CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
CC of the invention have CDRs from 10D5 and human framework sequences. These
CC humanised antibodies have binding affinities (affinity and epitope
CC location) approximately the same as those of the mouse 10D5 antibody. The
CC invention includes antibodies, single chain antibodies, and their
CC fragments, as well as nucleotide sequences, vectors, transformed host
CC cells, and methods of using the humanised antibody to treat, prevent,
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 453 AA;

Query Match 78.3%; Score 670; DB 6; Length 453;
Best Local Similarity 81.5%; Pred. No. 1.6e-52;
Matches 128; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 1 LTCTFGSFLITRGVGDWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKTSKQ 60
DB 20 LTCTFGSFLSTSGMGVSWIRQPPGKALEWLAHLYWDDDKRYNPSLSKSLRLTISKDTSKSQ 79
QY 61 VLTLTNTNMDPVDATYTCVRRPITPVLVDANDYWGQGLTVTVSSASTKGPSVFLAPCSR 120
DB 80 VLTLTNTNMDPVDATYTCVRRPITPVLVDANDYWGQGLTVTVSSASTKGPSVFLAPCSR 139
QY 121 STSESTAALGCLVKDYPPPEPTVTVSWNSGALTSGVHTF 157
DB 140 STSGTAAALGCLVKDYPPPEPTVTVSWNSGALTSGVHTF 176

RESULT 8
ABP58289
ID ABP58289 standard; protein; 472 AA.
XX
AC ABP58289;
XX
DT 23-OCT-2003 (revised)
DT 31-MAR-2003 (first entry)
XX
DE Humanised 10D5 antibody heavy chain.
XX
KW Monoclonal antibody; 10D5; complementarity determining region; CDR;
KW mouse; human; humanised antibody; antibody; Alzheimer's disease;
KW Down's syndrome; cerebral amyloid angiopathy; neuroprotective; nootropic.
XX
OS Mus sp.
OS Homo sapiens.
OS Chimeric.
XX
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FH Key Location/Qualifiers
FT Peptide 1..19
FT Peptide /label= Signal_peptide
FT Peptide 20..472
FT Peptide /label= Mature_protein
FT Region /note= "the mature light chain is claimed in Claim 5"
FT Region 20..142
FT Region /note= "light chain variable region, claimed in Claim 4"
FT Region 50..56
FT Region /note= "CDR1"
FT Region 71..86
FT Region /note= "CDR2"
FT Region 119..131
FT Region /note= "CDR3"
XX
PN WO200288307-A2.
XX
PD 07-NOV-2002.
XX
PF 26-APR-2002; 2002WO-US011854.
XX
PR 30-APR-2001; 2001US-0287653P.
XX
PA (ELIL ) LILLY & CO ELI.
XX
PI Hinton PR, Vasquez M;
XX
DR WPI; 2003-183836/18.
XX
DR N-PSDB; ABZ24639, ABZ24641.
XX
PT New humanized 10D5 antibody, useful for the manufacture of a medicament
PT for treating Down's syndrome, clinical or pre-clinical Alzheimer's
PT disease or cerebral amyloid angiopathy.
XX
PS Disclosure; Page 13-15; 52pp; English.
XX
CC The present sequence is the protein sequence of the heavy chain of a
CC humanised antibody of the present invention. In the variable portion, the
CC complementarity determining regions (CDRs) originate from murine
CC monoclonal antibody 10D5 and the framework region originates from human
CC germline VH segment DP-28 and J segment JH4. Novel humanised antibodies
CC of the invention have CDRs from 10D5 and human framework sequences. These
CC humanised antibodies have binding affinities (affinity and epitope
CC location) approximately the same as those of the mouse 10D5 antibody. The
CC invention includes antibodies, single chain antibodies, and their
CC fragments, as well as nucleotide sequences, vectors, transformed host
CC cells, and methods of using the humanised antibody to treat, prevent,
CC alleviate, reverse or otherwise ameliorate symptoms and/or pathology
CC associated with Down's syndrome, (pre-)clinical Alzheimer's disease or
CC (pre-)clinical cerebral amyloid angiopathy, and to inhibit formation or
CC reduce Abeta plaque in the brain. (Updated on 23-OCT-2003 to standardise
CC OS field)
XX
SQ Sequence 472 AA;

Query Match 78.3%; Score 670; DB 6; Length 472;
Best Local Similarity 81.5%; Pred. No. 1.6e-52;
Matches 128; Conservative 8; Mismatches 21; Indels 0; Gaps 0;

QY 1 LTCTFGSFLITRGVGDWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKTSKQ 60
DB 39 LTCTFGSFLSTSGMGVSWIRQPPGKALEWLAHLYWDDDKRYNPSLSKSLRLTISKDTSKSQ 98
QY 61 VLTLTNTNMDPVDATYTCVRRPITPVLVDANDYWGQGLTVTVSSASTKGPSVFLAPCSR 120
DB 99 VLTLTNTNMDPVDATYTCVRRPITPVLVDANDYWGQGLTVTVSSASTKGPSVFLAPSSK 158
QY 121 STSESTAALGCLVKDYPPPEPTVTVSWNSGALTSGVHTF 157
DB 159 STSGTAAALGCLVKDYPPPEPTVTVSWNSGALTSGVHTF 195

RESULT 9
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AD71908
ID ADF71908 standard; protein; 448 AA.
XX
AC ADF71908;
XX
DT 26-FEB-2004 (first entry)
XX
DE Hu3G8VH-1G1 amino acid sequence SEQ ID NO:107.
XX
KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN W02003101485-A1.
XX
PD 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US017111.
XX
PR 30-MAY-2002; 2002US-0384689P.
PR 10-JAN-2003; 2003US-0439320P.
XX
XX (MACR-) MACROGENICS INC.
XX
PI Johnson LS, Huang L, Li H, Tuallion N;
XX
DR WPI; 2004-042985/04.
XX
XX Novel anti-CD16A antibody comprising complementarity determining regions
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
PT lacks effector function, useful for treating deleterious immune response.
XX
PS Disclosure; SEQ ID NO 107; 103pp; English.
XX
CC The present invention describes an anti-CD16A antibody (I) comprising a
CC VH domain comprising complementarity determining regions (CDRs) derived
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an FC region derived from a human IgG heavy chain, where the FC region
CC lacks effector function or is modified to reduce binding to an FC
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis,
CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence

CC is used in the exemplification of the present invention.
XX
SQ Sequence 448 AA;
XX
Query Match 77.6%; Score 664.5; DB 8; Length 448;
Best Local Similarity 81.1%; Pred. No. 4.9e-52;
Matches 129; Conservative 9; Mismatches 12; Indels 9; Gaps 2;
XX
QY 1 LCTFSGFSLLITRGVGVWIRQPPGKALQWLALYNNDDKRYSPSLKSLRTITKDTSKNQ 60
DB 20 LCTFSGFSLLSTSGMGVWIRQPPGKALELHIMWDDDKRYNPALKSRUTISKDTSKNQ 79
QY 61 VLVTMTNMDPVDATYYCAHFFDSSGYTP--FDSMGQGTLLVSSASTKGPSVFPLAPC 118
DB 80 VLVTMTNMDPVDATYYCAR-----INPAWYMGQGTLLVSSASTKGPSVFPLAPS 132
QY 119 SRSTSTSTAALGCLVXDYFPPEPVTVSWNSGALTSGVHTF 157
DB 133 SKSTSGTAAALGCLVXDYFPPEPVTVSWNSGALTSGVHTF 171
XX
RESULT 10
AD71912
ID ADF71912 standard; protein; 448 AA.
XX
AC ADF71912;
XX
DT 26-FEB-2004 (first entry)
XX
DE Hu3G8VH-5G1Ag amino acid sequence SEQ ID NO:111.
XX
KW anti-CD16A antibody; mouse; 3G8 antibody; humanised anti-CD16A antibody;
KW immune response; haemostatic; antirheumatic; antiarthritic;
KW dermatological; immunosuppressive; antiinflammatory; antianaemic;
KW vasotropic; nephrotropic; neuroprotective; antipsoriatic; uropathic;
KW ophthalmological; antiasthmatic; inflammatory response;
KW autoimmune disease; idiopathic thrombocytopenic purpura;
KW rheumatoid arthritis; systemic lupus erythematosus;
KW autoimmune haemolytic anaemia; scleroderma;
KW autoantibody triggered urticaria; pemphigus; vasculitis syndrome;
KW systemic vasculitis; Goodpasture's syndrome; multiple sclerosis;
KW psoriatic arthritis; ankylosing spondylitis; Sjogren's syndrome;
KW Reiter's syndrome; Kawasaki's disease; polymyositis; dermatomyositis;
KW allergic asthma.
XX
OS Synthetic.
OS Mus sp.
OS Homo sapiens.
XX
PN W02003101485-A1.
XX
PD 11-DEC-2003.
XX
XX 29-MAY-2003; 2003WO-US017111.
XX
PF 30-MAY-2002; 2002US-0384689P.
PR 10-JAN-2003; 2003US-0439320P.
XX
XX (MACR-) MACROGENICS INC.
XX
PA Johnson LS, Huang L, Li H, Tuallion N;
XX
DR WPI; 2004-042985/04.
XX
XX Novel anti-CD16A antibody comprising complementarity determining regions
PT derived from mouse 3G8 antibody and humanized anti-CD16A antibody that
PT lacks effector function, useful for treating deleterious immune response.
XX
PS Disclosure; SEQ ID NO 111; 103pp; English.
XX
CC The present invention describes an anti-CD16A antibody (I) comprising a
CC VH domain comprising complementarity determining regions (CDRs) derived
CC from the mouse 3G8 antibody heavy chain and a VL domain comprising CDRs
CC derived from the mouse 3G8 antibody light chain and a VL domain comprising CDRs
CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
CC antibody (II) that lacks effector function and comprises all six CDRs of
CC mouse antibody 3G8. Also described is a method (M1) for reducing a
CC deleterious immune response in a mammal in need of such reduction, which
CC involves administering to the mammal a CD16A binding protein comprising
CC an FC region derived from a human IgG heavy chain, where the FC region
CC lacks effector function or is modified to reduce binding to an FC
CC effector ligand. (I) and (II) have haemostatic, antirheumatic,
CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
CC useful for reducing a deleterious immune response in a mammal which
CC involves administering to the mammal (I) or (II). The deleterious immune
CC response is an inflammatory response caused by autoimmune disease such as
CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis,
CC and also for treating diseases susceptible to treatment with intravenous
CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence

CC derived from the mouse 3G8 antibody light chain or a humanised anti-CD16A
 CC mouse antibody (II) that lacks effector function and comprises all six CDRs of
 CC mouse antibody 3G8. Also described is a method (MI) for reducing a
 CC deleterious immune response in a mammal in need of such reduction, which
 CC involves administering to the mammal a CD16A binding protein comprising
 CC an FC region derived from a human IGH heavy chain, where the FC region
 CC lacks effector function or is modified to reduce binding to an FC
 CC effector ligand. (I) and (II) have haemostatic, antithrombotic,
 CC antiarthritic, dermatological, immunosuppressive, antiinflammatory,
 CC antianaemic, vasotropic, nephrotropic, neuroprotective, antipsoriatic,
 CC uropathic, ophthalmological and antiasthmatic activities. (I) or (II) is
 CC useful for reducing a deleterious immune response in a mammal which
 CC involves administering to the mammal (I) or (II). The deleterious immune
 CC response is an inflammatory response caused by autoimmune disease such as
 CC idiopathic thrombocytopenic purpura (ITP), rheumatoid arthritis (RA),
 CC systemic lupus erythematosus (SLE), autoimmune haemolytic anaemia (AHA),
 CC scleroderma, autoantibody triggered urticaria, pemphigus, vasculitis
 CC syndrome, systemic vasculitis, Goodpasture's syndrome, multiple sclerosis
 CC (MS), psoriatic arthritis, ankylosing spondylitis, Sjogren's syndrome,
 CC Reiter's syndrome, Kawasaki's disease, polymyositis and dermatomyositis
 CC and also for treating diseases susceptible to treatment with intravenous
 CC immunoglobulin (IVIg) therapy e.g., allergic asthma. The present sequence
 CC is used in the exemplification of the present invention.

XX Sequence 448 AA;

Query Match 77.6%; Score 664.5; DB 8; Length 448;
 Best Local Similarity 81.1%; Pred. No. 4.9e-52;
 Matches 129; Conservative 9; Mismatches 12; Indels 9; Gaps 2;

Qy 1 LTCFSGSLITRGVGDWIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 60
 Db 20 LTCFSGSLITRGVGDWIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 79
 Qy 61 VVLTMTNMDPVDATYYCAHFFDSSGYYP--FDSWGQGLVSVSSASTKGPSVFPPLAPC 118
 Db 80 VVLTMTNMDPVDATYYCAQ-----INPAFWYWGQGLTVTVSSASTKGPSVFPPLAPS 132

Qy 119 SRSTSESTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTF 157
 Db 133 SKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTF 171

RESULT 11
 ADJ32130
 ID ADJ32130 standard; protein; 228 AA.

AC ADJ32130;
 XX 22-APR-2004 (first entry)
 DT Human interferon-gamma antibody heavy chain amino acid sequence SeqIDB4.
 DE antibody; antigen binding domain; interferon-gamma; INF-gamma;
 KW antagonist antibody; antiinflammatory; immunosuppressive;
 KW autoimmune disease; inflammatory condition; human; heavy chain.
 XX Homo sapiens.

XX US2003099647-A1.
 XX 29-MAY-2003.
 XX 05-OCT-2001; 2001US-00972656.
 XX 05-OCT-2001; 2001US-00972656.
 XX (DESH/) DESHPANDE R V.
 XX (TSAI/) TSAI M.

XX Deshpande RV, Tsai M;
 XX WPI; 2003-696068/66.

DR N-PSDB; ADJ32129.

XX New antibody or antigen binding domain, or its fragment, variant or
 PT derivative, which binds to an interferon-gamma protein, useful for
 PT preparing a composition for preventing or treating inflammatory or
 PT autoimmune disorders.

XX Claim 10; SEQ ID NO 84; 113pp; English.

XX This invention relates to a novel antibody or antigen binding domain, or
 CC its fragment, variant or derivative, which binds to an interferon-gamma
 CC (INF-gamma) protein, and is an antagonist antibody. The invention may be
 CC useful for the development of compounds with an antiinflammatory or
 CC immunosuppressive activity through action as interferon-gamma agonists. A
 CC composition containing the antibody is useful for preventing or treating
 CC an autoimmune disease and an inflammatory condition. The present sequence
 CC is that of an antibody heavy chain of a human IFN-gamma antibody which
 CC may be part of the invention.

XX Sequence 228 AA;

Query Match 77.6%; Score 664; DB 7; Length 228;
 Best Local Similarity 78.6%; Pred. No. 2.5e-52;
 Matches 125; Conservative 11; Mismatches 21; Indels 2; Gaps 1;

Qy 1 LTCFSGSLITRGVGDWIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 60
 Db 20 LTCFSGSLITRGVGDWIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTITKDTSKNQ 79
 Qy 61 VVLTMTNMDPVDATYYCAHFFDSSGYYP--FDSWGQGLVSVSSASTKGPSVFPPLAPC 118
 Db 80 VVLTMTNMDPVDATYYCAHRLVRYGYSTGGFDVWGQGLTVTVSSASTKGPSVFPPLAPS 139
 Qy 119 SRSTSESTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTF 157
 Db 140 SKSTSGGTAALGCLVKDYFPEPTVTVSNWNSGALTSGVHTF 178

RESULT 12
 ABP66596
 ID ABP66596 standard; protein; 450 AA.

AC ABP66596;
 XX 04-DEC-2002 (first entry)
 DT Human RSV antibody variable heavy chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.

XX Homo sapiens.
 XX WO200243660-A2.
 XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.
 XX 28-NOV-2000; 2000US-00724396.
 XX 28-NOV-2000; 2000US-00724531.
 XX (MEDI-) MEDIUMMUNE INC.

XX Young JF, Koenig S, Johnson LS;
 XX WPI; 2002-706803/76.

XX Antibody for treating respiratory syncytial virus (RSV) infection,
 PT

PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 XX binds to RSV antigen.

PS Disclosure; Page 279-281; 298pp; English.

XX The invention relates to a novel antibody comprising a variable heavy
 CC (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention

XX Sequence 450 AA;

Query Match 75.3%; Score 644.5; DB 5; Length 450;
 Best Local Similarity 79.0%; Pred. No. 3.3e-50;
 Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGSLITRGVGVDMTRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
 Db 20 LTCTFSGSLSTAGMSVGMIRQPPGKALEWLADIWDDKDYNPSSLKSLRLTISKDTSKNQ 79
 Qy 61 VLVTMTNMDPVDATYTCYCAHHFFDSSGYPFDSWGQGLTVSVSSASTKGSPVPLAPCSR 120
 Db 80 VLVKVTNMDPADTATYTCARDMI--TNFY-FDVMGQGTITVTVSSASTKGSPVPLAPSSK 136
 Qy 121 STSESTAALGCLVKDYPPEPVTVSWNSGALTSVGHVF 157
 Db 137 STSGTAAALGCLVKDYPPEPVTVSWNSGALTSVGHVF 173

RESULT 13

ID ABP66594 standard; protein; 450 AA.

AC ABP66594;

DT 04-DEC-2002 (first entry)

XX Human RSV antibody variable heavy chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.

OS Homo sapiens.

XX WO200243660-A2.

XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.

XX 28-NOV-2000; 2000US-00724396.

XX 28-NOV-2000; 2000US-00724531.

XX (MEDI-) MEDIUMMUNE INC.

XX Young JF, Koenig S, Johnson LS;

XX

DR WPI; 2002-706803/76.

XX Antibody for treating respiratory syncytial virus (RSV) infection,
 PT comprises a variable heavy/light domain or complementarity determining
 PT regions 1 - 3 of variable light/heavy chains, that immunospecifically
 PT binds to RSV antigen.

XX Disclosure; Page 277-278; 298pp; English.

XX The invention relates to a novel antibody comprising a variable heavy
 CC (VH) domain, variable light (VL) domain, VH complementarity determining
 CC region (CDR)-1, VH CDR2, VH CDR3, VL CDR1, VL CDR2 or VL CDR3, where the
 CC antibody immunospecifically binds to a respiratory syncytial virus (RSV)
 CC antigen, and where the antibody is not SYNAGIS (RTM). The antibody of the
 CC invention has virucide, pulmonary, antiinflammatory, cardiant, anti-HIV,
 CC and immunostimulant activity. The polynucleotides of the invention may
 CC have a use in a vaccine, and in gene therapy. The antibody is useful for
 CC treating or ameliorating a RSV infection in a human. The antibody is also
 CC useful for preventing, treating or ameliorating one or more symptoms
 CC associated with RSV infection in a mammal, e.g. cystic fibrosis,
 CC bronchopulmonary dysplasia, congenital heart disease, congenital
 CC immunodeficiency or acquired immunodeficiency, or after a bone marrow
 CC transplant. The sequence represents a variable domain of a human RSV
 CC antibody of the invention

XX Sequence 450 AA;

Query Match 75.3%; Score 644.5; DB 5; Length 450;
 Best Local Similarity 79.0%; Pred. No. 3.3e-50;
 Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGSLITRGVGVDMTRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
 Db 20 LTCTFSGSLSTAGMSVGMIRQPPGKALEWLADIWDDKDYNPSSLKSLRLTISKDTSKNQ 79
 Qy 61 VLVTMTNMDPVDATYTCYCAHHFFDSSGYPFDSWGQGLTVSVSSASTKGSPVPLAPCSR 120
 Db 80 VLVKVTNMDPADTATYTCARDMI--TNFY-FDVMGQGTITVTVSSASTKGSPVPLAPSSK 136
 Qy 121 STSESTAALGCLVKDYPPEPVTVSWNSGALTSVGHVF 157
 Db 137 STSGTAAALGCLVKDYPPEPVTVSWNSGALTSVGHVF 173

RESULT 14

ID ABP66598 standard; protein; 450 AA.

AC ABP66598;

DT 04-DEC-2002 (first entry)

XX Human RSV antibody variable heavy chain.

XX Human; variable heavy domain; variable light domain; CDR; VH; VL; RSV;
 KW complementarity determining region; respiratory syncytial virus;
 KW virucide; pulmonary; antiinflammatory; cardiant; anti-HIV; vaccine;
 KW immunostimulant; gene therapy; cystic fibrosis; bone marrow transplant;
 KW bronchopulmonary dysplasia; congenital heart disease;
 KW congenital immunodeficiency; acquired immunodeficiency.

OS Homo sapiens.

XX WO200243660-A2.

XX 06-JUN-2002.

XX 28-NOV-2001; 2001WO-US044807.

XX 28-NOV-2000; 2000US-00724396.

XX 28-NOV-2000; 2000US-00724531.

XX (MEDI-) MEDIUMMUNE INC.

XX

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 84.3771 Seconds
(without alignments)
620.051 Million cell updates/sec

Title: US-09-784-950-39
Perfect score: 856
Sequence: 1 LTCTFSGFSLITRGVGDWV.....PVTVWNSGALTSVHTFQL 159

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	700.5	81.8	518	14	US-10-225-108A-10
2	700.5	81.8	518	15	US-10-461-148-4
3	678.5	79.3	448	15	US-10-449-566-115
4	664.5	77.6	448	15	US-10-449-566-107
5	664.5	77.6	448	15	US-10-449-566-111
6	664	77.6	228	10	US-09-972-656-84
7	644.5	75.3	450	9	US-09-996-288-210
8	644.5	75.3	450	9	US-09-996-288-238
9	644.5	75.3	450	9	US-09-996-288-240
10	644.5	75.3	450	9	US-09-996-288-242
11	644.5	75.3	450	9	US-09-996-288-244
12	644.5	75.3	450	9	US-09-996-288-246
13	644.5	75.3	450	10	US-09-996-265-210

14	644.5	75.3	450	10	US-09-996-265-238	Sequence 238, App
15	644.5	75.3	450	10	US-09-996-265-240	Sequence 240, App
16	644.5	75.3	450	10	US-09-996-265-242	Sequence 242, App
17	644.5	75.3	450	10	US-09-996-265-244	Sequence 244, App
18	644.5	75.3	450	10	US-09-996-265-246	Sequence 246, App
19	644.5	75.3	450	16	US-10-900-230-210	Sequence 210, App
20	644.5	75.3	450	16	US-10-900-230-238	Sequence 238, App
21	644.5	75.3	450	16	US-10-900-230-240	Sequence 240, App
22	644.5	75.3	450	16	US-10-900-230-242	Sequence 242, App
23	644.5	75.3	450	16	US-10-900-230-244	Sequence 244, App
24	644.5	75.3	450	16	US-10-900-230-246	Sequence 246, App
25	643.5	75.2	450	9	US-09-996-288-208	Sequence 208, App
26	643.5	75.2	450	10	US-09-996-265-208	Sequence 208, App
27	643.5	75.2	450	16	US-10-900-230-208	Sequence 208, App
28	641.5	74.9	450	9	US-09-996-288-232	Sequence 232, App
29	641.5	74.9	450	9	US-09-996-288-234	Sequence 234, App
30	641.5	74.9	450	9	US-09-996-288-236	Sequence 236, App
31	641.5	74.9	450	9	US-09-996-288-248	Sequence 248, App
32	641.5	74.9	450	10	US-09-996-265-232	Sequence 232, App
33	641.5	74.9	450	10	US-09-996-265-234	Sequence 234, App
34	641.5	74.9	450	10	US-09-996-265-236	Sequence 236, App
35	641.5	74.9	450	10	US-09-996-265-238	Sequence 238, App
36	641.5	74.9	450	16	US-10-900-230-232	Sequence 232, App
37	641.5	74.9	450	16	US-10-900-230-234	Sequence 234, App
38	641.5	74.9	450	16	US-10-900-230-236	Sequence 236, App
39	641.5	74.9	450	16	US-10-900-230-248	Sequence 248, App
40	640.5	74.8	450	9	US-09-996-288-45	Sequence 45, Appl
41	640.5	74.8	450	9	US-09-996-288-226	Sequence 226, App
42	640.5	74.8	450	9	US-09-996-288-252	Sequence 252, App
43	640.5	74.8	450	9	US-09-996-288-254	Sequence 254, App
44	640.5	74.8	450	9	US-09-996-288-256	Sequence 256, App
45	640.5	74.8	450	10	US-09-996-265-226	Sequence 226, App

ALIGNMENTS

RESULT 1
US-10-225-108A-10
; Sequence 10, Application US/10225108A
; Publication No. US20030157112A1
; GENERAL INFORMATION:
; APPLICANT: HOOPER, Craig
; APPLICANT: DIETZSCHOLD, Bernhard
; TITLE OF INVENTION: Recombinant Antibodies, and Compositions
; TITLE OF INVENTION: and Methods for Making Them
; FILE REFERENCE: 8321-110
; CURRENT APPLICATION NUMBER: US/10/225.108A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: US 09/848,832
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/204,518
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/314,023
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 518
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-108A-10

Query Match 81.8%; Score 700.5; DB 14; Length 518;

Best Local Similarity 84.2%; Pred. No. 3.8e-47;

Matches 133; Conservative 9; Mismatches 13; Indels 3; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGDWIRQPGKALQWLALYIYNDKRYSPSLKRLTITKTSKQ 60

Db 39 LTCTFSGFSLITSGVGVGWIRQPGKALEWTLIYDWDKRYSPSLNRVIRKDTSKQ 98

Qy 61 VLWTMTNDPVDATYTYCAHHFFDSSGYYP-FDSWGQGLTVSVSSASTKGSVPFLAPCS 119

GENERAL INFORMATION:
APPLICANT: JOHNSON, Leslie S.
APPLICANT: HUANG, Ling
APPLICANT: LI, Hua
APPLICANT: TUAILLON, Nadine
TITLE OF INVENTION: CD16A BINDING PROTEINS AND USE FOR THE
TREATMENT OF IMMUNE DISORDERS
FILE REFERENCE: 529392000100
CURRENT APPLICATION NUMBER: US/10/449,566
CURRENT FILING DATE: 2003-05-29
PRIOR APPLICATION NUMBER: 60/384,689
PRIOR FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/439,320
PRIOR FILING DATE: 2003-01-10
NUMBER OF SEQ ID NOS: 119
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 111
LENGTH: 448
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic Construct
US-10-449-566-111

Query Match 77.6%; Score 664.5; DB 15; Length 448;
Best Local Similarity 81.1%; Pred. No. 2.2e-44;
Matches 129; Conservative 9; Mismatches 12; Indels 9; Gaps 2;
Qy 1 LTCTFSGFSLLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCTFSGFSLLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 79
Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSVFPPLAPC 118
Db 80 VLWTMTNMDPVDATYYCAQ-----INPAFWAGQGLTVTVSSASTKGPSVFPPLAPS 132
Qy 119 SRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
Db 133 SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 171

RESULT 6
US-09-972-656-84
Sequence 84, Application US/09972656
Publication No. US20030099647A1
GENERAL INFORMATION:
APPLICANT: Deshpande, Rajendra
APPLICANT: Tsai, Mei-Mei
TITLE OF INVENTION: Fully Human Antibody Fab Fragments with Human Interferon-Gamma
Neutralizing Activity
FILE REFERENCE: A-799
CURRENT APPLICATION NUMBER: US/09/972,656
CURRENT FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 135
SOFTWARE: PatentIn version 3.0
SEQ ID NO 84
LENGTH: 228
TYPE: PRT
ORGANISM: Homo sapiens
US-09-972-656-84

Query Match 77.6%; Score 664; DB 10; Length 228;
Best Local Similarity 78.6%; Pred. No. 1.2e-44;
Matches 125; Conservative 11; Mismatches 21; Indels 2; Gaps 1;
Qy 1 LTCTFSGFSLLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCTFSGFSLLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 79
Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYP--FDSWGQGLTVSVSSASTKGPSVFPPLAPC 118
Db 80 VLWTMTNMDPVDATYYCAHRLVRYGGYSTGDFDWGQGLTVTVSSASTKGPSVFPPLAPS 139

Qy 119 SRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
Db 140 SKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 178

RESULT 7
US-09-996-288-210
Sequence 210, Application US/09996288
Patent No. US20020177126A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 210
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-210

Query Match 75.3%; Score 644.5; DB 9; Length 450;
Best Local Similarity 79.0%; Pred. No. 8.5e-43;
Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;
Qy 1 LTCTFSGFSLLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCTFSGFSLLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 79
Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLTVSVSSASTKGPSVFPPLAPCSR 120
Db 80 VLWTMTNMDPVDATYYCARSMI--TNFY-FDVGQGLTVTVSSASTKGPSVFPPLAPSSK 136
Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

RESULT 8
US-09-996-288-238
Sequence 238, Application US/09996288
Patent No. US20020177126A1
GENERAL INFORMATION:
APPLICANT: Young, James
APPLICANT: Scott, Koenig
APPLICANT: Leslie, Johnson
TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
and Treatment
FILE REFERENCE: 10271-047-999
CURRENT APPLICATION NUMBER: US/09/996,288
CURRENT FILING DATE: 2001-11-28
NUMBER OF SEQ ID NOS: 259
SOFTWARE: PatentIn version 3.1
SEQ ID NO 238
LENGTH: 450
TYPE: PRT
ORGANISM: Homo sapiens
US-09-996-288-238

Query Match 75.3%; Score 644.5; DB 9; Length 450;
Best Local Similarity 79.0%; Pred. No. 8.5e-43;
Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;
Qy 1 LTCTFSGFSLLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCTFSGFSLLTRGVGDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 79
Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLTVSVSSASTKGPSVFPPLAPCSR 120

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Db      80  VVLKVTNMDPADTATYYCARDMI--TFNY-EDVWVGQGTVTTVSSASTKGPSVEPLAPSSK 136
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      121 STSESTAALGCLVKDYPPEPTVTVSNSGALTSGVHTP 157
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      137 STSGGTAALGCLVKDYPPEPTVTVSNSGALTSGVHTF 173
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 9
US-09-996-288-240
; Sequence 240, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-240

```

Query Match	75.3%;	Score 644.5;	DB 9;	Length 450;
Best Local Similarity	79.0%;	Pred. No. 8.5e-43;		
Matches 124;	Conservative 11;	Mismatches 19;	Indels 3;	Gaps 2

Qy	1	LCTCTSGSLIRGRGVGDWIRQPPCKALQWLALYWNDDKRYSPSLKSRLLTIKDTSKNQ	60
Db	20	LCTCTSGSLTAGMSVGIIRQPPCKALEWLADLWDDKDYNPFLKSRLLTIKDTSKNQ	79
Qy	61	VVLVTNNMDPVDATATYYCAHHFFDPSGYYPFDSWGQGLTVSVSSASTKGPSVFPFLPCSR	120
Db	80	VVLKVTNNMDPADATATYYCARSMI--TNFY-EDVWGQGLTVTVSSASTKGPSVFPFLPSSK	136
Qy	121	STSESTAALGCLVKDYFPPEPVTVSNNSGALTSGVHTF	157
Db	137	STSGGTAALGCLVKDYFPPEPVTVSNNSGALTSGVHTF	173

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RESULT 10
US-09-996-288-242
; Sequence 242, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 242
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-242

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[illegible]

Db	20	LTCTFSGSLTAGMSVCGWIRQPGKALEWLADIWDDKKDYNPSLKSRLTISKDTSKNQ	79
Qy	61	VVLFWNMNDPVDTATYYCAHHFFDSGGYYPPDSWGQGLTVSVSSASTKGPSVFPLAPCSR	120
Db	80	VVLKVTNMNDPATATYYCARDMI--TNYF-FDVWGQGLTVTVSSASTKGPSVFPLAPSSK	136
Qy	121	STSESTALGCLVKDYFPEPVTVSWNSGALTSGVHTF	157
Db	137	STSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTF	173

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RESULT 11
US-09-996-288-244
; Sequence 244, Application US/09996288
; Patent No. US20020177126A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 244
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-244

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Qy	121	STSESTAALGCLVKDYFPEPVTVSNWNGALTSGVHTF	157
Db	137	STSGTAALGCLVKDYFPEPVTVSNWNGALTSGVHTF	173

Qy	1	LTCFSGSLITRGVGVDWIRQPPCKALQWLAL1YWNDDKRYSPSLKSLTITKDTSKNQ	60
Db	20	LTCFSGSLSTAGSVSGWIRQPPCKALEWLAIWNDDKDYNP SLKSLTITSKDTSKNQ	79
Qy	61	VVLWTNNMPVDATYTYCAHHFFDSSGGYPPFDSWGQGLTVSVSSASTGSPSVFPLAPCSR	120
Db	80	VVLKVTNNDPADTATYTCARDMI--TNEY-FDVWGQGLTVTVSVSSASTGSPSVFPLAPSSK	136
Qy	121	STSESTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF	157
Db	137	STSGTAALGCLVKDYFPEPVTVSNWNSGALTSGVHTF	173

RESULT 13
 US-09-996-265-210
 ; Sequence 210, Application US/09996265
 ; Publication No. US20030091584A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, James
 ; APPLICANT: Scott, Koenig
 ; APPLICANT: Leslie, Johnson
 ; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
 ; TITLE OF INVENTION: and Treatment
 ; FILE REFERENCE: 10271-048-999
 ; CURRENT APPLICATION NUMBER: US/09/996,265
 ; CURRENT FILING DATE: 2001-11-28
 ; NUMBER OF SEQ ID NOS: 259
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 210
 ; LENGTH: 450
 ; TYPE: prt
 ; ORGANISM: Homo sapiens
 US-09-996-265-210

		Query Match	75.3%; Score 644.5; DB 10; Length 450;
		Best Local Similarity	79.0%; Pred. No. 8.5e-43;
		Matches 124; Conservative	11; Mismatches 19; Indels 3; Gaps 2;
Qy	1	LTCFSGFSLITRGVGDWIRQPCKALOWLALIYWNDDKRYSPSLKRLIITKDTSNQ	60
Dd	20	LTCFSGFSLSLAGSVGWIRQPCKALEWLADIWDDKKDYNPSLKRLIISKDTSNQ	79
Qy	61	VVLTMNTMNDPVDATYYCAHHFFDSSGYPPDSWGQGTLVSVSASSTKGPSVFPLAPCSR	120
Dd	80	VVLKVNTMDPADTATYYCARSMI--TNFY-FDVWGQTIVTVSSASTKGPSVFPLAPSSK	136
Qy	121	STSSESTAALGCLVKDYPPEPVTVSWNSGALTSGVHTF	157
Dd	137	STSGCTAALGCLVKDYPPEPVTVSWNSGALTSGVHTF	173

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RESULT 14
US-09-996-265-238
; Sequence 238, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 238
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-238

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	Query Match	75.3%	Score 644.5	DB 10	Length 450
	Best Local Similarity	79.0%	Pred. No. 8.5e-43		
	Matches 124	Conservative 11	Mismatches 13	Indels 3	Gaps 2
Qy	1	LTCTFSGFSLITRCGVGDWITROPGKALOWIALIYNWDDKEYSPSLKSLRTLTITTKDTSKQ	60		
Db	20	LTCTFSGFSLSTAGMSVGNIRQPPGKALEWADLWDDKDYINPSLKSRLTITSKDTSKQ	79		
Qy	61	VWLTMTNMDPVDATYYCAHHFFDSSGYPYPPDSGQGTLVSVSSASTKGPSVFPLAPCSR	120		
Db	80	VWLKVTNMDPADTATYYCARDMI--TFYF-FDVWGQGTVTVTSSASTKGPSVFPLAPSSK	136		
Qy	121	STSESTAAALGCLVKDYPPEPVTVSWNSGALTSGVHTF	157		
Db	137	STSGGTAAALGCLVKDYFPPEPVTVSWNSGALTSGVHTF	173		

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RESULT 15
US-09-996-265-240
; Sequence 240, Application US/09996265
; Publication No. US20030091584A1
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-048-999
; CURRENT APPLICATION NUMBER: US/09/996,265
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 240
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-265-240

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Query Match	75.3%	Score 644.5	DB 10	Length 450
Best Local Similarity	79.0%	Pred. No. 8.5e-43		
Matches 124	Conservative 11	Mismatches 13	Indels 3	Gaps 2
Qy 1	LTCTFSGFSLITRGVGDWIRQPPGKALQWLALIWYNDKKEYSPSLKSLRLTITTKDTSKQ	60		
Db				
Qy 20	LTCTFSGFSLSLTAGMSVGWIRQPPGKALEWLADIWDDKDYNSPKSLRLTITTKDTSKQ	79		
Db				
Qy 61	VLLTMTNMDPVDATYYCAHHFDFSSGYPYPPDSWGQGTLSVSSASTKGPVSFPLAPCSR	120		
Db				
Qy 80	VLLKVTNMDPADTATYYCARSMI--TFYF-FDVWGQGTITVSSASTKGPVSFPLAPSSK	136		
Db				
Qy 121	STSESTAAIGCLVKDYPPEPVTVSWNSGALTSGVHVF	157		
Db				
Qy 137	STSGGTAAIGCLVKDYPPEPVTVSWNSGALTSGVHVF	173		
Db				

Search completed: March 8, 2005, 07:05:58
Job time : 85.3771 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 17.4831 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-39

Perfect score: 856

Sequence: 1 LTCTFSGFSLITRGVGDWV.....PVTVWSNGALTSVGHVFQL 159

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	644.5	75.3	450	4	US-09-996-288-210
2	644.5	75.3	450	4	US-09-996-288-238
3	644.5	75.3	450	4	US-09-996-288-240
4	644.5	75.3	450	4	US-09-996-288-242
5	644.5	75.3	450	4	US-09-996-288-244
6	644.5	75.3	450	4	US-09-996-288-246
7	643.5	75.2	450	4	US-09-996-288-208
8	641.5	74.9	450	4	US-09-996-288-232
9	641.5	74.9	450	4	US-09-996-288-234
10	641.5	74.9	450	4	US-09-996-288-236
11	641.5	74.9	450	4	US-09-996-288-248
12	640.5	74.8	450	4	US-09-996-288-226
13	640.5	74.8	450	4	US-09-996-288-252
14	640.5	74.8	450	4	US-09-996-288-254
15	640.5	74.8	450	4	US-09-996-288-256
16	640.5	74.8	475	4	US-09-740-002-27
17	639.5	74.7	450	4	US-09-996-288-212
18	639.5	74.7	450	4	US-09-996-288-214
19	638.5	74.6	450	4	US-09-996-288-228
20	633	73.9	451	4	US-09-996-288-230
21	632.5	73.9	450	4	US-09-996-288-218
22	632.5	73.9	450	4	US-09-996-288-222
23	632.5	73.9	450	4	US-09-996-288-224
24	632.5	73.9	450	4	US-09-996-288-250
25	631.5	73.8	450	4	US-09-996-288-216
26	631.5	73.8	450	4	US-09-996-288-220
27	623.5	72.8	462	4	US-09-288-942A-7

28	611.5	71.4	475	4	US-09-740-002-25	Sequence 25, Appl
29	559.5	65.4	172	4	US-09-472-087-7	Sequence 7, Appl
30	559.5	65.4	172	4	US-09-472-087-86	Sequence 86, Appl
31	532.5	62.2	473	3	US-09-049-672A-4	Sequence 4, Appl
32	532	62.1	499	3	US-09-049-672A-1	Sequence 1, Appl
33	530.5	62.0	241	4	US-09-726-219A-187	Sequence 187, App
34	530.5	62.0	832	3	US-08-630-820-7	Sequence 7, Appl
35	530.5	62.0	832	4	US-09-273-453-7	Sequence 7, Appl
36	529.5	61.9	167	4	US-09-472-087-74	Sequence 74, Appl
37	529.5	61.9	463	4	US-09-472-087-1	Sequence 1, Appl
38	529.5	61.9	463	4	US-09-472-087-63	Sequence 63, Appl
39	529.5	61.9	463	4	US-09-472-087-64	Sequence 64, Appl
40	526.5	61.5	255	3	US-09-171-945-57	Sequence 57, Appl
41	525	61.3	166	4	US-09-472-087-75	Sequence 75, Appl
42	525	61.3	464	4	US-09-472-087-2	Sequence 2, Appl
43	525	61.3	464	4	US-09-472-087-66	Sequence 66, Appl
44	523.5	61.2	463	4	US-09-472-087-4	Sequence 4, Appl
45	523.5	61.2	463	4	US-09-472-087-68	Sequence 68, Appl

ALIGNMENTS

RESULT 1

US-09-996-288-210
; Sequence 210, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 210
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-210

Query Match 75.3%; Score 644.5; DB 4; Length 450;

Best Local Similarity 79.0%; Pred. No. 1.2e-54;

Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGDWVIRQPGKALOWALIYWNDDKRYSPSLKSLRLITKDTSKNQ 60

Db 20 LTCTFSGFSLITRGVGDWVIRQPGKALEWLIWDDKRYSPSLKSLRLITKDTSKNQ 79

Qy 61 VLTWTNMDPVTATYCAHHFFDSSGYPPDSSGQGLVSVSSASTKGPVFPPLAPCSR 120

Db 80 VLVKVTNMDPVTATYCAHSMI--TNYF-FDVNGQGTVTVSSASTKGPVFPPLAPSSK 136

Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSVGHVTF 157

Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSVGHVTF 173

RESULT 2

US-09-996-288-238
; Sequence 238, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288

; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 246
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-246

Query Match 75.3%; Score 644.5; DB 4; Length 450;
Best Local Similarity 79.0%; Pred. No. 1.2e-54;
Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGVWDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCTFSGFSLSTAGMSVGVIRQPPGKALEWLADIWDDKKDYNPSLKSRLTISKDTSKNQ 79

Qy 61 VVLTMTNMDPVDATATYCAHHFFDSSGYPPDSSGQGTLSVSSASTKGPSVFPPLAPCSR 120
Db 80 VVLTMTNMDPADTATYCARMI--TNFY-FDVWGQGTITVSSASTKGPSVFPPLAPSSK 136

Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

RESULT 7

US-09-996-288-208
; Sequence 208, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 208
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-208

Query Match 75.2%; Score 643.5; DB 4; Length 450;
Best Local Similarity 79.0%; Pred. No. 1.5e-54;
Matches 124; Conservative 11; Mismatches 19; Indels 3; Gaps 2;

Qy 1 LTCTFSGFSLITRGVGVWDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCTFSGFSLSTAGMSVGVIRQPPGKALEWLADIWDDKKDYNPSLKSRLTISKDTSKNQ 79

Qy 61 VVLTMTNMDPVDATATYCAHHFFDSSGYPPDSSGQGTLSVSSASTKGPSVFPPLAPCSR 120
Db 80 VVLTMTNMDPADTATYCARSMI--TNFY-FDVWGQGTITVSSASTKGPSVFPPLAPSSK 136

Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

RESULT 8

US-09-996-288-232
; Sequence 232, Application US/09996288

; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 232
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-232

Query Match 74.9%; Score 641.5; DB 4; Length 450;
Best Local Similarity 79.0%; Pred. No. 2.4e-54;
Matches 124; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

Qy 1 LTCTFSGFSLITRGVGVWDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCTFSGFSLSTAGMSVGVIRQPPGKALEWLADIWDDKKDYNPSLKSRLTISKDTSKNQ 79

Qy 61 VVLTMTNMDPVDATATYCAHHFFDSSGYPPDSSGQGTLSVSSASTKGPSVFPPLAPCSR 120
Db 80 VVLTMTNMDPADTATYCAR--DMIENWYFDVWGQGTITVSSASTKGPSVFPPLAPSSK 136

Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

RESULT 9

US-09-996-288-234
; Sequence 234, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 234
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-234

Query Match 74.9%; Score 641.5; DB 4; Length 450;
Best Local Similarity 79.0%; Pred. No. 2.4e-54;
Matches 124; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

Qy 1 LTCTFSGFSLITRGVGVWDWIRQPPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCTFSGFSLSTAGMSVGVIRQPPGKALEWLADIWDDKKDYNPSLKSRLTISKDTSKNQ 79

Qy 61 VVLTMTNMDPVDATATYCAHHFFDSSGYPPDSSGQGTLSVSSASTKGPSVFPPLAPCSR 120
Db 80 VVLTMTNMDPADTATYCAR--DMIENWYFDVWGQGTITVSSASTKGPSVFPPLAPSSK 136

Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

```
RESULT 10
US-09-996-288-236
; Sequence 236, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 236
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-236

Query Match 74.9%; Score 641.5; DB 4; Length 450;
Best Local Similarity 79.0%; Pred. No. 2.4e-54;
Matches 124; Conservative 10; Mismatches 20; Indels 3; Gaps 1;

Qy 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTIITKDTSKNQ 60
Db 20 LTCTFGSFLSTAGMSVGMIRQPPGKALEWLADIWDDKKHYNPSLKDLRTISKDTSKNQ 79

Qy 61 VLVTMTNMDPVDATYYCAHHFFDSSGYYPFDSGQGTLYSVSSASTKGPSVFPPLAPCSR 120
Db 80 VLKVTNMDPADTATYYCAR---DMIFNFYFDVWGQGTIVTVSSASTKGPSVFPPLAPSSK 136

Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

RESULT 11
US-09-996-288-248
; Sequence 248, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 248
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-248

Query Match 74.9%; Score 641.5; DB 4; Length 450;
Best Local Similarity 78.3%; Pred. No. 2.4e-54;
Matches 123; Conservative 11; Mismatches 20; Indels 3; Gaps 2;

Qy 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTIITKDTSKNQ 60
Db 20 LTCTFGSFLSTAGMSVGMIRQPPGKALEWLADIWDDKKHYNPSLKDLRTISKDTSKNQ 79

Qy 61 VLVTMTNMDPVDATYYCAHHFFDSSGYYPFDSGQGTLYSVSSASTKGPSVFPPLAPCSR 120
Db 80 VLKVTNMDPADTATYYCARSMI--TWNY-FDVWGQGTIVTVSSASTKGPSVFPPLAPSSK 136

Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
; ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

RESULT 12
US-09-996-288-226
; Sequence 226, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 226
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-226

Query Match 74.8%; Score 640.5; DB 4; Length 450;
Best Local Similarity 78.3%; Pred. No. 3e-54;
Matches 123; Conservative 10; Mismatches 21; Indels 3; Gaps 1;

Qy 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTIITKDTSKNQ 60
Db 20 LTCTFGSFLSTAGMSVGMIRQPPGKALEWLADIWDDKKHYNPSLKDLRTISKDTSKNQ 79

Qy 61 VLVTMTNMDPVDATYYCAHHFFDSSGYYPFDSGQGTLYSVSSASTKGPSVFPPLAPCSR 120
Db 80 VLKVTNMDPADTATYYCAR---DMIFNFYFDVWGQGTIVTVSSASTKGPSVFPPLAPSSK 136

Qy 121 STSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTF 173

RESULT 13
US-09-996-288-252
; Sequence 252, Application US/09996288
; Patent No. 6818216
; GENERAL INFORMATION:
; APPLICANT: Young, James
; APPLICANT: Scott, Koenig
; APPLICANT: Leslie, Johnson
; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis
; TITLE OF INVENTION: and Treatment
; FILE REFERENCE: 10271-047-999
; CURRENT APPLICATION NUMBER: US/09/996,288
; CURRENT FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 259
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 252
; LENGTH: 450
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-996-288-252

Query Match 74.8%; Score 640.5; DB 4; Length 450;
Best Local Similarity 78.3%; Pred. No. 3e-54;
Matches 123; Conservative 10; Mismatches 21; Indels 3; Gaps 1;

Qy 1 LTCTFGSFLITRGVGVDMIRQPPGKALQWLALYIWNDDKRYSPSLKSLRLTIITKDTSKNQ 60
Db 20 LTCTFGSFLSTAGMSVGMIRQPPGKALEWLADIWDDKKHYNPSLKDLRTISKDTSKNQ 79

Qy 61 VLVTMTNMDPVDATYYCAHHFFDSSGYYPFDSGQGTLYSVSSASTKGPSVFPPLAPCSR 120
Db 80 VLKVTNMDPADTATYYCAR---DMIFNFYFDVWGQGTIVTVSSASTKGPSVFPPLAPSSK 136
```

Qy 121 STSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 173

RESULT 14

US-09-996-288-254

; Sequence 254, Application US/09996288

; Patent No. 6818216

; GENERAL INFORMATION:

; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 254

; LENGTH: 450

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-996-288-254

Query Match 74.8%; Score 640.5; DB 4; Length 450;
Best Local Similarity 78.3%; Pred. No. 3e-54;
Matches 123; Conservative 10; Mismatches 21; Indels 3; Gaps 1;

Qy 1 LTCFTSGFSLITRGVGVNDWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCFTSGFSLTAGMSVGVIRQPGKALEWLDIWDKHYNPSLKDRLTISKDTSKNQ 79

Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFLAPCSR 120
Db 80 VLKVTNMDPADTATYYCAR---DMIFNFYFDVWGQGTTVTVSSASTKGPSVFLAPSSK 136

Qy 121 STSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 173

RESULT 15

US-09-996-288-256

; Sequence 256, Application US/09996288

; Patent No. 6818216

; GENERAL INFORMATION:

; APPLICANT: Young, James

; APPLICANT: Scott, Koenig

; APPLICANT: Leslie, Johnson

; TITLE OF INVENTION: Methods of Administering/Dosing Anti-RSV Antibodies for Prophylaxis

; TITLE OF INVENTION: and Treatment

; FILE REFERENCE: 10271-047-999

; CURRENT APPLICATION NUMBER: US/09/996,288

; CURRENT FILING DATE: 2001-11-28

; NUMBER OF SEQ ID NOS: 259

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 256

; LENGTH: 450

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-996-288-256

Query Match 74.8%; Score 640.5; DB 4; Length 450;
Best Local Similarity 78.3%; Pred. No. 3e-54;
Matches 123; Conservative 10; Mismatches 21; Indels 3; Gaps 1;

Qy 1 LTCFTSGFSLITRGVGVNDWIRQPGKALQWLALYWNDDKRYSPSLKSLRLTITKDTSKNQ 60
Db 20 LTCFTSGFSLTAGMSVGVIRQPGKALEWLDIWDKHYNPSLKDRLTISKDTSKNQ 79

Qy 61 VLWTMTNMDPVDATYYCAHHFFDSSGYYPFDSWGQGLVSVSSASTKGPSVFLAPCSR 120
Db 80 VLKVTNMDPADTATYYCAR---DMIFNFYFDVWGQGTTVTVSSASTKGPSVFLAPSSK 136
Qy 121 STSESTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 157
Db 137 STSGTAALGCLVKDYPPPEPVTVSWNSGALTSGVHTF 173

Search completed: March 8, 2005, 05:54:14

Job time : 17.4831 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 11.8686 Seconds
(without alignments)
1353.842 Million cell updates/sec

Title: US-09-784-950-40

Perfect score: 867
Sequence: 1 GGLVQPGGSLRLSCAASGF.....SWNLGALTSGVHTFPAVLQS 167

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: pir1.*
- 2: pir2.*
- 3: pir3.*
- 4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	623.5	71.9	548	2	S38864
2	590	68.1	213	2	S68213
3	582	67.1	143	2	S23624
4	576.5	66.5	254	2	B31790
5	555.5	64.1	220	2	S68211
6	555.5	64.1	444	2	PC4436
7	546	63.0	220	2	A49444
8	535.5	61.8	241	2	S69131
9	518	59.7	160	2	S05271
10	514.5	59.3	470	2	S22080
11	497.5	57.4	249	2	S59340
12	495.5	57.2	124	2	S20782
13	493.5	56.9	469	2	S37483
14	492	56.7	509	2	S17597
15	491	56.6	231	2	PC4155
16	489	56.4	246	2	S38950
17	489	56.4	446	2	S40295
18	485	55.9	119	2	S31108
19	484.5	55.9	108	2	PH1648
20	483.5	55.8	214	2	PC4202
21	481.5	55.5	147	2	I37780
22	481	55.5	138	2	S31666
23	480.5	55.4	572	2	B46529
24	480	55.4	119	2	D36005
25	479	55.2	119	2	S31107
26	478	55.1	140	2	S31686
27	477	55.0	123	2	S31114
28	477	55.0	140	2	S31588
29	476.5	55.0	120	2	S48798

30	476	54.9	119	2	C36005	Ig heavy chain V r
31	476	54.9	221	2	S49220	Ig gamma-1 chain -
32	471.5	54.4	112	2	PH1647	Ig heavy chain V r
33	469	54.1	109	2	PH1649	Ig heavy chain V r
34	468.5	54.0	135	2	I37778	Ig variable region
35	467.5	53.9	475	2	S01321	Ig gamma-2b chain
36	466.5	53.8	114	2	S46391	Ig heavy chain V r
37	465.5	53.7	120	2	S49590	Ig heavy chain V r
38	465	53.6	134	2	S31679	Ig heavy chain V r
39	464	53.5	134	2	S31699	Ig heavy chain V r
40	463.5	53.5	136	2	S31587	Ig heavy chain V r
41	460.5	53.1	114	2	S46390	Ig heavy chain V r
42	460.5	53.1	114	2	S31120	Ig heavy chain - h
43	460	53.1	121	2	I35673	Ig heavy chain - h
44	460	53.1	127	2	S38489	Ig heavy chain - h
45	459	52.9	123	2	S26794	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S38864

Ig epsilon chain C region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001

C;Accession: S38864

R;Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A;Description: Combination of a defined specificity and desired isotype by cloning of an

A;Reference number: S38864

A;Accession: S38864

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-548 <KIP>

A;Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;353-421/Domain: immunoglobulin homology <IMM>

Query Match 71.9%; Score 623.5; DB 2; Length 548;

Best Local Similarity 70.3%; Pred. No. 2.2e-42;

Matches 121, Conservative 17, Mismatches 29; Indels 5; Gaps 1;

Qy 1 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWVSTISVSGITTYVDSVKGR 60

Db 8 GGLVQPGGSLRLSCAASGLTFSYGMWVRQIPDKRLWVATISSGCTTYYPDSVKGR 67

Qy 61 FTISRDNKNTLYLQNSLRADTAIVYCAK-----IFGVVWGQGLVTVSSASTKGPS 115

Db 68 FTISRDNKNTLYLQNSLRADTAIVYCAK-----IFGVVWGQGLVTVSSASTKGPS 127

Qy 116 VFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTFPAVLQS 167

Db 128 VFPLAPCSAAQTNSMTVLGCLVKGYFPEPVTVSWNIGALTSGVHTFPAVLQS 179

RESULT 2

S68213

Ig heavy chain (Mab03-1) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C;Accession: S68213

R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Imanaka, T.

FEBS Lett. 375, 273-276, 1995

A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin

A;Reference number: S68211; MUID:96085223; PMID:7498516

A;Accession: S68213

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-213 <TAK>

A;Cross-references: UNIPROT:Q91Z05; EMBL:D29667

C;Superfamily: immunoglobulin C region; immunoglobulin homology

F;137-201/Domain: immunoglobulin homology <IMM>

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Query Match 68.1%; Score 590; DB 2; Length 213;
Best Local Similarity 68.0%; Pred. No. 3.9e-40;
Matches 115; Conservative 18; Mismatches 34; Indels 2; Gaps 1;

QY 1 GGGVLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 60
DB 8 GGGVLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 67

QY 61 FTISRDNKSNLYLQMSLRAEDTAVYCAKRI--IFGVWVGQGLTVTVSSASTKGPSVFP 118
DB 68 FTISRDNKSNLYLQMSLRAEDTAVYCAKRI--IFGVWVGQGLTVTVSSASTKGPSVFP 127

QY 119 LAPCSRSTSTSTALGCLVKDYPEPTVTSNWLKALTSGLVHTPPAVLQS 167
DB 128 LAPCGDITGSSVTLGCLVKGYFPEPVTVTVNSGSLSSVHTPPALLQS 176

RESULT 3
S23624
IG heavy chain V region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S23624
R/Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gill, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;
J. Exp. Med. 175, 831-842, 1992
A/Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from
A/Reference number: S23623; MUID:92156804; PMID:1740665
A/Accession: S23624
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-143 <OLE>
A/Cross-references: EMBL:X59703; NID:g32012; PIDN:CAA42224.1; PID:g32013
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 67.1%; Score 582; DB 2; Length 143;
Best Local Similarity 84.6%; Pred. No. 1.1e-39;
Matches 115; Conservative 6; Mismatches 13; Indels 2; Gaps 1;

QY 1 GGGVLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 60
DB 8 GGGVLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 67

QY 61 FTISRDNKSNLYLQMSLRAEDTAVYCAKRI--GVWVGQGLTVTVSSASTKGPSVFP 118
DB 68 FTISRDNKSNLYLQMSLRAEDTAVYCAKRI--GVWVGQGLTVTVSSASTKGPSVFP 127

QY 119 LAPCSRSTSTSTALG 134
DB 128 LAPCSRSTSGTALG 143

RESULT 4
B31790
IG heavy chain V region (17/9) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C/Accession: B31790
R/Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A/Title: Preliminary crystallographic data, primary sequence, and binding data for an
A/Reference number: A92686; MUID:89034213; PMID:3182835
A/Accession: B31790
A/Molecule type: mRNA
A/Residues: 1-254 <SCH>
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/15-98/Domain: immunoglobulin homology <IMM>

Query Match 66.5%; Score 576.5; DB 2; Length 254;
Best Local Similarity 66.9%; Pred. No. 5.6e-39;
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```
Matches 121; Conservative 19; Mismatches 26; Indels 15; Gaps 6;

QY 1 GGGVLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 60
DB 8 GGGVLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 67

QY 61 FTISRDNKSNLYLQMSLRAEDTAVYCAKRI-----FGVWVGQGLTVTVSSASTKGP 114
DB 68 FTISRDNKSNLYLQMSLRAEDTAVYCAKRI-----FGVWVGQGLTVTVSSASTKGP 126

QY 115 SVPLAPCSR--STSTSTALGCLVKDYPEPTVTSNWLKALTSGLVHTPPAVLQ 166
DB 127 SVPLAPCSR--STSTSTALGCLVKDYPEPTVTSNWLKALTSGLVHTPPAVLQ 186

QY 167 S 167
DB 187 S 187

RESULT 5
S68211
IG heavy chain (Mab13-1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000
C/Accession: S68211
R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A/Reference number: S68211; MUID:96085223; PMID:7498516
A/Accession: S68211
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-220 <TAK>
A/Cross-references: EMBL:D29669; NID:g473958; PIDN:BA06140.1; PID:g473959
A/Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequence
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F/136-200/Domain: immunoglobulin homology <IMM>

Query Match 64.1%; Score 555.5; DB 2; Length 220;
Best Local Similarity 62.8%; Pred. No. 2.3e-37;
Matches 108; Conservative 22; Mismatches 37; Indels 5; Gaps 3;

QY 1 GGGVLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISV--SGITTYVDSVK 58
DB 4 GGGVLVPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISV--SGITTYVDSVK 63

QY 59 GRTISRDNKSNLYLQMSLRAEDTAVYCAKRI--IFGVWVGQGLTVTVSSASTKGPS 115
DB 64 GRTISRDNKSNLYLQMSLRAEDTAVYCAKRI--IFGVWVGQGLTVTVSSASTKGPS 123

QY 116 VFPLAPCSRSTSTSTALGCLVKDYPEPTVTSNWLKALTSGLVHTPPAVLQS 167
DB 124 VFPLAPGSAQTNSMTLGLCLVKGYFPEPVTVTVNSGSLSSGVHTPPAVLQS 175

RESULT 6
PC4436
monoclonal antibody 13-1 heavy chain - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000
C/Accession: PC4436
R/Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.;
Biochem. Biophys. Res. Commun. 240, 566-572, 1997
A/Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A/Reference number: JCS810; MUID:98063277; PMID:9398605
A/Accession: PC4436
A/Molecule type: protein
A/Residues: 1-444 <AKA>
C/Comment: This catalytic antibody has peroxidase oxidase activity. It is directed against
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F/251-320/Domain: immunoglobulin homology <IMM>
F/22/Disulfide bonds: interchain (to 98) #status predicted
F/99/Disulfide bonds: interchain (to 109) #status predicted
```

Query Match 64.1%; Score 555.5; DB 2; Length 444;
Best Local Similarity 62.8%; Pred. No. 4.7e-37;
Matches 108; Conservative 22; Mismatches 37; Indels 5; Gaps 3;

QY 1 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISV--SGITTYVDSVK 58
DB 8 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISV--SGITTYVDSVK 67

QY 59 GRFTISRDNSKNTLYLQMSLRADTAIVYCAK--RIFGV-VWGQGLTVTVSSASTKGPS 115
DB 68 GRFTISRDNSKNTLYLQMSLRADTAIVYCAK--RIFGV-VWGQGLTVTVSSASTKGPS 127

QY 116 VFPAPCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
DB 128 VYLPAPGSAQTSMVLTGLCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 179

RESULT 7
A49444
Ig gamma-1 heavy chain (New) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-Mar-1994 #sequence_revision 03-Mar-1994 #text_change 16-Jul-1999
C:Accession: A49444
R:Saul, P.A.; Poljak, R.J.
Proteins 14, 363-371, 1992
A:Title: Crystal structure of human immunoglobulin fragment Fab New refined at 2.0 A resolution
A:Reference number: A49444; MUID:93066153; PMID:1438175
A:Accession: A49444
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-220 <SAU>
A:Note: sequence modified after extraction from NCBI backbone
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-202/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 546; DB 2; Length 220;
Best Local Similarity 64.1%; Pred. No. 1.3e-36;
Matches 109; Conservative 22; Mismatches 35; Indels 4; Gaps 3;

QY 1 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISVSGITTYVDSVKGR 60
DB 8 GPGVLVRESQTLSTCTVSGTSFDDYVWTVKQPPGRLGWIYGYFTG-TTLDPSPGR 66

QY 61 FTISRDNSKNTLYLQMSLRADTAIVYCAKRI--GV-VWGQGLTVTVSSASTKGPSVF 117
DB 67 VTMLVNTSKQFSLRLSSVTHADTAIVYCAKRLTAGGIDVWGQGLTVTVSSASTKGPSVF 126

QY 118 PLAPCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
DB 127 PLAPSSKSTSGTAAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 176

RESULT 8
S69131
Ig heavy chain (DOT) - human (fragment)
N:Alternate names: anti-riboflavin IGG Fd fragment
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C:Accession: S69131
R:Stoppini, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A:Reference number: S69130; MUID:95255298; PMID:7737190
A:Accession: S69131
A:Molecule type: protein
A:Residues: 1-241 <STO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>
F:140-205/Domain: immunoglobulin homology <IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 61.8%; Score 535.5; DB 2; Length 241;
Best Local Similarity 63.1%; Pred. No. 9.9e-36;
Matches 106; Conservative 22; Mismatches 31; Indels 9; Gaps 4;

QY 7 PGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISV--VSGITTYVDSVKGRFTISR 65
DB 14 PGASVRLSCASGAFENYIHWVRQAPKGLWGMGFNPVAGAVS--SEKFRDLVMS 71

QY 66 DNSKNTLYLQMSLRADTAIVYCAK----RIFGV-VWGQGLTVTVSSASTKGPSVPL 119
DB 72 DTSANTVSMQLRNLRSDDTGRYFCARVSYDFSQVGMVWGQGLTVTVSSASTKGPSVPL 131

QY 120 APCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
DB 132 APCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 179

RESULT 9
S05271
Ig heavy chain precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: S05271; S04602
R:Kishimoto, T.
submitted to the EMBL Data Library, March 1989
A:Reference number: S05270
A:Accession: S05271
A:Molecule type: mRNA
A:Residues: 1-160 <KIS1>
A:Cross-references: UNIPROT:Q96BB9; EMBL:X14584
R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.
Nucleic Acids Res. 17, 4385, 1989
A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of a
A:Reference number: S04601; MUID:89296497; PMID:2500644
A:Accession: S04602
A:Molecule type: mRNA
A:Residues: 1-144 <KIS2>
A:Cross-references: EMBL:X14584
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-160/Product: Ig heavy chain (fragment) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 59.7%; Score 518; DB 2; Length 160;
Best Local Similarity 77.3%; Pred. No. 1.6e-34;
Matches 102; Conservative 7; Mismatches 13; Indels 10; Gaps 2;

QY 1 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISVSGITTYVDSVKGR 60
DB 27 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISVSGITTYVDSVKGR 86

QY 61 FTISRDNSKNTLYLQMSLRADTAIVYCAKRI-----FGV-VWGQGLTVTVSSAS 110
DB 87 FTISRDNSKNTLYLQMSLRADTAIVYCAKRVGVISVYVYGMVWGQGLTVTVSSGS 146

QY 111 TKGPSVFPPLAPC 122
DB 147 ASATPLPPLVSC 158

RESULT 10
S22080
Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
N:Alternate names: Ig gamma-1 chain C region (Clone 8.10)
C:Species: Bos primigenius taurus (cattle)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S22080; S06610; A31303
R:Sanders, P.G.
submitted to the EMBL Data Library, November 1991
A:Reference number: S22080

```
A;Accession: S22080
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-470 <SAN>
R;Cross-references: EMBL:X62916; NID:g439; PIDN:CAA44699.1; PID:g440
R;Symons, D.B.A.; Clarkon, C.A.; Beale, D.
Mol. Immunol. 26, 841-850, 1989
A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2
A;Reference number: S06610; MUID:90097956; PMID:2513487
A;Accession: S06610
A;Molecule type: DNA
A;Residues: 142-470 <SYM>
A;Cross-references: EMBL:X16701
A;Note: the sequence was determined from the germline gene
C;Genetics:
A;Gene: Ig CH gamma-1
A;Introns: 98/1; 111/1; 221/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
F;161-225/Domain: immunoglobulin homology <IMM>
F;318/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 59.3%; Score 514.5; DB 2; Length 470;
Best Local Similarity 57.7%; Pred. No. 9.3e-34;
Matches 101; Conservative 23; Mismatches 42; Indels 9; Gaps 2;

Qy 1 GGGIVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GPSLVKPSQTLSTCTVSGFSLSSYALTWRQAPGKALEWVGGIT-SGGTTYNPALKSR 85
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGV-----WGQGLTVTVSSASTK 112
Db 86 LSITKENSQVLSVSVTPEDTATYYCARSTGEVGDGAIDAWQGLLTVTVSSASTT 145
Qy 113 GPSVFPAPCSRSTSESTAALGCLVKDYPFPPTVTSWNLGALTSGVHTFPAVLQS 167
Db 146 APKVYPLSSCGDSSSTVTLGCLVSSYPPEPTVTWNSGALKSGVHTFPAVLQS 200

RESULT 11
S69340
Ig heavy chain VHIII-D-JH-CH3 region - human
C;Species: Homo sapiens (man)
C;Date: 28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change 21-Jan-2000
C;Accession: S69340
R;Khamlichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A;Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A;Reference number: S69339; MUID:95262687; PMID:7744049
A;Accession: S69340
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-249 <KHA>
A;Cross-references: EMBL:X81696
C;Superfamily: immunoglobulin C region; immunoglobulin homology
F;162-229/Domain: immunoglobulin homology <IMM>

Query Match 57.4%; Score 497.5; DB 2; Length 249;
Best Local Similarity 57.4%; Pred. No. 1.1e-32;
Matches 101; Conservative 19; Mismatches 47; Indels 9; Gaps 2;

Qy 1 GGGIVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVVQGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 86
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGV-----WGQGLTVTVSSASTK 112
Db 87 FTISRDNSENQLYLQMSLRAEDTAVYYCAKDVSVIHLPSAIFHWGGTRVIVSSGQPR 146
Qy 113 GPSVFPAPCSRSTSESTAALGCLVKDYPFPPTVTSW-NLGALTSGVHTFPAVLQS 167
Db 147 EPQVYTLPPSRSEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPPVLDS 202
```

RESULT 12

```
S20782
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C;Accession: S20782
R;Mortari, F.; Wang, J.; Schroeder, H.W.
submitted to the EMBL Data Library, April 1992
A;Description: Analysis of the IGA and IGH rearranged VH repertoire of human cord blood
A;Reference number: S20765
A;Accession: S20782
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-124 <MOR>
A;Cross-references: EMBL:Z11946; NID:g33897; PIDN:CAA78003.1; PID:g33898
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
```

Query Match 57.2%; Score 495.5; DB 2; Length 124;
Best Local Similarity 85.5%; Pred. No. 7.8e-33;
Matches 100; Conservative 3; Mismatches 5; Indels 9; Gaps 2;

```
Qy 1 GGGIVQGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db 8 GGGIVQGGSLRLSCAASGFTFSYAMSWVRQAPGEGLEWVSTISGSDSTYYADSVKGR 67
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGV-----WGQGLTVTVSS 108
Db 68 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGVPHFDYWGQGLTVTVSS 124
```

RESULT 13

```
S37483
Ig gamma-2a chain - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S37483
R;Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A;Reference number: S37483
A;Accession: S37483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-469 <DUC>
A;Cross-references: EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PID:g406253
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: immunoglobulin
F;276-345/Domain: immunoglobulin homology <IMM>
```

Query Match 56.9%; Score 493.5; DB 2; Length 469;
Best Local Similarity 52.9%; Pred. No. 4.4e-32;
Matches 91; Conservative 34; Mismatches 42; Indels 5; Gaps 1;

```
Qy 1 GGGIVQGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db 27 GPGLVPEASVKLSCKASGFTFTDYINWVKPQGGKLGKIGWIPASGNTKYNENFGK 86
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGV-----WGQGLTVTVSSASTKPS 115
Db 87 ATLTVDTSSSTAYWQLSSLTSEDVAVYFCARAMGATATLLDYWGQGLTLTVSSAKTTAPS 146
Qy 116 VFPLAPCSRSTSESTAALGCLVKDYPFPPTVTSWNLGALTSGVHTFPAVLQS 167
Db 147 VYPLAPVCGDITGSSVTGLCLVKGFYPPPTVLTWNSGSLSSGVHTFPAVLQS 198
```

RESULT 14

```
S17597
Ig delta chain (WIE) - human
N;Alternate names: myeloma protein WIE
C;Species: Homo sapiens (man)
```


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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 62.3661 Seconds
(without alignments)
1371.214 Million cell updates/sec

Title: US-09-784-950-40
Perfect score: 867
Sequence: 1 GGGLVQGGSLRLSCAASGF.....SWNLGALTSGVHTFPAVLQ 167

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	740	85.4	464	Q6MZU6	Q6mz6 homo sapien
2	726.5	83.8	465	Q6P6C4	Q6p6c4 homo sapien
3	724	83.5	478	Q6PI81	Q6pi81 homo sapien
4	723	83.4	470	Q6PJ44	Q6pj44 homo sapien
5	710.5	81.9	475	Q6MZ06	Q6mz06 homo sapien
6	709	81.8	472	Q6N089	Q6n089 homo sapien
7	705.5	81.4	473	Q6MZV7	Q6mzv7 homo sapien
8	704	81.2	466	Q6IN78	Q6in78 homo sapien
9	677.5	78.1	475	Q6GMW7	Q6gmw7 homo sapien
10	672.5	77.6	544	Q6PJ95	Q6pj95 homo sapien
11	663	76.5	480	Q6N094	Q6n094 homo sapien
12	657	75.8	466	Q6N096	Q6n096 homo sapien
13	656	75.7	470	Q6Z5W1	Q6z5w1 homo sapien
14	654	75.4	493	Q68CN4	Q68cn4 homo sapien
15	647.5	74.7	473	Q6P055	Q6p055 homo sapien
16	645	74.4	521	Q6N4Y9	Q6n4y9 homo sapien
17	641	73.9	482	Q6Z351	Q6z351 homo sapien
18	632	72.9	417	Q6N093	Q6n093 homo sapien
19	616.5	71.1	481	Q6N097	Q6n097 homo sapien
20	597	68.9	458	Q65ZQ1	Q65zq1 homo sapien
21	596.5	68.8	473	Q91Z05	Q91z05 mus musculus
22	594.5	68.6	471	Q66K04	Q66k04 mus musculus
23	585	67.5	464	Q6PIP8	Q6pip8 mus musculus
24	577.5	66.6	597	Q66BB9	Q66bb9 homo sapien
25	572.5	66.0	473	Q6TC63	Q6tc63 homo sapien
26	566	65.3	476	Q6GMX1	Q6gmx1 homo sapien
27	565.5	65.2	469	Q7Z7P5	Q7z7p5 homo sapien
28	563.5	65.0	518	Q6N030	Q6n030 homo sapien
29	563	64.9	613	Q6WUK1	Q6wuk1 homo sapien
30	553.5	63.8	465	Q6GMX6	Q6gmx6 homo sapien
31	552	63.7	606	Q6GMY2	Q6gmy2 homo sapien

32	550	63.4	208	2	Q6ZP87	Q6zpb7 homo sapien
33	549.5	63.4	475	2	Q6N095	Q6n095 homo sapien
34	541	62.4	476	2	Q6MZX7	Q6mzx7 homo sapien
35	539	62.2	480	2	Q6PJF1	Q6pjf1 homo sapien
36	537	61.9	573	2	Q6WU38	Q6wu38 homo sapien
37	522	60.2	493	2	Q6GMX2	Q6gmx2 homo sapien
38	516.5	59.6	494	2	Q6K6E8	Q6k6e8 homo sapien
39	513.5	59.2	147	2	Q9Y509	Q9y509 homo sapien
40	510	58.8	473	2	Q9DBL4	Q9dbl4 mus musculus
41	504.5	58.2	463	2	Q99LC4	Q99lc4 mus musculus
42	499.5	57.6	487	2	Q99KA4	Q99ka4 mus musculus
43	498.5	57.5	465	2	Q6PJB2	Q6pjb2 mus musculus
44	497.5	57.4	487	2	Q6ZVX0	Q6zvx0 homo sapien
45	497	57.3	499	2	Q8N5K4	Q8n5k4 homo sapien

ALIGNMENTS

RESULT 1
Q6MZU6 PRELIMINARY; PRT; 464 AA.
AC Q6MZU6; 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C15213.
GN Name=DKFZp686C15213;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RG The German Human cDNA Consortium;
RA Bloeker H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640874; CAB45931.1; -.
DR HSSP; P01861; 1ADO.
DR InterPro; IPR003599; Ig-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2; 3.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOW_N.
KW Hypothetical protein_
SQ SEQUENCE 464 AA; 51099 MW; 2FCA72C66E8A0ABC CRC64;

Query Match 85.4%; Score 740; DB 2; Length 464;
Best Local Similarity 85.4%; Pred. No. 1.4e-62;
Matches 146; Conservative 9; Mismatches 12; Indels 4; Gaps 3;

Qy	1	GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPKGLWVSTISV-SGITTYVDSVKG	59
Db	27	GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPKGLWVSSFRGGSYEYVADS VKG	86
Qy	60	RFTISRDNKNILYQWNSLRAEDTAVVYCAKRI--FGV-VWGQCTLVTVSSASTKGPSV	116
Db	87	RFTISRDNKNILYQWNSLRAEDTAVVYCAKRI--FGV-VWGQCTLVTVSSASTKGPSV	146
Qy	117	FPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 167	
Db	147	FPLAPCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 197	

RESULT 2

```
Q6P6C4
ID Q6P6C4 PRELIMINARY; PRT; 465 AA.
AC Q6P6C4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RT TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC062335; AAHE2335.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 465 AA; 51325 MW; FDDB9348ADC37B6D CRC64;

Query Match 83.8%; Score 726.5; DB 2; Length 465;
Best Local Similarity 82.5%; Pred. No. 2.7e-61;
Matches 14; Conservative 8; Mismatches 17; Indels 5; Gaps 1;

Qy 2 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGRF 61
Db 28 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGRF 87
Qy 62 TISRDNSKNILYQMNLSRAEDTAVYCAK-----RIFGVVWGQGLTVTVSSASTKGPSV 116
Db 88 TISRDNARTLTLYQMNLSRLAEEDTAVYCAKIPGRCFYDFWGHGTLTVTVSSASTKGPSV 147
Qy 117 PFLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQ 167
Db 148 PFLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQ 198

RESULT 3
Q6PI81 PRELIMINARY; PRT; 478 AA.
AC Q6PI81
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RT TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC041037; AAH41037.1; -.
DR HSSP; P01861; 1ADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00407; IGcl; 3.
DR PROSITE; PS50835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 478 AA; 52666 MW; 17BED38D917970D6 CRC64;

Query Match 83.5%; Score 724; DB 2; Length 478;
Best Local Similarity 79.0%; Pred. No. 4.9e-61;
Matches 143; Conservative 6; Mismatches 18; Indels 14; Gaps 1;

Qy 1 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 86
Qy 61 FTISRDNSKNILYQMNLSRAEDTAVYCAK-----RIFGVVWGQGLTVTV 106
Db 87 FTISRDNAKNSLYQMNLSRAEDTAVYCAKFEFTTMTTNADYFYFMDVWGKGTITV 146
Qy 107 SSASTKGPSVFPPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQ 166
Db 147 SSASTKGPSVFPPLAPCSRSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQ 206
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Qy 167 S 167
Db 207 S 207

RESULT 4
Q6PJA4 PRELIMINARY; PRT; 470 AA.
ID Q6PJA4
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smaluk D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strauberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7849556A11FD7D99 CRC64;

Query Match 83.4%; Score 723; DB 2; Length 470;
Best Local Similarity 82.7%; Pred. No. 6e-61;
Matches 143; Conservative 5; Mismatches 19; Indels 6; Gaps 1;

Qy 1 GGGVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
27 GGGVQPGGSLRLSCWVGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 86
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 FTISRDNSKNLYLQMSLRADTAIVYCAK-----RIFGVVVGQGLTVTVSSASTKGP 114
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 FTISRDNAKNSLYLQMSLRADTAIVYCAKDGSSWRDWFDPWGQGLTVTVSSASTKGP 146
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 5
Q6MZQ6 PRELIMINARY; PRT; 475 AA.
ID Q6MZQ6
AC Q6MZQ6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686G11190.
GN Name=DKF2p686G11190;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Lauber J., Bahr A., Mewes H.W., Weil B., Amid C., Osanger A., Fobo G.,
RA Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640947; CAB45972.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 475 AA; 52043 MW; B7EAE255A26F4B8E CRC64;

Query Match 81.9%; Score 710.5; DB 2; Length 475;
Best Local Similarity 79.2%; Pred. No. 9.6e-60;
Matches 141; Conservative 11; Mismatches 15; Indels 11; Gaps 2;

Qy 1 GGGVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
27 GGGVQPGGSLRLSCAASGFTFRNYANWVRQAPGKLEWVSGISSGVTYYADSVKGR 86
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 FTISRDNSKNLYLQMSLRADTAIVYCAK---RIFGV-----VWGQGLTVTVSSA 109
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
87 FTISGDI STNTLYLQMSLRADTAIVYCARADYDQVSPAYWYFDWGRGLTVSVSAA 146
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 6
Q6N089 PRELIMINARY; PRT; 472 AA.
ID Q6N089
AC Q6N089;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKF2p686P15220.
GN Name=DKF2p686P15220;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RC TISSUE=Human rectum tumor;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640627; CAE45781.1; -.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 472 AA; 51724 MW; 26CB340D0046D279 CRC64;

Query Match 81.8%; Score 709; DB 2; Length 472;
Best Local Similarity 81.1%; Pred. No. 1.3e-59;
Matches 142; Conservative 6; Mismatches 19; Indels 8; Gaps 2;

Qy 1 GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 FTISRDNSKNILYLQMSLRAEDTAVYYCAKRI-----FGV-VMQQGLVTVSSASTK 112
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 87 FTISRDNGKSLYLQMSLRAEDTALYYCAKEIGAHNFYFYGMVWGQGITVTVSSASTK 146
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 113 GPSVFPPLAPCSRSTSESTAALGCLVKDYPPEPTVTSWNLGALTSVGVHTFPAVLQS 167
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 147 GPSVFPPLAPSSKSTSGGTAALGCLVKDYPPEPTVTSWNSGALTSVGVHTFPAVLQS 201
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 7
Q6MZV7 PRELIMINARY; PRT; 473 AA.
AC Q6MZV7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686C11235.
GN Name=DKFZp686C11235;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human small intestine;
RA Bloecher H., Boecher M., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640853; CAE45920.1; -.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.

SQ SEQUENCE 473 AA; 52121 MW; 9476AE4C0BFC447 CRC64;

Query Match 81.4%; Score 705.5; DB 2; Length 473;
Best Local Similarity 79.0%; Pred. No. 2.9e-59;
Matches 139; Conservative 11; Mismatches 17; Indels 9; Gaps 1;

Qy 1 GGGLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 FTISRDNSKNILYLQMSLRAEDTAVYYCAK-----IFGVVNGQTLTVSSAST 111
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 87 FTISRDNARNSLYLQMSLRAEDTAVYYCARQNEHTSPWYPSFFDYWGQGLVTVSSAST 146
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 112 KGPSVFPPLAPCSRSTSESTAALGCLVKDYPPEPTVTSWNLGALTSVGVHTFPAVLQS 167
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy 147 KGPSVFPPLAPSSKSTSGGTAALGCLVKDYPPEPTVTSWNSGALTSVGVHTFPAVLQS 202
Db |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 8
Q6IN78 PRELIMINARY; PRT; 466 AA.
AC Q6IN78;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE IGHG1 protein.
GN Name=IGHG1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RN [1]
RP "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral Nervous System;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072419; AAH72419.1; -.
DR HSP; P01861; 1ADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig-cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
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DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 466 AA; 50853 MW; 53EB0BCDE81076E CRC64;
Query Match 81.2%; Score 704; DB 2; Length 466;
Best Local Similarity 82.4%; Pred. No. 4e-59;
Matches 140; Conservative 6; Mismatches 20; Indels 4; Gaps 2;
Qy 1 GGGVLPQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVLPQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISVSGITTYVDSVKGR 85
Qy 61 FTISRDNKNLYLQMSLRADTAIVYCAKRIQGV---VMGQGTLVTVSSASTKGPSVF 117
Db 86 FTISRDNKNLYLQMSLRADTAIVYCAKRIQGV---VMGQGTLVTVSSASTKGPSVF 145
Qy 118 PLAPCSRSTSESTAALGCLVDPPEPVTVMNGLGALTSVGHVTFPAVLQS 167
Db 146 PLAPSSKSTSGTAAALGCLVDPPEPVTVMNGLGALTSVGHVTFPAVLQS 195
RESULT 9
Q6GMW7
ID Q6GMW7 PRELIMINARY; PRT; 475 AA.
AC Q6GMW7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073782; AAH73782.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003599; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 475 AA; 51987 MW; 2A1P55D736860F8 CRC64;
Query Match 78.1%; Score 677.5; DB 2; Length 475;
Best Local Similarity 77.0%; Pred. No. 1.4e-56;
Matches 137; Conservative 8; Mismatches 22; Indels 11; Gaps 2;
Qy 1 GGGVLPQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVLPQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISVSGITTYVDSVKGR 86
Qy 61 FTISRDNKNLYLQMSLRADTAIVYCAKRIQGV---VMGQGTLVTVSSASTKGPSVF 109
Db 87 FTISRDNKNLYLQMSLRADTAIVYCAKRIQGV---VMGQGTLVTVSSASTKGPSVF 146
Qy 110 STKGPSVFPPLAPCSRSTSESTAALGCLVDPPEPVTVMNGLGALTSVGHVTFPAVLQS 167
Db 147 STKGPSVFPPLAPCSRSTSESTAALGCLVDPPEPVTVMNGLGALTSVGHVTFPAVLQS 204
RESULT 10
Q6PJ95
ID Q6PJ95 PRELIMINARY; PRT; 544 AA.
AC Q6PJ95
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019046; AAH19046.1; -.
DR HGSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 3.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 4.

```

DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 544 AA; 60102 MW; 1895814B2297C668 CRC64;

Query Match
Best Local Similarity 77.6%; Score 672.5; DB 2; Length 544;
Matches 136; Conservative 5; Mismatches 25; Indels 13; Gaps 2;

QY 1 GGGVOPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
DB 27 GGGVOPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 86
QY 61 FTISRDNSKNILYLQMSLRAEDTAVYYCAK-----RIFGVWVGQGLTVTVSS 108
DB 87 FTISRDNSKNILYLQMSLRAEDTAVYYCAKDPWYSNSWFLTNFD-SWGRGTLTVTVSS 145
QY 109 ASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTTTPAVLQS 167
DB 146 ASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTTTPAVLQS 204

RESULT 11
Q6N094 ID Q6N094 PRELIMINARY; PRT; 480 AA.
AC Q6N094;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein DKFZp686O01196;
GN Name=DKFZp686O01196;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640622; CAB45776.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52612 MW; 225247F3D35AEC18 CRC64;

Query Match
Best Local Similarity 76.5%; Score 663; DB 2; Length 480;
Matches 131; Conservative 15; Mismatches 21; Indels 16; Gaps 2;

QY 1 GGGVOPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
DB 27 GGGVOPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 86
QY 61 FTISRDNSKNILYLQMSLRAEDTAVYYCAK-----RIFGVW-----WGQGLTV 104
DB 87 FTISRDNSKNILYLQMSLRAEDTAVYYCAKRGWVPAGPTSTSGPVHRNWFDPGQGLTV 146
QY 105 TVSSASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTTTPAV 164
DB 147 TVSSASTKGPSVFFLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTTTPAV 206

```

```

QY 165 LQS 167
DB 207 LQS 209

RESULT 12
Q6N096 ID Q6N096 PRELIMINARY; PRT; 466 AA.
AC Q6N096;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein DKFZp686I15196;
GN Name=DKFZp686I15196;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human esophagus tumor;
RG The German Human cDNA Consortium;
RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Oeanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX640620; CAB45774.1; -.
DR HSP; P01861; IADQ.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 50926 MW; 01E91B748D6D57C4 CRC64;

Query Match
Best Local Similarity 75.8%; Score 657; DB 2; Length 466;
Matches 131; Conservative 12; Mismatches 24; Indels 2; Gaps 1;

QY 1 GGGVOPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
DB 27 GGGVOPGGSLRLSCAASGTFSSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 86
QY 61 FTISRDNSKNILYLQMSLRAEDTAVYYCAKIFGVV--WGQGLTVTVSSASTKGPSVFP 118
DB 87 FTISRDNSKNILYLQMSLRAEDTAVYYCARGFGNPDQMGQGLTVTVSSASTKGPSVFP 146
QY 119 LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTTTPAVLQS 167
DB 147 LAPCSRSTSESTAALGCLVKDYFPEPVTVSWNIGALTSGVHTTTPAVLQS 195

RESULT 13
Q7Z5W1 ID Q7Z5W1 PRELIMINARY; PRT; 470 AA.
AC Q7Z5W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

```


[illegible]

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 77.4257 Seconds
(without alignments)
834.206 Million cell updates/sec

Title: US-09-784-950-40

Perfect score: 867

Sequence: 1 GGLVQGGSLRLSCAAGF.....SWNLGALTGVHTFPVQLQS 167

Scoring table: BLOSUM62DX
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	867	100.0	167	2 AAY34308	Aay34308 IgG antib
2	788	90.9	465	7 ADD93783	Add93783 Monoclonal
3	780	90.0	470	5 ABG77158	Abg77158 Germline
4	780	90.0	470	8 ADR28580	Adr28580 Human ant
5	774.5	89.3	467	6 ABP71365	Abp71365 Anti-OPGL
6	772	89.0	458	8 ADP07903	Adp07903 Human imm
7	769.5	88.8	445	6 AAO31101	Aao31101 Human A2-
8	767	88.5	470	5 ABG77157	Abg77157 Amino aci
9	767	88.5	470	8 ADR28579	Adr28579 Human ant
10	765.5	88.3	443	2 AA113564	Aa113564 Humanised
11	764.5	88.2	466	8 ADL93667	Adl93667 Human CD4
12	764	88.1	217	6 ABR01503	Abro1503 Human ant
13	764	88.1	444	6 ABR55342	Ab55342 Amino aci
14	763.5	88.1	367	6 ABP55467	Abp55467 MALF3 pr
15	763.5	88.1	462	8 ADL93670	Adl93670 Human CD4
16	763	88.0	217	6 ABR01505	Abro1505 Human ant
17	762.5	87.9	222	6 ABR01508	Abro1508 Human ant
18	761.5	87.8	220	6 ABR01519	Abro1519 Human ant
19	760.5	87.7	222	6 ABR01515	Abro1515 Human ant
20	760	87.7	217	6 ABR01509	Abro1509 Human ant
21	760	87.7	224	7 ADJ32114	Adj32114 Human int
22	758.5	87.5	224	6 ABR01513	Abro1513 Human ant
23	757.5	87.4	473	5 ABR015162	Abg77162 Germline
24	757.5	87.4	473	8 ADR28584	Adr28584 Human ant
25	757	87.3	221	6 ABR01506	Abro1506 Human ant

26	756.5	87.3	218	6 ABR01507	Abro1507 Human ant
27	756	87.2	221	6 ABR01534	Abro1534 Human ant
28	756	87.2	227	4 AAB75051	Aab75051 TRO005 Hu
29	755	87.1	217	6 ABR01504	Abro1504 Human ant
30	754.5	87.0	220	6 ABR01517	Abro1517 Human ant
31	754.5	87.0	462	8 ADL93668	Adl93668 Human CD4
32	754.5	87.0	464	8 ADL93661	Adl93661 Human CD4
33	753.5	86.9	462	8 ADL93660	Adl93660 Human CD4
34	752.5	86.8	224	6 ABR01511	Abro1511 Human ant
35	752	86.7	451	8 ADH34584	Adh34584 008 heavy
36	752	86.7	470	7 ADE28475	Ade28475 Human ant
37	751	86.6	463	8 ADL93665	Adl93665 Human CD4
38	750.5	86.6	628	6 ABJ38670	Abj38670 Fab expre
39	750.5	86.6	638	6 ADA89103	Ada89103 Phage dis
40	750.5	86.6	638	6 ADA90139	Ada90139 Anti-Abet
41	750.5	86.6	638	6 ADA91410	Ada91410 Anti-Abet
42	750.5	86.6	747	7 ADG74355	Adg74355 MSPRO lig
43	749.5	86.4	223	7 ADJ32132	Adj32132 Human int
44	749.5	86.4	460	8 ADL93664	Adl93664 Human CD4
45	749.5	86.4	468	8 ADL93666	Adl93666 Human CD4

ALIGNMENTS

RESULT 1
AAY34308
ID AAY34308 standard; protein; 167 AA.
XX
AC AAY34308;
XX
DT 19-NOV-1999 (first entry)
XX
DE IgG antibody 2.6.1 heavy chain sequence.
XX
KW Antibody: CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.
XX
OS Homo sapiens.
XX
PN WO9945031-A2.
XX
PD 10-SEP-1999.
XX
PF 03-MAR-1999; 99WO-US004583.
XX
PR 03-MAR-1998; 98US-00034607.
PR 03-FEB-1999; 99US-00244253.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;
PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;
XX
FI WPI; 1999-540816/45.
XX
N-PSDB; AAZ20409.
XX
PT New monoclonal antibody, used for treating e.g. graft versus host
PT disease, cancer, autoimmune diseases and inflammatory diseases.
XX
PS Claim 60; Fig 33; 245pp; English.
XX
CC This sequence represents the heavy chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

AC ABG77158;
XX
DT 24-OCT-2002 (first entry)
XX
DE Germline protein sequence of anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6.
XX
KW Insulin-like growth factor I receptor; antibody; human; cytostatic;
KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-IR; tumour;
KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
KW acromegaly; gigantism; psoriasis; atherosclerosis.
XX
OS Homo sapiens.
XX
XX WO200253596-A2.
XX
PD 11-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-US051113.
XX
XX 05-JAN-2001; 2001US-0259927P.
XX
XX (PFIZ) PFIZER INC.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
XX WPI; 2002-575410/61.
XX
XX Novel humanized, chimeric monoclonal antibody that specifically binds to
XX insulin-like growth factor I (IGF-I) receptor useful for inhibiting
XX binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
XX
XX Disclosure; Fig 19B; 172pp; English.
XX
XX This invention relates to a novel humanised, chimeric or human monoclonal
XX antibody or its antigen binding portion that specifically binds to
XX insulin-like growth factor I receptor (IGF-IR). The antibodies of the
XX invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
XX IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
XX phosphorylation. The antibodies of the invention are useful for
XX diagnosing the presence or location of an IGF-IR-expressing tumour in a
XX subject. The antibody or its antigen-binding portion is also useful for
XX treating cancer in a human. The method for this further involves an anti
XX neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
XX antibodies may also be useful for increasing IGF-IR activity and thus
XX restoring IGF-IR activity in a condition characterised by low IGF-IR
XX levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
XX also useful for inducing apoptosis of specific cells in a patient, and to
XX treat non-cancerous states or disease, e.g. acromegaly, gigantism,
XX psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
XX minimise the immunogenic and allergic responses intrinsic to mouse or
XX mouse-derived monoclonal antibodies and thus increase the efficacy
XX and safety of the administered antibodies. The present sequence
XX represents an anti-insulin-like growth factor I receptor antibody of the
XX invention
XX
SQ Sequence 470 AA;
Query Match 90.0%; Score 780; DB 5; Length 470;
Best Local Similarity 87.6%; Pred. No. 8.6e-57;
Matches 155; Conservative 3; Mismatches 9; Indels 10; Gaps 2;
QY 1 GGGLVOPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITYYVDSVKGR 60
DB 27 GGGLVOPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITYYVDSVKGR 86
QY 61 FTISRDNKNTLYLQMSRLAEADTAIVYCAK-----RIFGV-VWGQTLTVTSSAS 110
DB 87 FTISRDNKNTLYLQMSRLAEADTAIVYCAKGGSGWYIIYGGYGVGGTITVTVSSAS 146
QY 111 TKGPSVFLAPCSRSTSESTAAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167
DB 147 TKGPSVFLAPCSRSTSESTAAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 203

RESULT 4
ADR28580
ID ADR28580 standard; protein; 470 AA.
XX
XX ADR28580;
XX AC
XX 18-NOV-2004 (first entry)
DT
XX Human anti-IGF-IR antibody DP-47(3-23)/D6-19/JH6 protein SEQ ID NO:46.
XX
XX aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;
KW I-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;
KW neurodegenerative disorder; human;
KW anti-insulin-like growth factor I receptor antibody;
KW anti-IGF-IR antibody; cytostatic; immunosuppressive; endocrine;
KW vasotropic; neuroprotective; nootropic; antithyroid; vaccine;
KW gene therapy.
XX
XX Homo sapiens.
OS
XX WO2004071529-A2.
XX
XX 26-AUG-2004.
PD
XX 03-FEB-2004; 2004WO-IB000366.
XX
XX 13-FEB-2003; 2003US-0447353P.
XX
XX (PFIZ) PFIZER PROD INC.
XX
XX Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;
PI Cusmano JD, Guyot DJ, Page KL;
XX WPI; 2004-625776/60.
XX
XX Treating or preventing aging or a disorder (e.g. multiple myeloma,
XX autoimmune disease or neurodegenerative disorder) in humans comprises
XX administering an amount of a human anti-insulin-like growth factor I
XX receptor antibody.
XX
XX Disclosure; SEQ ID NO 46; 105pp; English.
XX
XX The present invention describes a method for treating or preventing aging
XX or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
XX disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
XX ischaemia or neurodegenerative disorder) in a mammal. The method
XX comprises administering to the mammal an amount of a human anti-insulin-
XX like growth factor I receptor (IGF-IR) antibody. Also described is a
XX pharmaceutical composition for treating or preventing the above-mentioned
XX disorder in a mammal, comprising an amount of the human anti-IGF-IR
XX antibody and a pharmaceutical carrier. The composition has cytostatic,
XX immunosuppressive, endocrine, vasotropic, neuroprotective, nootropic and
XX antithyroid activities, and can be used in vaccines and in gene therapy.
XX The method and composition are useful for preventing or treating aging or
XX a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
XX disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
XX ischaemia or neurodegenerative disorder) in mammals, such as humans. The
XX human IGF-IR antibody is used in preparing a composition for the
XX treatment or prevention of the above-mentioned disorders. The present
XX sequence represents a human anti-IGF-IR antibody heavy chain amino acid
XX sequence, which is used in the exemplification of the present invention.
XX
SQ Sequence 470 AA;
Query Match 90.0%; Score 780; DB 8; Length 470;
Best Local Similarity 87.6%; Pred. No. 8.6e-57;
Matches 155; Conservative 3; Mismatches 9; Indels 10; Gaps 2;
QY 1 GGGLVOPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITYYVDSVKGR 60
DB 27 GGGLVOPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITYYVDSVKGR 86

QY	61	FTISRDNKNTLYLQNNSLRAEDTAVVYCAK-----RIFGV-VWGQGLTVTVSSAS	110
DB	87	FTISRDNKNTLYLQNNSLRAEDTAVVYCAKGYSSGMYYYYGMDVWGQGLTVTVSSAS	146
QY	111	TKGSPVFPPLAPCSRSTSESTAALGCLVKDYPPEPTVTSNWLGALTSGVHTFPFVLOS	167
DB	147	TKGSPVFPPLAPCSRSTSESTAALGCLVKDYPPEPTVTSNWLGALTSGVHTFPFVLOS	203
RESULT 5			
ABP71365	ID	ABP71365 standard; protein; 467 AA.	
XX	AC	ABP71365;	
XX	AC		
DT	28-APR-2003	(first entry)	
XX	DE	Anti-OPGL-1 antibody heavy chain.	
XX	DE		
KW	KW	Osteoprotegerin ligand; osteopathic; antiinflammatory; antirheumatic;	
KW	KW	antiarthritic; cytostatic; OPGL; anti-OPGL-1; antibody.	
XX	OS	Mus musculus.	
XX	OS		
XX	Key	Location/Qualifiers	
XX	Key	1..19	
XX	Key	/note= "IgG2 signal peptide"	
XX	Key	20..141	
XX	Key	/note= "variable region"	
XX	Key	142..467	
XX	Key	/note= "constant region"	
XX	Key	WO2003002713-A2.	
XX	Key		
XX	Key	09-JAN-2003.	
XX	Key		
XX	Key	25-JUN-2002; 2003WO-US020181.	
XX	Key		
XX	Key	26-JUN-2001; 2001US-0301172P.	
XX	Key	(ABGE-) ABGENIX INC.	
XX	Key	(AMGE-) AMGEN INC.	
XX	Key	Boyle WJ, Martin FH, Corvalan JR, Davis GC;	
XX	Key	WPI; 2003-210262/20.	
XX	Key	N-PSDB; AB259147.	
XX	Key		
XX	Key	New antibodies that interact with osteoprotegerin ligands, useful for	
XX	Key	treating osteopenic disorders, e.g. osteoporosis, bone loss from	
XX	Key	arthritis, Paget's disease, osteopenia, osteomyelitis, hypercalcemia and	
XX	Key	osteonecrosis.	
XX	Key	Claim 1; Fig 2; 144pp; English.	
XX	Key		
XX	Key	The invention relates to antibodies that interact with osteoprotegerin	
XX	Key	ligands (OPGL). The antibody is useful for detecting the level of OPGL in	
XX	Key	a biological sample. The antibody, or the pharmaceutical composition	
XX	Key	comprising the antibody, is also useful for treating osteopenic disorder,	
XX	Key	an inflammatory condition with attendant bone loss, an autoimmune	
XX	Key	condition with attendant bone loss in a patient or rheumatoid arthritis	
XX	Key	in a patient. In particular, the antibody or composition is useful for	
XX	Key	treating bone diseases, e.g. osteoporosis, bone loss from arthritis,	
XX	Key	Paget's disease, osteopenia, endocrine osteoporosis (e.g. Cushing's	
XX	Key	syndrome or acromegaly), osteogenesis imperfecta, homocystinuria, Menkes'	
XX	Key	syndrome, Riley-Day syndrome, osteomyelitis, hypercalcemia, or	
XX	Key	osteonecrosis. The present sequence represents an anti-OPGL-1 antibody	
XX	Key	heavy chain	
XX	Key		
SQ	SQ	Sequence 467 AA;	

Best Local Similarity 88.5%; Pred. No. 2.5e-56;		Matches 154; Conservative 2; Mismatches 11; Indels 7; Gaps 1;	
QY	1	G G G L V P G G S L R L S C A A S G F T F S S Y A M S W R Q A P G K G L E W V S T I S V S G I T T Y Y V D S V K G R	60
Db	27	G G G L V P G G S L R L S C A A S G F T F S S Y A M S W R Q A P G K G L E W S G I T S G G S T Y Y A D S V K G R	86
QY	61	F T I S R D N S K N I L Y L O M N S L R A E D T A V Y Y C A K R I F G V V - - - - - W Q G G T L V T V S S A S T K G	113
Db	87	F T I S R D N S K N T L Y L O M N S L R A E D T A V Y Y C A K D P G T T V I M S W F D P W G Q G T L V T V S S A S T K G	146
QY	114	P S V F P L A P C S R S T S E S T A A L G C L I K D Y F P E P V T V S W N L G A L T S G V H T F P P A V L Q S	167
Db	147	P S Y F P L A P C S R S T S E S T A A L G C L I K D Y F P E P V T V S W N S G A L T S G V H T F P P A V L Q S	200
RESULT 6			
ADP07903			
ID	ADP07903 standard; protein; 458 AA.		
XX	ADP07903;		
XX	AC AC		
XX	29-JUL-2004 (first entry)		
DT			
XX	Human immunoglobulin heavy chain variable region.		
XX	monoclonal antibody; tumour growth factor-beta type II receptor;		
KW	TGF-beta type II receptor; kidney disease; nephrosclerosis;		
KW	pulmonary fibrosis; liver cirrhosis; blood-vessel restenosis;		
KW	arteriosclerosis; psoriasis; scleroderma; atopy; keloid; arthritis;		
XX	human; heavy chain variable region.		
XX			
OS	Homo sapiens.		
OS			
PN	JP2004121001-A.		
XX			
PD	22-APR-2004.		
XX			
PF	07-AUG-2002; 2002JP-00230651.		
XX			
PR	07-AUG-2002; 2002JP-00230600.		
XX			
PA	(NISR) JAPAN TOBACCO INC.		
XX			
DR	WPI; 2004-322721/30.		
DR	N-PSDB; ADP07902.		
XX			
PT	Novel monoclonal antibody coupled with human transforming growth factor		
PT	(TGF)-beta type II receptor, useful for treating or preventing		
PT	arteriosclerosis, psoriasis, scleroderma, atopy, keloid, arthritis.		
PS	Claim 29; SEQ ID NO 7; 78pp; Japanese.		
XX			
CC	The invention comprises a monoclonal antibody coupled with human tumour		
CC	growth factor-beta (TGF-beta) type II receptor. The monoclonal antibody		
CC	coupled with human TGF-beta type II receptor of the invention is useful		
CC	for treating or preventing: kidney disease, nephrosclerosis, pulmonary		
CC	fibrosis, liver cirrhosis, blood-vessel restenosis, arteriosclerosis,		
CC	psoriasis, scleroderma, atopy, keloid and arthritis. The present amino		
CC	acid sequence represents a human immunoglobulin heavy chain variable		
XX			
XX	Sequence 458 AA;		
Query Match 89.0%; Score 772; DB 8; Length 458;			
Best Local Similarity 91.0%; Pred. No. 3.9e-56;			
Matches 152; Conservative 3; Mismatches 10; Indels 2; Gaps 1;			
QY	1	G G G L V P G G S L R L S C A A S G F T F S S Y A M S W R Q A P G K G L E W V S T I S V S G I T T Y Y V D S V K G R	60
Db	27	G G G L V P G G S L R L S C A A S G F T F S S Y A M S W R Q A P G K G L E W I S V I S V G G S T Y Y A D S V K G R	86
QY	61	F T I S R D N S K N I L Y L O M N S L R A E D T A V Y Y C A K R I F G V V W G Q G T L V T V S S A S T K G S V P P L A	120

Query Match 89.3%; Score 774.5; DB 6; Length 467;

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Db      87 FTISRDNSKNTLYLQMNLSRAEDTAVYVC--EIAARIQGGQGLTVTVSSASTKGSVPFPLA 144
Qy      121 PCSRSTSESTAALGCLVKDYPPPEPTVTVSNLGGALTSVGHVHTFPVAVLQS 167
Db      145 PCSRSTSESTAALGCLVKDYPPPEPTVTVSNLGGALTSVGHVHTFPVAVLQS 191

RESULT 7
AAO31101
ID      AAO311101 standard; protein; 445 AA.
XX      AC      AAO311101;
XX      DT      06-OCT-2003 (first entry)
XX      DE      Human A2-G8 SCF antibody heavy chain variable and constant region.
XX      KW      Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;
XX      KW      steel factor; c-kit ligand; gene therapy.
XX      OS      Homo sapiens.
XX      PN      WO2003051311-A2.
XX      PD      26-JUN-2003.
XX      PF      16-DEC-2002; 2002WO-US040227.
XX      PR      17-DEC-2001; 2001US-0342174P.
XX      PA      (FARB ) BAYER. CORP.
XX      PI      Takeuchi T, Tomkinson A, Neben S;
XX      DR      WPI; 2003-523500/49.
XX      PT      New purified human antibody that binds to stem cell factor protein,
XX      PT      useful for preparing a composition for treating asthma.
XX      PS      Claim 9; Page 47; 94pp; English.
XX      CC      The invention provides human antibodies that bind to stem cell factor
XX      CC      (SCF) protein. SCF is also known as mast cell growth factor, steel factor
XX      CC      or c-kit ligand. Antibodies of the invention are useful for preparing
XX      CC      compositions for treating asthma. They are also used in gene therapy. The
XX      CC      present sequence is human SCF antibody heavy chain variable and constant
XX      CC      region
XX      SQ      Sequence 445 AA;
XX      Query Match      88.8%; Score 769.5; DB 6; Length 445;
XX      Best Local Similarity      89.4%; Pred. No. 6.1e-56;
XX      Matches 152; Conservative 3; Mismatches 12; Indels 3; Gaps 1;

Qy      1 GGGVLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db      5 GGGVLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLEWVSTISVSGITTYVDSVKGR 64
Qy      61 FTISRDNSKNTLYLQMNLSRAEDTAVYVCARIFGV---VWGQGLTVTVSSASTKGSVPF 117
Db      65 FTISRDNSKNTLYLQMNLSRAEDTAVYVCARRDPFAHFDVWGQGLTVTVSSASTKGSVPF 124
Qy      118 PLAPCSKSTSESTAALGCLVKDYPPPEPTVTVSNLGGALTSVGHVHTFPVAVLQS 167
Db      125 PLAPSSKSTSGTAAALGCLVKDYPPPEPTVTVSNLGGALTSVGHVHTFPVAVLQS 174

RESULT 8
ABG77157
ID      ABG77157 standard; protein; 470 AA.
XX      AC      ABG77157;

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XX      24-OCT-2002 (first entry)
XX      DE      Amino acid sequence of anti-IGF-1R antibody 2.13.2 Vh domain.
XX      KW      Insulin-like growth factor I receptor; antibody; human; cytostatic;
XX      KW      osteopathic; antiatherosclerotic; antipapillary; IGF-1R; tumour;
XX      KW      anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
XX      KW      acromegaly; gigantism; psoriasis; atherosclerosis.
XX      OS      Homo sapiens.
XX      PN      WO200253596-A2.
XX      PD      11-JUL-2002.
XX      PF      20-DEC-2001; 2001WO-US051113.
XX      PR      05-JAN-2001; 2001US-0259927P.
XX      PA      (PFIZ ) PFIZER INC.
XX      PA      (ABGE-) ABGENIX INC.
XX      PI      Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX      DR      WPI; 2002-575410/61.
XX      PT      Novel humanized, chimeric monoclonal antibody that specifically binds to
XX      PT      insulin-like growth factor I (IGF-1) receptor useful for inhibiting
XX      PT      binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
XX      PS      Claim 16; Fig 19B; 172pp; English.
XX      CC      This invention relates to a novel humanised, chimeric or human monoclonal
XX      CC      antibody or its antigen binding portion that specifically binds to
XX      CC      insulin-like growth factor I receptor (IGF-1R). The antibodies of the
XX      CC      invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
XX      CC      IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
XX      CC      phosphorylation. The antibodies of the invention are useful for
XX      CC      diagnosing the presence or location of an IGF-IR-expressing tumour in a
XX      CC      subject. The antibody or its antigen-binding portion is also useful for
XX      CC      treating cancer in a human. The method for this further involves an anti
XX      CC      neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
XX      CC      antibodies may also be useful for increasing IGF-IR activity and thus
XX      CC      restoring IGF-IR activity in a condition characterised by low IGF-IR
XX      CC      levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
XX      CC      also useful for inducing apoptosis of specific cells in a patient, and to
XX      CC      treat non-cancerous states or disease, e.g. acromegaly, gigantism,
XX      CC      psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
XX      CC      minimise the immunogenic and allergic responses intrinsic to mouse or
XX      CC      mouse-derived monoclonal antibodies and thus increase the efficacy
XX      CC      and safety of the administered antibodies. The present sequence
XX      CC      represents an anti-insulin-like growth factor I receptor antibody of the
XX      CC      invention
XX      SQ      Sequence 470 AA;
XX      Query Match      88.5%; Score 767; DB 5; Length 470;
XX      Best Local Similarity      85.3%; Pred. No. 1e-55;
XX      Matches 151; Conservative 6; Mismatches 10; Indels 10; Gaps 2;

Qy      1 GGGVLVQPGGSLRLSCAASGFTFSYAMSVWRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db      27 GGGVLVQPGGSLRLSCTASGFTFSYAMSVWRQAPGKGLEWVSTISVSGITTYVDSVKGR 86
Qy      61 FTISRDNSKNTLYLQMNLSRAEDTAVYVCARI-----FGV-VWGQGLTVTVSSAS 110
Db      87 FTISRDNSRTTLYLQMNLSRAEDTAVYVCARDLQWSDSYTYYYGMDVWGQGLTVTVSSAS 146
Qy      111 TKGPSVFPPLAPCSKSTSESTAALGCLVKDYPPPEPTVTVSNLGGALTSVGHVHTFPVAVLQS 167
Db      147 TKGPSVFPPLAPCSKSTSESTAALGCLVKDYPPPEPTVTVSNLGGALTSVGHVHTFPVAVLQS 203

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RESULT 9
 ADR28579 ID ADR28579 standard; protein; 470 AA.
 AC AC
 XX ADR28579;
 XX 18-NOV-2004 (first entry)
 DT XX
 DE Human anti-IGF-IR antibody heavy chain 2.13.2 protein SEQ ID NO:45.
 XX
 XX aging; multiple myeloma; liquid tumour; liver cancer; thymus disorder;
 KW T-cell-mediated autoimmune disease; endocrinological disorder; ischaemia;
 KW neurodegenerative disorder; human;
 KW anti-insulin-like growth factor I receptor antibody;
 KW anti-IGF-IR antibody; cytostatic; immunosuppressive; endocrine;
 KW vasotropic; neuroprotective; nootropic; antithyroid; vaccine;
 KW gene therapy.
 XX
 XX Homo sapiens.
 OS XX
 XX W02004071529-A2.
 PN XX
 PD 26-AUG-2004.
 XX
 XX 03-FEB-2004; 2004WO-IB000366.
 PF XX
 XX 13-FEB-2003; 2003US-0447353P.
 PR XX
 XX (PFIZ) PFIZER PROD INC.
 PA XX
 XX Cohen BD, Bedian V, Wang HF, Obrocea M, Gomez-Navarro J;
 PI Cuamano JD, Guyot DJ, Page KL;
 PI WPI; 2004-625776/60.
 DR XX
 XX Treating or preventing aging or a disorder (e.g. multiple myeloma,
 PT autoimmune disease or neurodegenerative disorder) in humans comprises
 PT administering an amount of a human anti-insulin-like growth factor I
 PT receptor antibody.
 XX
 XX Disclosure; SEQ ID NO 45; 105pp; English.
 PS
 XX The present invention describes a method for treating or preventing aging
 CC or a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
 CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
 CC ischaemia or neurodegenerative disorder) in a mammal. The method
 CC comprises administering to the mammal an amount of a human anti-insulin-
 CC like growth factor I receptor (IGF-IR) antibody. Also described is a
 CC pharmaceutical composition for treating or preventing the above-mentioned
 CC disorder in a mammal, comprising an amount of the human anti-IGF-IR
 CC antibody and a pharmaceutical carrier. The composition has cytostatic,
 CC immunosuppressive, endocrine, vasotropic, neuroprotective, nootropic and
 CC antithyroid activities, and can be used in vaccines and in gene therapy.
 CC The method and composition are useful for preventing or treating aging or
 CC a disorder (e.g. multiple myeloma, liquid tumour, liver cancer, thymus
 CC disorder, T-cell-mediated autoimmune disease, endocrinological disorder,
 CC ischaemia or neurodegenerative disorder) in mammals, such as humans. The
 CC human IGF-IR antibody is used in preparing a composition for the
 CC treatment or prevention of the above-mentioned disorders. The present
 CC sequence represents a human anti-IGF-IR antibody heavy chain amino acid
 CC sequence, which is used in the exemplification of the present invention.
 XX
 SQ Sequence 470 AA;
 Query Match 88.5%; Score 767; DB 8; Length 470;
 Best Local Similarity 85.3%; Pred. No. 1e-55;
 Matches 151; Conservative 6; Mismatches 10; Indels 10; Gaps 2;
 QY 1 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSTISVSGITTYVDSVKGR 60
 DB 27 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSTISVSGITTYVDSVKGR 86
 61 FTISRDNKNILYQWNSLRAEDTAVYYCAKRI-----FGV-VWQGGTLVTVSSAS 110
 87 FTISRDNKRTLLYQWNSLRAEDTAVYYCAKDLGSDSYYYGMDVWVGQTTTVTVSSAS 146
 111 TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPPPVTVSWNIGLALTSGVHTFPAVLQS 167
 147 TKGPSVFPLAPCSRSTSESTAALGCLVKDYFPPPVTVSWNSGALTSGVHTFPAVLQS 203
 RESULT 10
 AAW13564 ID AAW13564 standard; protein; 443 AA.
 XX AC AAW13564;
 XX 17-OCT-2003 (revised)
 DT 03-JUN-1997 (first entry)
 DT XX
 DE Humanised anti-L-selectin antibody HuDreg 55 heavy chain.
 XX
 XX L-selectin; humanised antibody; HuDreg 55; acute organ damage;
 KW organ failure; poly-trauma; haemorrhagic-traumatic shock.
 KW
 XX Mus; sp.
 OS Homo sapiens.
 OS Chimeric.
 XX PN W09706822-A1.
 XX 27-FEB-1997.
 PD XX
 XX 14-AUG-1996; 96WO-US013152.
 PF XX
 XX 17-AUG-1995; 95EP-00112895.
 PR 19-SEP-1995; 95EP-00114696.
 PR 27-DEC-1995; 95US-00578953.
 XX
 XX (PROT-) PROTEIN DESIGN LABS INC.
 PA (BOEF) BOEHRINGER MANNHEIM GMBH.
 XX
 XX Haselbeck A, Schumacher G, Co M, Martin U;
 PI WPI; 1997-165036/15.
 DR N-PSDB; AAT61281.
 DR
 XX Using anti-selectin antibody to prevent acute organ damage and multiple
 PT organ failure - during extracorporeal circulation or following
 PT polytrauma, e. g. haemorrhagic-traumatic shock.
 XX
 PS Disclosure; Page 34-36; 52pp; English.
 XX
 CC Humanised anti-L-selectin antibody HuDreg 55 comprises 2 heavy chains
 CC each having the sequence given in AAW13564 and 2 light chains each having
 CC the sequence given in AAW13563. These are encoded by the cDNA clones
 CC given in AAT61281 and AAT61280. HuDreg 55 can be used to prevent multiple
 CC organ failure associated with polytrauma and for the prevention of acute
 CC organ damage associated with extracorporeal blood circulation. The
 CC antibody inhibits interaction between the carbohydrate-recognising domain
 CC of the selectin and the corresponding cell surface receptor. (Updated on
 CC 17-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 443 AA;
 Query Match 88.3%; Score 765.5; DB 2; Length 443;
 Best Local Similarity 88.8%; Pred. No. 1.3e-55;
 Matches 150; Conservative 6; Mismatches 10; Indels 3; Gaps 2;
 QY 1 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSTISVSGITTYVDSVKGR 60
 DB 8 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPGKGLWVSTISVSGITTYVDSVKGR 66
 61 FTISRDNKNILYQWNSLRAEDTAVYYCAKRIFGV--VWQGGTLVTVSSASTGPSVFP 118
 86 FTISRDNKRTLLYQWNSLRAEDTAVYYCAKDLGSDSYYYGMDVWVGQTTTVTVSSAS 146

Db 67 FTISRDNKNTLYLQMSLRAEDTAVVYCARDYDGYDWGGTLVTVSSASTKGP3VFP 126
QY 119 LAPCSRSTSESTAALGCLVKDYFFPEPVTVSNWLGALTSVGVHTFPAVLQS 167
Db 127 LAPCSRSTSESTAALGCLVKDYFFPEPVTVSNWLGALTSVGVHTFPAVLQS 175
RESULT 11
ADL93667
ID ADL93667 standard; protein; 466 AA.
XX AC ADL93667;
XX DT 17-JUN-2004 (first entry)
XX DE Human CD44-binding antibody heavy chain HAE-F1-heavy SEQ ID NO:162.
XX KW human; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;
KW antiinflammatory; immunosuppressive; antiarthritic; antirheumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX OS Homo sapiens.
XX PN WO2004024750-A2.
XX PD 25-MAR-2004.
XX PF 15-SEP-2003; 2003WO-US029318.
XX PR 13-SEP-2002; 2002US-0410758P.
XX PR 09-MAY-2003; 2003US-0469123P.
XX PA (DYAX-) DYAX CORP.
XX FI Rondon IJ, Edge A, Baribault Kent R;
XX DR WPI; 2004-270003/25.
XX PT New protein comprising a light chain (LC) immunoglobulin variable domain
PT sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX PS Disclosure; SEQ ID NO 162; 128pp; English.
XX CC The invention relates to a novel isolated protein comprising a light
CC chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
CC immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CDR3 of the LC variable domain sequence. A protein of the invention has
CC cytostatic, antiinflammatory, immunosuppressive, antiarthritic,
CC antirheumatic, dermatological, vasotropic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for
CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a human CD44-binding
CC antibody heavy chain.
XX SQ Sequence 466 AA;
Query Match 88.2%; Score 764.5; DB 8; Length 466;
Best Local Similarity 87.2%; Pred. No. 1.7e-55;
Matches 150; Conservative 5; Mismatches 12; Indels 5; Gaps 2;
QY 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLVWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTFSYPYGMWVRQAPGKGLVWVSSISPSGTTLYADSVKGR 86

QY 61 FTISRDNKNTLYLQMSLRAEDTAVVYCAKR---IFGV--VMGGTLVTVSSASTKGPS 115
Db 87 FTISRDNKNTLYLQMSLRAEDTAVVYCARQKSSLSGAFDINGGTMVTVSSASTKGPS 146
QY 116 VFPLAPCSRSTSESTAALGCLVKDYFFPEPVTVSNWLGALTSVGVHTFPAVLQS 167
Db 147 VFPLAPCSRSTSESTAALGCLVKDYFFPEPVTVSNWLGALTSVGVHTFPAVLQS 198
RESULT 12
ABR01503
ID ABR01503 standard; protein; 217 AA.
XX AC ABR01503;
XX DT 16-APR-2003 (first entry)
XX DE Human anti-TIMP-1 antibody heavy chain #1.
XX KW Human; antibody; tissue inhibitor of metalloprotease-1; TIMP-1; VLCDR3;
KW matrix metalloprotease; MMP; variable heavy chain; VHCDR3; hepatotropic;
KW variable light chain; cytostatic; nephrotropic; cardiant; liver fibrosis;
KW alcoholic liver disease; cardiac fibrosis; acute coronary syndrome;
KW lupus nephritis; glomerulosclerotic renal disease; lung cancer;
KW idiopathic pulmonary fibrosis; benign prostate hypertrophy; colon cancer.
XX OS Homo sapiens.
XX PN WO200286085-A2.
XX PD 31-OCT-2002.
XX PF 24-APR-2002; 2002WO-US012801.
XX PR 24-APR-2001; 2001US-0285683P.
XX PA (FARB) BAYER CORP.
XX PA (MORP-) MORPHOSYS AG.
XX PI Pan C, Knorr AM, Schauer M, Hirth-Dietrich C, Kraft S, Krebs B;
XX DR WPI; 2003-129114/12.
XX DR N-PSDB; ABZ74774.
XX PT New human anti-TIMP-1 (tissue inhibitor of metalloprotease-1) antibodies,
PT for diagnosing or ameliorating the symptoms of a disorder in which TIMP-1
PT is elevated, e.g. liver fibrosis, benign prostate hypertrophy or lung
PT cancer.
XX PS Claim 20; Page 148; 228pp; English.
XX CC The invention relates to a novel purified preparation of a human
CC antibody, which binds to a tissue inhibitor of metalloprotease-1 (TIMP-1)
CC and neutralises a matrix metalloprotease (MMP)-inhibiting activity of TMP
CC -1. The antibody comprises a variable heavy chain (VHC)DR3 region and a
CC variable light chain (VLC)DR3 region. An antibody preparation of the
CC invention has hepatotropic, cytostatic, nephrotropic and cardiant
CC activity. The human antibody is useful for decreasing an MMP-inhibiting
CC activity of a TIMP-1. It is especially useful for ameliorating the
CC symptoms of a disorder in which TIMP-1 is elevated, e.g. liver fibrosis,
CC alcoholic liver disease, cardiac fibrosis, acute coronary syndrome, lupus
CC nephritis, glomerulosclerotic renal disease, idiopathic pulmonary
CC fibrosis, benign prostate hypertrophy, lung cancer or colon cancer. The
CC antibody is also useful for detecting a TIMP-1 in a test preparation, or
CC in diagnosing a disorder in which a TIMP-1 level is elevated. The
CC sequences shown in ABR01502-ABR01545 represent the heavy chain regions of
CC a human anti-TIMP-1 antibody of the invention
XX SQ Sequence 217 AA;
Query Match 88.1%; Score 764; DB 6; Length 217;
Best Local Similarity 89.8%; Pred. No. 8e-56;
Matches 150; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

QY 1 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISVSGITTYVDSVKGR 60
DB 8 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSAISGGSTTYADSVKGR 67
QY 61 FTISRDNSKNILYLQMSLRAEDTAVYCAKRIFGVVMVGQGLTVTVSSASTKGPSVPLA 120
DB 68 FTISRDNSKNILYLQMSLRAEDTAVYCAR--FMDIWGQGLTVTVSSASTKGPSVPLA 125
QY 121 PCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
DB 126 PSSKSTSGGTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 172
RESULT 13
ABR55342
ID ABR55342 standard; protein; 444 AA.
XX
AC ABR55342;
XX
DT 29-JUL-2003 (first entry)
XX
DE Amino acid sequence of a grafted VH chaine for anti-KDR antibody.
XX
KW Antibody; kinase insert domain-containing receptor; KDR; antibody VR165;
KW complementarity determining region; vascular endothelial growth factor;
KW CDR; VEGF; inflammation; psoriasis; rheumatoid arthritis; tumour.
XX
OS Synthetic.
XX
PN WO2003031475-A2.
XX
PD 17-APR-2003.
XX
PF 10-OCT-2002; 2002WO-GB004619.
XX
PR 10-OCT-2001; 2001GB-00024317.
XX
PA (CELL-) CELTECH R & D LTD.
XX
PI Popplewell AG, Tickle SP, Zinkewich-Peotti K, Morrison RK;
XX
DR WPI; 2003-441133/41.
XX
PT Novel antibody molecules having specificity for human kinase insert
PT domain-containing receptors, useful for treating inflammation, psoriasis,
PT rheumatoid arthritis, tumor growth and metastasis.
XX
PS Claim 16; Fig 21; 57pp; English.
XX
CC The specification describes an antibody molecule which has specificity
CC for human kinase insert domain-containing receptor (KDR). The antibody
CC comprises complementarity determining regions (CDRs) from the heavy and
CC light chain variable domains of the murine monoclonal antibody VR165.
CC This antibody is specific for human KDR. The antibody of the invention
CC blocks vascular endothelial growth factor (VEGF) binding to KDR.
CC Antibodies of the invention are useful for treating a pathology in which
CC VEGF and/or KDR are implicated, and in the manufacture of a medicament
CC for the treatment of a pathology in which VEGF and/or KDR are implicated.
CC This includes inflammation, psoriasis, rheumatoid arthritis, and tumour
CC growth or metastasis. The present sequence represents a grafted VH chain,
CC comprising a VR165 CDR regions and a human framework. It is used to
CC produce antibody molecules of the invention
XX
SQ Sequence 444 AA;
Query Match 88.1%; Score 764; DB 6; Length 444;
Best Local Similarity 87.7%; Pred. No. 1.8e-55;
Matches 150; Conservative 4; Mismatches 11; Indels 6; Gaps 2;
QY 1 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVSTISVSGITTYVDSVKGR 60
DB 8 GGGVLVQGGSLRLSCAASGFTFSYAMSVWRQAPKGLWVATITSGGTYVDSVKGR 67

QY 61 FTISRDNSKNILYLQMSLRAEDTAVYCAKRIFGV---VMQGLTVTVSSASTKGPSV 116
DB 68 FTISRDNAKNTLYLQMSLRAEDTAVYCYVR--IGEDALDYWGQGLTVTVSSASTKGPSV 125
QY 117 FPLAPCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
DB 126 FPLAPCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 176
RESULT 14
ABP55467
ID ABP55467 standard; protein; 367 AA.
XX
AC ABP55467;
XX
DT 18-FEB-2003 (first entry)
XX
DE MALLI3 protein sequence SEQ ID NO:453.
XX
KW Library; cleavage; display; diverse family.
XX
OS Synthetic.
XX
PN WO200283872-A2.
XX
PD 24-OCT-2002.
XX
PF 17-APR-2002; 2002WO-US012405.
XX
PR 17-APR-2001; 2001US-00837306.
PR 24-OCT-2001; 2001US-00000516.
PR 25-OCT-2001; 2001US-00045674.
XX
PA (LADN/) LADNER R C.
PA (COHE/) COHEN E H.
PA (NAST/) NASTRI H G.
PA (ROOK/) ROOKEY K L.
PA (HOET/) HOET R.
PA (HOOG/) HOOGENBOOM H R J M.
XX
PI Ladner RC, Cohen EH, Nastri HG, Rookey KL, Hoet R;
PI Hoogenboom HRJM;
XX
WPI; 2003-093015/08.
XX
PT Cleaving single-stranded nucleic acid sequences at a desired location by
PT contacting the nucleic acid with an single strand oligonucleotide
PT complementary to a nucleic acid region where cleavage is desired.
XX
PS Disclosure; Page 400-401; 485pp; English.
XX
CC The present invention describes a method for cleaving single-stranded
CC nucleic acid sequences at a desired location. Also described: (1) methods
CC for displaying or expressing a member of a diverse family of peptides,
CC polypeptides or proteins on the surface of a genetic package and
CC collectively displaying at least a part of the diversity of the family,
CC where the displayed or expressed peptide, polypeptide or protein is
CC encoded at least in part by a nucleic acid that has been cleaved at a
CC desired location; (2) a method for preparing single-stranded nucleic
CC acids; (3) a method for preparing a library comprising a collection of
CC genetic packages that display a member of a diverse family of peptides,
CC polypeptides or proteins and that collectively display at least a portion
CC of the family; (4) a vector comprising a DNA sequence encoding an
CC antibody variable region linked to a version of F11 anchor which does
CC not mediate infection of phage particles, and wild-type gene III; (5) a
CC method for producing a population or a library of immunoglobulin genes;
CC and (6) a library of immunoglobulins that comprise members having at
CC least one variable domain in which at least one of CDR1 and CDR2 contain
CC synthetic diversity and CDR3 diversity is captured from B cells. The
CC method is useful for cleaving single-stranded nucleic acid sequences at a
CC desired location, which can be subsequently used to produce libraries or
CC genetic packages that display and/or express a diverse family of

CC peptides, polypeptides or proteins. ABZ37510 to ABZ37510 and ABP55464 to
CC ABP55499 represent sequences used in the exemplification of the present
CC invention
XX
SQ Sequence 367 AA;
Query Match 88.1%; Score 763.5; DB 6; Length 367;
Best Local Similarity 87.2%; Pred. No. 1.6e-55;
Matches 150; Conservative 4; Mismatches 13; Indels 5; Gaps 1;
Qy 1 GGGVLVQPGGSLRLSCAASGFTFFSSYAMSVWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 30 GGGVLVQPGGSLRLSCAASGFTFFSSYAMSVWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 89
Qy 61 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV-----VWGQGLTVTVSSASTKGPS 115
Db 90 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV-----VWGQGLTVTVSSASTKGPS 149
Qy 116 VPLAPCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167
Db 150 VPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 201

RESULT 15

ADL93670
ID ADL93670 standard; protein; 462 AA.
XX
AC ADL93670;
XX
DT 17-JUN-2004 (first entry)
XX
DE Human CD44-binding antibody heavy chain BE-A11-heavy SEQ ID NO:169.
XX
KW human; CD44; light chain immunoglobulin variable domain;
KW heavy chain immunoglobulin variable domain; immunoglobulin; cytostatic;
KW anti-inflammatory; immunosuppressive; anti-arthritis; anti-rheumatic;
KW dermatological; vasotropic; neuroprotective; antibody therapy;
KW inflammatory disorders; rheumatoid arthritis; lupus; restenosis;
KW graft versus host response; multiple sclerosis; neoplastic disorder;
KW cancer; antibody.
XX
OS Homo sapiens.
XX
PN WO2004024750-A2.
XX
PD 25-MAR-2004.
XX
PF 15-SEP-2003; 2003WO-US029318.
XX
PR 13-SEP-2002; 2002US-0410758P.
PR 09-MAY-2003; 2003US-0469123P.
XX
PA (DYAX-) DYAX CORP.
XX
PI Rondon IJ, Edge A, Baribault Kent R;
XX
DR WPI; 2004-270003/25.
XX

PT New protein comprising a light chain (LC) immunoglobulin variable domain
sequence and a heavy chain (HC) immunoglobulin variable domain sequence,
PT useful for preparing a composition for treating inflammatory or
PT neoplastic disorders.
XX
PS Disclosure; SEQ ID NO 165; 128pp; English.
XX
CC The invention relates to a novel isolated protein comprising a light
chain (LC) immunoglobulin variable domain sequence and a heavy chain (HC)
immunoglobulin variable domain sequence that form an antigen binding site
CC with binding affinity for the human CD44 extracellular domain and where
CC CDR3 of the LC variable domain sequence. A protein of the invention has
CC cytostatic, anti-inflammatory, immunosuppressive, anti-arthritis,
CC anti-rheumatic, dermatological, vasotropic, and neuroprotective activity,
CC and may have a use in antibody therapy. The protein is useful for

CC preparing a composition for treating inflammatory disorders, e.g.,
CC rheumatoid arthritis, lupus, restenosis, graft versus host response or
CC multiple sclerosis or neoplastic disorder, which is a malignant or
CC metastatic cancer. The present sequence represents a human CD44-binding
CC antibody heavy chain.
XX
SQ Sequence 462 AA;

Query Match 88.1%; Score 763.5; DB 8; Length 462;
Best Local Similarity 88.7%; Pred. No. 2e-55;
Matches 149; Conservative 4; Mismatches 14; Indels 1; Gaps 1;
Qy 1 GGGVLVQPGGSLRLSCAASGFTFFSSYAMSVWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTFFSKYSMEWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 86
Qy 61 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV-VWGQGLTVTVSSASTKGPSVPL 119
Db 87 FTISRDNKNILYLQMNLSRAEDTAVYYCARDSTGMDVWGQGLTVTVSSASTKGPSVPL 146
Qy 120 APCSRSTSESTAALGCLVKDYFPEPTVTSWNLGALTSGVHTFPAVLQS 167
Db 147 APCSRSTSESTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQS 194

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Job time : 78.4257 secs

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OM protein - protein search, using sw model

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(without alignments)
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Perfect score: 867
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Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 329044822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	788	90.9	465	14	US-10-401-344-2
2	780	90.0	470	15	US-10-038-591-46
3	774.5	89.3	467	15	US-10-180-648-2
4	769.5	88.8	445	14	US-10-320-231A-79
5	767	88.5	470	15	US-10-038-591-45
6	765.5	88.3	443	9	US-09-917-410-4
7	764.5	88.2	466	16	US-10-663-244-162
8	764	88.1	217	16	US-10-128-520-140
9	763.5	88.1	367	15	US-10-045-674-453
10	763.5	88.1	368	11	US-09-837-306-196
11	763.5	88.1	462	16	US-10-663-244-165
12	763	88.0	217	16	US-10-128-520-142
13	762.5	87.9	222	16	US-10-128-520-145

14	761.5	87.8	220	16	US-10-128-520-156
15	760.5	87.7	222	16	US-10-128-520-152
16	760	87.7	217	16	US-10-128-520-146
17	760	87.7	224	10	US-09-972-656-68
18	758.5	87.5	224	16	US-10-128-520-150
19	757.5	87.4	473	15	US-10-038-591-50
20	757	87.3	221	16	US-10-128-520-143
21	756.5	87.3	218	16	US-10-128-520-144
22	756	87.2	221	16	US-10-128-520-171
23	755	87.1	217	16	US-10-128-520-141
24	754.5	87.0	462	16	US-10-128-520-154
25	754.5	87.0	462	16	US-10-663-244-163
26	754.5	87.0	464	16	US-10-663-244-156
27	753.5	86.9	462	16	US-10-663-244-155
28	752.5	86.8	224	16	US-10-128-520-148
29	752	86.7	470	15	US-10-292-088-78
30	751	86.6	463	16	US-10-663-244-160
31	749.5	86.4	223	10	US-09-972-656-86
32	749.5	86.4	460	16	US-10-663-244-159
33	749.5	86.4	468	16	US-10-663-244-161
34	748.5	86.3	464	16	US-10-663-244-158
35	747	86.2	469	16	US-10-663-244-164
36	745	85.9	449	9	US-09-736-371B-21
37	745	85.9	449	15	US-10-463-442-21
38	745	85.9	451	9	US-09-822-698A-26
39	743	85.7	470	15	US-10-292-088-62
40	743	85.7	470	15	US-10-038-591-49
41	742	85.6	469	16	US-10-663-244-157
42	742	85.6	474	10	US-09-848-832-3
43	742	85.6	474	14	US-10-225-108A-3
44	742	85.6	474	15	US-10-461-148-1
45	742	85.6	519	16	US-10-312-354-19

ALIGNMENTS

RESULT 1
US-10-401-344-2
; Sequence 2, Application US/10401344
; Publication No. US20030194404A1
; GENERAL INFORMATION:
; APPLICANT: Schering Corporation and Abgenix, Inc.
; APPLICANT: Corvalan, Jose
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO INTERLEUKIN-5 AND METHODS AND COMPOUNDS
; TITLE OF INVENTION: COMPRISING SAME
; FILE REFERENCE: L101564W1
; CURRENT APPLICATION NUMBER: US/10/401,344
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 465
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
; LOCATION: (1)..(19)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: Variable Region
; LOCATION: (20)..(138)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CH1 Region
; LOCATION: (139)..(236)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: Hinge Region
; LOCATION: (237)..(248)
; OTHER INFORMATION:
; FEATURE:

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; NAME/KEY: CH2 Region
; LOCATION: (249)..(358)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: CH3 Region
; LOCATION: (359)..(465)
; OTHER INFORMATION:
US-10-401-344-2

Query Match          90.9%; Score 788; DB 14; Length 465;
Best Local Similarity 90.6%; Pred. No. 1.2e-50;
Matches 155; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

Qy 1 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
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Db 27 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISGSGSTYADSVKGR 86
    |||||

Qy 61 FTISRDNSKNTLYLQWNSLRADTAIVYCAKRIFG-----VVGQGLTVTVSSASTKGPSV 116
    |||||
Db 87 FTISRDNSKNTLYLQWNSLRADTAIVYCAKERYNNYLYHWGQGLTVTVSSASTKGPSV 146
    |||||

Qy 117 FPLAPCSRSTSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ 167
    |||||
Db 147 FPLAPCSRSTSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ 197
    |||||

RESULT 2
US-10-038-591-46
; Sequence 46, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 46
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-46

Query Match          90.0%; Score 780; DB 15; Length 470;
Best Local Similarity 87.6%; Pred. No. 4.6e-50;
Matches 155; Conservative 3; Mismatches 9; Indels 10; Gaps 2;

Qy 1 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
    |||||
Db 27 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGSGSTYADSVKGR 86
    |||||

Qy 61 FTISRDNSKNTLYLQWNSLRADTAIVYCAK-----RIFGV-VVGQGLTVTVSSAS 110
    |||||
Db 87 FTISRDNSKNTLYLQWNSLRADTAIVYCAKGYSSGWYVYVYVYVYVYVYVYVYVYVYV 146
    |||||

Qy 111 TKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ 167
    |||||
Db 147 TKGPSVFLAPCSRSTSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ 203
    |||||

RESULT 3
US-10-180-648-2
; Sequence 2, Application US/10180648
; Publication No. US20040033535A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Boyle, William J
; APPLICANT: Martin, Francis H
; APPLICANT: Corvalan, Jose R
; APPLICANT: Davis, C. Geoffrey
; TITLE OF INVENTION: Antibodies to OPG
; FILE REFERENCE: 06843.0049-00000
; CURRENT APPLICATION NUMBER: US/10/180,648
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 60/301,172
; PRIOR FILING DATE: 2001-06-26
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-180-648-2

Query Match          89.3%; Score 774.5; DB 15; Length 467;
Best Local Similarity 88.5%; Pred. No. 1.2e-49;
Matches 154; Conservative 2; Mismatches 11; Indels 7; Gaps 1;

Qy 1 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
    |||||
Db 27 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSGITGSGSTYADSVKGR 86
    |||||

Qy 61 FTISRDNSKNTLYLQWNSLRADTAIVYCAKRIFGV-----WGQGLTVTVSSASTKG 113
    |||||
Db 87 FTISRDNSKNTLYLQWNSLRADTAIVYCAKDPGTTVMSWFPWGGTTLTVTVSSASTKG 146
    |||||

Qy 114 PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ 167
    |||||
Db 147 PSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ 200
    |||||

RESULT 4
US-10-320-231A-79
; Sequence 79, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 79
; LENGTH: 445
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic sequence
US-10-320-231A-79

Query Match          88.8%; Score 769.5; DB 14; Length 445;
Best Local Similarity 89.4%; Pred. No. 2.6e-49;
Matches 152; Conservative 3; Mismatches 12; Indels 3; Gaps 1;

Qy 1 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
    |||||
Db 5 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGSGSTYADSVKGR 64
    |||||

Qy 61 FTISRDNSKNTLYLQWNSLRADTAIVYCAKRIFGV---VMGQGLTVTVSSASTKGPSV 117
    |||||
Db 65 FTISRDNSKNTLYLQWNSLRADTAIVYCARROFFFAHFDVWGQGLTVTVSSASTKGPSV 124
    |||||

Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQ 167
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Db 125 PLAPSSKTSCTAALGCLVKDYFPEPVTVSNWNGALTSVGHVTPPAVLQS 174
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RESULT 5
US-10-038-591-45
; Sequence 45, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PP2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-45
Query Match 88.5%; Score 767; DB 15; Length 470;
Best Local Similarity 85.3%; Pred. No. 4.3e-49;
Matches 151; Conservative 6; Mismatches 10; Indels 10; Gaps 2;
Qy 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVLVQPGGSLRLSCTASGFTFSYAMWVRQAPGKGLWVSAISGSGITTFYADSVKGR 86
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRI-----FGV-VWGQGLTVTVSSAS 110
Db 87 FTISRDNSTRTLYLQMSLRAEDTAVYYCAKDLGWSDSYIIYGMVWGQGLTVTVSSAS 146
Qy 111 TKGPSVPLPCSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSVGHVTPPAVLQS 167
Db 147 TKGPSVPLPCSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSVGHVTPPAVLQS 203
RESULT 6
US-09-917-410-4
; Sequence 4, Application US/09917410
; Patent No. US20020098183A1
; GENERAL INFORMATION:
; APPLICANT: MARTIN, Ulrich; HASELBECK, Anton; SCHUMACHER, Guenther;
; CO, Man S.
; TITLE OF INVENTION: ANTI-I-SELECTIN ANTIBODIES FOR PREVENTION OF
; MULTIPLE ORGAN FAILURE AFTER POLYTRAUMA AND FOR
; PREVENTION OF ACUTE ORGAN DAMAGE AFTER
; EXTRACORPOREAL BLOOD CIRCULATION
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII, WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/917,410
; FILING DATE: 26-Jul-2001

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: <Unknown>
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US20020098183A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PFF/NDH/SLH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-917-410-4
Query Match 88.3%; Score 765.5; DB 9; Length 443;
Best Local Similarity 88.8%; Pred. No. 5.2e-49;
Matches 150; Conservative 6; Mismatches 10; Indels 3; Gaps 2;
Qy 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 8 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVASISTGG-STIYPDSVKGR 66
Qy 61 FTISRDNKNILYLQMSLRAEDTAVYYCAKRIFGV-VWGQGLTVTVSSASTKGPSVFP 118
Db 67 FTISRDNKNTLYLQMSLRAEDTAVYYCARDYDYGQGLTVTVSSASTKGPSVFP 126
Qy 119 LAPCSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSVGHVTPPAVLQS 167
Db 127 LAPCSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSVGHVTPPAVLQS 175
RESULT 7
US-10-663-244-162
; Sequence 162, Application US/10663244
; Publication No. US20040110933A1
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 162
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-663-244-162
Query Match 88.2%; Score 764.5; DB 16; Length 466;
Best Local Similarity 87.2%; Pred. No. 6.5e-49;
Matches 150; Conservative 5; Mismatches 12; Indels 5; Gaps 2;
Qy 1 GGGVLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVLVQPGGSLRLSCAASGFTFSYGMWVRQAPGKGLWVSSISPSTGGLTVYADSVKGR 86

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; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: MALIA3 protein
; OTHER INFORMATION: sequence
; US-10-045-674-453

Query Match      88.1%; Score 764; DB 16; Length 217;
Best Local Similarity 89.8%; Pred. No. 3.4e-49;
Matches 150; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy 1 GGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db 8 GGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 67
Qy 61 FTISRDNKNTLYLQMSLRAEDTAVYCAKRIFGVVMGQGLTVTVSSASTKGPSVFPLA 120
Db 68 FTISRDNKNTLYLQMSLRAEDTAVYCAR--FMDIWGQGLTVTVSSASTKGPSVFPLA 125
Qy 121 PCRSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
Db 126 PSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 172

RESULT 9
US-10-045-674-453
; Sequence 453, Application US/10045674
; Publication No. US2003023233A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: US/10/045,674
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 09/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 453
; LENGTH: 367

Qy 61 FTISRDNKNTLYLQMSLRAEDTAVYCAKRIFGVVMGQGLTVTVSSASTKGPS 115
Db 87 FTISRDNKNTLYLQMSLRAEDTAVYCARQKRESSIGAFDINGQGTMTVTVSSASTKGPS 146
Qy 116 VFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
Db 147 VFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 198

RESULT 8
US-10-128-520-140
; Sequence 140, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-128-520-140

Query Match      88.1%; Score 764; DB 16; Length 217;
Best Local Similarity 89.8%; Pred. No. 3.4e-49;
Matches 150; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy 1 GGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db 8 GGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 67
Qy 61 FTISRDNKNTLYLQMSLRAEDTAVYCAKRIFGVVMGQGLTVTVSSASTKGPSVFPLA 120
Db 68 FTISRDNKNTLYLQMSLRAEDTAVYCAR--FMDIWGQGLTVTVSSASTKGPSVFPLA 125
Qy 121 PCRSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
Db 126 PSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 172

RESULT 9
US-10-045-674-453
; Sequence 453, Application US/10045674
; Publication No. US2003023233A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: US/10/045,674
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 09/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 453
; LENGTH: 367
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```
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: MALIA3 protein
; OTHER INFORMATION: sequence
; US-10-045-674-453

Query Match      88.1%; Score 763.5; DB 15; Length 367;
Best Local Similarity 87.2%; Pred. No. 6.1e-49;
Matches 150; Conservative 4; Mismatches 13; Indels 5; Gaps 1;

Qy 1 GGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db 30 GGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 89
Qy 61 FTISRDNKNTLYLQMSLRAEDTAVYCAKRIFGV-----VMGQGLTVTVSSASTKGPS 115
Db 90 FTISRDNKNTLYLQMSLRAEDTAVYCAKDEGTGYAFDINGQGTMTVTVSSASTKGPS 149
Qy 116 VFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
Db 150 VFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 201

RESULT 10
US-09-837-306-196
; Sequence 196, Application US/09837306
; Publication No. US20040029113A1
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES OF GENETIC
; TITLE OF INVENTION: PACKAGES THAT COLLECTIVELY DISPLAY THE MEMBERS OF A
; FILE REFERENCE: DYAX/002
; CURRENT APPLICATION NUMBER: US/09/837,306
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; NUMBER OF SEQ ID NOS: 428
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 196
; LENGTH: 368
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: MALIA3
; US-09-837-306-196

Query Match      88.1%; Score 763.5; DB 11; Length 368;
Best Local Similarity 87.2%; Pred. No. 6.1e-49;
Matches 150; Conservative 4; Mismatches 13; Indels 5; Gaps 1;

Qy 1 GGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 60
Db 30 GGGLVQPGGSLRLSCLASGFTFSSYAMSWVRQAPGKLEWVSTISVSGITTYVDSVKGR 89
Qy 61 FTISRDNKNTLYLQMSLRAEDTAVYCAKRIFGV-----VMGQGLTVTVSSASTKGPS 115
Db 90 FTISRDNKNTLYLQMSLRAEDTAVYCAKDEGTGYAFDINGQGTMTVTVSSASTKGPS 149
Qy 116 VFPLAPCSRSTSESTAALGCLVKDYFPEPTVSNLGLTSGVHTFPAVLQS 167
Db 150 VFPLAPSSKSTSGTAAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQS 201

RESULT 11
US-10-663-244-165
; Sequence 165, Application US/10663244
; Publication No. US20040110933A1
```



```
; GENERAL INFORMATION:
; APPLICANT: Rondon, Isaac J.
; APPLICANT: Edge, Albert
; APPLICANT: Kent, Rachel Baribault
; TITLE OF INVENTION: CD44 LIGANDS
; FILE REFERENCE: 10280-063001
; CURRENT APPLICATION NUMBER: US/10/663,244
; CURRENT FILING DATE: 2003-09-15
; PRIOR APPLICATION NUMBER: US 60/410,758
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: US 60/469,123
; PRIOR FILING DATE: 2003-05-09
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165
; LENGTH: 462
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
; US-10-663-244-165

Query Match      88.1%; Score 763.5; DB 16; Length 462;
Best Local Similarity 88.7%; Pred. No. 7.6e-49;
Matches 149; Conservative 4; Mismatches 14; Indels 1; Gaps 1;

Qy 1 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVLVQGGSLRLSCAASGFTFSYMEWVRQAPGKGLWVSRYPGGPTLYADSVKGR 86
Qy 61 FTISRDNKNILYLQWNSLRADTAIVYCAKRIQGV-VWGQGLTVTVSSASTKGPSVPL 119
Db 87 FTISRDNKNILYLQWNSLRADTAIVYCARDSYGMVWGQGLTVTVSSASTKGPSVPL 146
Qy 120 APCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 167
Db 147 APCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 194

RESULT 12
US-10-128-520-142
; Sequence 142, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-128-520-142

Query Match      88.0%; Score 763; DB 16; Length 217;
Best Local Similarity 89.8%; Pred. No. 4e-49;
Matches 150; Conservative 4; Mismatches 11; Indels 2; Gaps 1;

Qy 1 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 8 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGGSTYYADSVKGR 67
Qy 61 FTISRDNKNILYLQWNSLRADTAIVYCAKRIQGVVWGQGLTVTVSSASTKGPSVPLA 120
Db 68 FTISRDNKNILYLQWNSLRADTAIVYCAR--FLDIWGQGLTVTVSSASTKGPSVPLA 125
Qy 121 PCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 167
| :||| |
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Db 126 PSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 172

RESULT 13
US-10-128-520-145
; Sequence 145, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-128-520-145

Query Match      87.9%; Score 762.5; DB 16; Length 222;
Best Local Similarity 88.2%; Pred. No. 4.5e-49;
Matches 150; Conservative 5; Mismatches 12; Indels 3; Gaps 1;

Qy 1 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 8 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGGSTYYADSVKGR 67
Qy 61 FTISRDNKNILYLQWNSLRADTAIVYCAKRIQGV---VWGQGLTVTVSSASTKGPSVF 117
Db 68 FTISRDNKNILYLQWNSLRADTAIVYCARVWRLGSLFDIWGQGLTVTVSSASTKGPSVF 127
Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 167
Db 128 PLAPSKRSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 177

RESULT 14
US-10-128-520-156
; Sequence 156, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-128-520-156

Query Match      87.8%; Score 761.5; DB 16; Length 220;
Best Local Similarity 89.3%; Pred. No. 5.3e-49;
Matches 150; Conservative 5; Mismatches 12; Indels 1; Gaps 1;

Qy 1 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSTISVSGITTYVDSVKGR 60
Db 8 GGGVLVQGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSAISGGSTYYADSVKGR 67
Qy 61 FTISRDNKNILYLQWNSLRADTAIVYCAKRI--FGVWGQGLTVTVSSASTKGPSVPL 119
Db 68 FTISRDNKNILYLQWNSLRADTAIVYCARLICYFDLWGQGLTVTVSSASTKGPSVPL 127
Qy 120 APCSRSTSESTAALGCLVKDYFPEPTVSWNLGALTSGVHTFPAVLQ 167
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Db 128 APSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 175

RESULT 15

US-10-128-520-152
; Sequence 152, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 152
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-128-520-152

Query Match 87.7%; Score 760.5; DB 16; Length 222;
Best Local Similarity 88.8%; Pred. No. 6.3e-49;
Matches 151; Conservative 4; Mismatches 12; Indels 3; Gaps 2;
Qy 1 GGGVLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISVSGITTYVYVDSVKGR 60
Db 8 GGGVLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGSTYYADSVKGR 67
Qy 61 FTISRDNSKNTLYLQMSLRAEDTAVYYCAK--RIFGV-VWGQGTLYTVSSASTKGPSVF 117
Db 68 FTISRDNSKNTLYLQMSLRAEDTAVYYCARYGAYFGLDYWGQGTLYTVSSASTKGPSVF 127
Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 167
Db 128 PLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQS 177

Search completed: March 8, 2005, 07:05:59
Job time : 89.6225 secs

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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:48:12 ; Search time 18.3627 Seconds
(without alignments)
678.897 Million cell updates/sec

Title: US-09-784-950-40

Perfect score: 867

Sequence: 1 GGGVQPGGSLRLSCAASG.....SWNLGALTSGVHTFPAVLQS 167

Scoring table:

BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued Patents AA.*
2: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
7: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	765.5	88.3	443	5	PCT-US96-13152-4
2	742	85.6	467	1	US-08-704-744-81
3	741	85.5	451	4	US-09-472-087-70
4	729.5	84.1	248	4	US-09-315-926A-80
5	727.5	83.9	463	4	US-09-472-087-1
6	727.5	83.9	463	4	US-09-472-087-63
7	727.5	83.9	463	4	US-09-472-087-64
8	726.5	83.8	463	4	US-09-472-087-4
9	726.5	83.8	463	4	US-09-472-087-68
10	724.5	83.6	169	4	US-09-472-087-5
11	724.5	83.6	169	4	US-09-472-087-73
12	719	82.9	464	4	US-09-472-087-2
13	719	82.9	464	4	US-09-472-087-66
14	718	82.8	225	4	US-09-456-090A-56
15	718	82.8	225	4	US-09-456-090A-60
16	718	82.8	225	4	US-09-456-090A-92
17	718	82.8	225	4	US-09-456-090A-90
18	718	82.8	225	4	US-09-453-234-56
19	718	82.8	225	4	US-09-453-234-60
20	718	82.8	225	4	US-09-453-234-70
21	718	82.8	225	4	US-09-453-234-92
22	717.5	82.8	174	4	US-09-472-087-12
23	717	82.7	470	4	US-09-859-053-32
24	717	82.7	470	4	US-09-859-053-36
25	715	82.5	225	4	US-09-456-090A-68
26	715	82.5	225	4	US-09-456-090A-106
27	715	82.5	225	4	US-09-453-234-68

28	715	82.5	225	4	US-09-453-234-106
29	712	82.1	225	4	US-09-456-090A-108
30	712	82.1	225	4	US-09-453-234-108
31	711.5	82.1	167	4	US-09-472-087-74
32	709	81.8	225	4	US-09-456-090A-94
33	709	81.8	225	4	US-09-453-234-94
34	708	81.7	225	4	US-09-456-090A-58
35	708	81.7	225	4	US-09-456-090A-110
36	708	81.7	225	4	US-09-453-234-58
37	708	81.7	225	4	US-09-453-234-110
38	706.5	81.5	233	2	US-08-480-753-2
39	706.5	81.5	233	3	US-09-041-889-9
40	706.5	81.5	233	3	US-08-837-058-9
41	706.5	81.5	233	4	US-09-417-264-9
42	706	81.4	225	4	US-09-456-090A-102
43	706	81.4	225	4	US-09-453-234-102
44	705.5	81.4	171	4	US-09-472-087-83
45	704	81.2	225	4	US-09-456-090A-98

ALIGNMENTS

RESULT 1

PCT-US96-13152-4
; Sequence 4, Application PC/TUS9613152
; GENERAL INFORMATION:
; APPLICANT: Martin, Ulrich, et al.
; TITLE OF INVENTION: Anti-selectin antibodies for prevention of multiple organ fai
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; ADDRESSEE: Attn: Norman D. Hanson
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Computer Disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/13152
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/578,953
; FILING DATE: 27-Dec-95
; APPLICATION NUMBER: EP 95 112 895.8
; FILING DATE: 17-Aug-95
; APPLICATION NUMBER: EP 95 114 969.9
; FILING DATE: 19-Sep-95
; ATTORNEY/AGENT INFORMATION:
; NAME: Norman D. Hanson
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: BOER 1059-PCT-PFF/NDH
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443
; TYPE: amino acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US96-13152-4

Query Match 88.3%; Score 765.5; DB 5; Length 443;
Best Local Similarity 88.8%; Pred. No. 2.4e-62; Indels 3; Gaps 2;
Matches 150; Conservative 6; Mismatches 10;

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QY 1 GGGLVQGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 8 GGGLVQGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 66
QY 61 FTISRDNKNTLYLQNMNSLAEDTAVYYCAKRIFGV--VMGQGLTVTVSSASTKGPSVFP 118
Db 67 FTISRDNKNTLYLQNMNSLAEDTAVYYCAKRIFGV--VMGQGLTVTVSSASTKGPSVFP 126
QY 119 LAPCSRSTSESTAALGCLVKDYRPEPTVSWNLGALTSGVHTFPAVLQS 167
Db 127 LAPCSRSTSESTAALGCLVKDYRPEPTVSWNSGALTSGVHTFPAVLQS 175

RESULT 2
US-08-704-744-81
; Sequence 81, Application US/08704744
; Patent No. 5705154
; GENERAL INFORMATION:
; APPLICANT: Dalié, Barbara
; APPLICANT: Miller, Kenneth
; APPLICANT: Murgolo, Nicholas
; APPLICANT: Tindall, Stephen
; TITLE OF INVENTION: Humanized Monoclonal Antibodies Against Human Interleukin-4
; NUMBER OF SEQUENCES: 90
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Schering-Plough Corporation
; STREET: 2000 Galloping Hill Road
; CITY: Kenilworth
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07033-0530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5.3
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/704,744
; FILING DATE: 06-SEPT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/208886
; FILING DATE: 10-MAR-1994
; APPLICATION NUMBER: PCT/US/95/02400
; FILING DATE: 08-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Foulke, Cynthia L.
; REGISTRATION NUMBER: 32,364
; REFERENCE/DOCKET NUMBER: JB0429K
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 298-2987
; TELEFAX: (908) 298-5388
; TELEX:
; INFORMATION FOR SEQ ID NO: 81:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-704-744-81

Query Match 85.6%; Score 742; DB 1; Length 467;
Best Local Similarity 83.2%; Pred. No. 3.7e-60;
Matches 144; Conservative 10; Mismatches 13; Indels 6; Gaps 1;

QY 1 GGGLVQGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGLVQGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 86
QY 61 FTISRDNKNTLYLQNMNSLAEDTAVYYCAKRIFGV-----VMGQGLTVTVSSASTKGP 114
Db 87 FTISRDNKNTLYLQNMNSLAEDTAVYYCAKRIFGV-----VMGQGLTVTVSSASTKGP 146
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QY 115 SVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNLGALTSGVHTFPAVLQS 167
Db 147 SVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNSGALTSGVHTFPAVLQS 199

RESULT 3
US-09-472-087-70
; Sequence 70, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 70
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-472-087-70

Query Match 85.5%; Score 741; DB 4; Length 451;
Best Local Similarity 82.5%; Pred. No. 4.4e-60;
Matches 146; Conservative 3; Mismatches 18; Indels 10; Gaps 1;

QY 1 GGGLVQGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 8 GGGLVQGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 67
QY 61 FTISRDNKNTLYLQNMNSLAEDTAVYYCAKRIFGV-----VMGQGLTVTVSSAS 110
Db 68 FTISRDNKNTLYLQNMNSLAEDTAVYYCARDPRGATLYYYGMDVMGQGLTVTVSSAS 127
QY 111 TKGPSVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNLGALTSGVHTFPAVLQS 167
Db 128 TKGPSVFPLAPCSRSTSESTAALGCLVKDYRPEPTVSWNSGALTSGVHTFPAVLQS 184

RESULT 4
US-09-315-926A-80
; Sequence 80, Application US/09315926A
; Patent No. 6498027
; GENERAL INFORMATION:
; APPLICANT: Havenga, Menzo
; APPLICANT: Verlinden, Stefan
; TITLE OF INVENTION: TARGETED DELIVERY THROUGH A CATIONIC AMINO ACID TRANSPORTER
; FILE REFERENCE: 2183-4080US
; CURRENT APPLICATION NUMBER: US/09/315,926A
; CURRENT FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 99201593.3
; PRIOR FILING DATE: 1999-05-20
; PRIOR APPLICATION NUMBER: EP 98201693.3
; PRIOR FILING DATE: 1998-05-20
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 80
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
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OTHER INFORMATION: Description of Artificial Sequence: phage
NAME/KEY: PEPTIDE
LOCATION: (1)..(248)
OTHER INFORMATION: /note="hCAT1 amino acid sequence"
US-09-315-926A-80

Query Match 84.1%; Score 729.5; DB 4; Length 248;
Best Local Similarity 83.7%; Pred. No. 2.4e-59;
Matches 144; Conservative 4; Mismatches 19; Indels 5; Gaps 1;
Qy 1 GGGVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 30 GGGVVQPGSLRLSCAASGFTSSYAMHWVRQAPGKGLEWAVISYDGSNKKYADSVKGR 89
Qy 61 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV-----VWGQGLTVTVSSASTKGPS 115
Db 90 FTISRDNKNILYLQMNLSRAEDTAVYYCARGITVTKSRFDYWGQGLTVTVSSASTKGPS 149
Qy 116 VPLAPCSRSTSESTAALGCLVKDYFPEPTVTSNLSGALTSGVHTFPAVLQS 167
Db 150 VPLAPSRKSTSGGTAALGCLVKDYFPEPTVTSNLSGALTSGVHTFPAVLQS 201

RESULT 5
US-09-472-087-1
Query Match 83.9%; Score 727.5; DB 4; Length 463;
Best Local Similarity 84.7%; Pred. No. 7.8e-59;
Matches 144; Conservative 5; Mismatches 18; Indels 3; Gaps 2;
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, ELLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 463
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-1

Query Match 83.9%; Score 727.5; DB 4; Length 463;
Best Local Similarity 84.7%; Pred. No. 7.8e-59;
Matches 144; Conservative 5; Mismatches 18; Indels 3; Gaps 2;
Qy 1 GGGVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVVQPGSLRLSCAASGFTSSYAMHWVRQAPGKGLEWAVISYDGSNKKYADSVKGR 86
Qy 61 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV--VWGQGLTVTVSSASTKGPSVF 117
Db 87 FTISRDNKNILYLQMNLSRAEDTAVYYCARGHGFDPDYWGQGLTVTVSSASTKGPSVF 146
Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPTVTSNLSGALTSGVHTFPAVLQS 167
Db 147 PLAPCSRSTSESTAALGCLVKDYFPEPTVTSNLSGALTSGVHTFPAVLQS 196

RESULT 6
US-09-472-087-63
Query Match 83.9%; Score 727.5; DB 4; Length 463;
Best Local Similarity 84.7%; Pred. No. 7.8e-59;
Matches 144; Conservative 5; Mismatches 18; Indels 3; Gaps 2;
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, ELLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 63
LENGTH: 463
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-63

Query Match 83.9%; Score 727.5; DB 4; Length 463;
Best Local Similarity 84.7%; Pred. No. 7.8e-59;
Matches 144; Conservative 5; Mismatches 18; Indels 3; Gaps 2;
Qy 1 GGGVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVVQPGSLRLSCAASGFTSSYAMHWVRQAPGKGLEWAVISYDGSNKKYADSVKGR 86
Qy 61 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV--VWGQGLTVTVSSASTKGPSVF 117
Db 87 FTISRDNKNILYLQMNLSRAEDTAVYYCARGHGFDPDYWGQGLTVTVSSASTKGPSVF 146
Qy 118 PLAPCSRSTSESTAALGCLVKDYFPEPTVTSNLSGALTSGVHTFPAVLQS 167
Db 147 PLAPCSRSTSESTAALGCLVKDYFPEPTVTSNLSGALTSGVHTFPAVLQS 196

RESULT 7
US-09-472-087-64
Query Match 83.9%; Score 727.5; DB 4; Length 463;
Best Local Similarity 84.7%; Pred. No. 7.8e-59;
Matches 144; Conservative 5; Mismatches 18; Indels 3; Gaps 2;
Patent No. 6682736
GENERAL INFORMATION:
APPLICANT: HANSON, DOUGLAS C.
APPLICANT: NEVEU, MARK J.
APPLICANT: MUELLER, ELLEN E.
APPLICANT: HANKE, JEFFREY H.
APPLICANT: GILMAN, STEVEN C.
APPLICANT: DAVIS, C. GEOFFREY
APPLICANT: CORVALAN, JOSE R.
TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
FILE REFERENCE: ABX-PF1
CURRENT APPLICATION NUMBER: US/09/472,087
CURRENT FILING DATE: 1999-12-23
PRIOR APPLICATION NUMBER: 60/113,647
PRIOR FILING DATE: 1998-12-23
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 64
LENGTH: 463
TYPE: PRT
ORGANISM: Homo sapiens
US-09-472-087-64

Query Match 83.9%; Score 727.5; DB 4; Length 463;
Best Local Similarity 84.7%; Pred. No. 7.8e-59;
Matches 144; Conservative 5; Mismatches 18; Indels 3; Gaps 2;
Qy 1 GGGVQPGGSLRLSCAASGFTSSYAMSWVRQAPGKGLEWVSTISVSGITTYVDSVKGR 60
Db 27 GGGVVQPGSLRLSCAASGFTSSYAMHWVRQAPGKGLEWAVISYDGSNKKYADSVKGR 86
Qy 61 FTISRDNKNILYLQMNLSRAEDTAVYYCAKRIFGV--VWGQGLTVTVSSASTKGPSVF 117
Db 87 FTISRDNKNILYLQMNLSRAEDTAVYYCARGHGFDPDYWGQGLTVTVSSASTKGPSVF 146


```
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-73

Query Match      83.6%; Score 724.5; DB 4; Length 169;
Best Local Similarity 85.2%; Pred. No. 4.4e-59;
Matches 144; Conservative 3; Mismatches 17; Indels 5; Gaps 2;

Qy 3 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGRFT 62
Db 1 GWQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGRFT 60

Qy 63 ISRDNSKNILYLQMSLRADTAIVYCAK--RIFGV---VWGQGLTVTVSSASTKGPSV 117
Db 61 ISRDNSKNILYLQMSLRADTAIVYCAKRIITPCMDVWGQGLTVTVSSASTKGPSV 120

Qy 118 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGLTSGVHTFPAVLQ 166
Db 121 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 169

RESULT 12
US-09-472-087-2
; Sequence 2, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-2

Query Match      82.9%; Score 719; DB 4; Length 464;
Best Local Similarity 83.0%; Pred. No. 4.7e-58;
Matches 142; Conservative 7; Mismatches 18; Indels 4; Gaps 2;

Qy 1 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGR 60
Db 27 GGGVVQPGSLRLSCTASGFTFSYGMHVRQAPGKGLEWVAVIYDGSNKHGYSVKGR 86

Qy 61 FTISRDNKNILYLQMSLRADTAIVYCAK--RI--FGVWGQGLTVTVSSASTKGPSV 116
Db 87 FTISSDNKNILYLQMSLRADTAIVYCARGLGSYFDYWGQGLTVTVSSASTKGPSV 146

Qy 117 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGLTSGVHTFPAVLQ 167
Db 147 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 197

RESULT 13
US-09-472-087-66
; Sequence 66, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-66

Query Match      82.9%; Score 719; DB 4; Length 464;
Best Local Similarity 83.0%; Pred. No. 4.7e-58;
Matches 142; Conservative 7; Mismatches 18; Indels 4; Gaps 2;

Qy 1 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGR 60
Db 27 GGGVVQPGSLRLSCTASGFTFSYGMHVRQAPGKGLEWVAVIYDGSNKHGYSVKGR 86

Qy 61 FTISRDNKNILYLQMSLRADTAIVYCAK--RI--FGVWGQGLTVTVSSASTKGPSV 116
Db 87 FTISSDNKNILYLQMSLRADTAIVYCARGLGSYFDYWGQGLTVTVSSASTKGPSV 146

Qy 117 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGLTSGVHTFPAVLQ 167
Db 147 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 197

RESULT 14
US-09-456-090A-56
; Sequence 56, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-3H
US-09-456-090A-56

Query Match      82.8%; Score 718; DB 4; Length 225;
Best Local Similarity 83.4%; Pred. No. 2.4e-58;
Matches 141; Conservative 5; Mismatches 21; Indels 2; Gaps 1;

Qy 1 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGR 60
Db 147 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 197
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; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 73
; LENGTH: 169
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-73

Query Match      83.6%; Score 724.5; DB 4; Length 169;
Best Local Similarity 85.2%; Pred. No. 4.4e-59;
Matches 144; Conservative 3; Mismatches 17; Indels 5; Gaps 2;

Qy 3 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGRFT 62
Db 1 GWQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGRFT 60

Qy 63 ISRDNSKNILYLQMSLRADTAIVYCAK--RIFGV---VWGQGLTVTVSSASTKGPSV 117
Db 61 ISRDNSKNILYLQMSLRADTAIVYCAKRIITPCMDVWGQGLTVTVSSASTKGPSV 120

Qy 118 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGLTSGVHTFPAVLQ 166
Db 121 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 169

RESULT 12
US-09-472-087-2
; Sequence 2, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PFI
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-472-087-2

Query Match      82.9%; Score 719; DB 4; Length 464;
Best Local Similarity 83.0%; Pred. No. 4.7e-58;
Matches 142; Conservative 7; Mismatches 18; Indels 4; Gaps 2;

Qy 1 GGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKGLEWVSTISVSGITTYVDVSKGR 60
Db 27 GGGVVQPGSLRLSCTASGFTFSYGMHVRQAPGKGLEWVAVIYDGSNKHGYSVKGR 86

Qy 61 FTISRDNKNILYLQMSLRADTAIVYCAK--RI--FGVWGQGLTVTVSSASTKGPSV 116
Db 87 FTISSDNKNILYLQMSLRADTAIVYCARGLGSYFDYWGQGLTVTVSSASTKGPSV 146

Qy 117 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNIGLTSGVHTFPAVLQ 167
Db 147 FLAPCSRSTSESTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQ 197
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Db 8 GGGVQPGRSRLRLSCAASGFTFSYGMHWRQAPFGKGLEWVTLITYDGNKYYADSVKGR 67
Qy 61 FTISRDNKNTLYLQMNLSRAEDTAVYYCAKRIFGV--VMQGQGLTVTVSSASTKGPSVFP 118
Db 68 FTISRDNKNTLYLQMNLSRAEDTAVYYCARDGIGYFDYMGQGLTVTVSSASTKGPSVFP 127
Qy 119 LAPCSRSTSESTAALGCLVKDYFPEPPTVSNLGLTSGVHTFPFPAVLQS 167
Db 128 LAPSSKSTSGGTAALGCLVKDYFPEPPTVSNWNSGALTSGVHTFPFPAVLQS 176

RESULT 15
US-09-456-090A-60
; Sequence 60, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lonberg, Nils
; TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
; FILE REFERENCE: 020015-000200US
; CURRENT APPLICATION NUMBER: US/09/456,090A
; CURRENT FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 110
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 60
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Homo sapiens
; OTHER INFORMATION: M1-5H
US-09-456-090A-60

Query Match 82.8%; Score 718; DB 4; Length 225;
Best Local Similarity 83.4%; Pred. No. 2.4e-58;
Matches 141; Conservative 5; Mismatches 21; Indels 2; Gaps 1;
Qy 1 GGGVQPGGSLRLSCAASGFTFSYAMSWVRQAPFGKGLEWVSTISVSGITTYVYVDSVKGR 60
Db 8 GGGVQPGRSRLRLSCAASGFTFSYGMHWRQAPFGKGLEWVTLITYDGNKYYADSVKGR 67
Qy 61 FTISRDNKNTLYLQMNLSRAEDTAVYYCAKRIFGV--VMQGQGLTVTVSSASTKGPSVFP 118
Db 68 FTISRDNKNTLYLQMNLSRAEDTAVYYCARDGIGYFDYMGQGLTVTVSSASTKGPSVFP 127
Qy 119 LAPCSRSTSESTAALGCLVKDYFPEPPTVSNLGLTSGVHTFPFPAVLQS 167
Db 128 LAPSSKSTSGGTAALGCLVKDYFPEPPTVSNWNSGALTSGVHTFPFPAVLQS 176

Search completed: March 8, 2005, 05:54:15
Job time : 19.3627 secs

[illegible]

Qy 123 PPSDEQLKSGTASVVCLLNFFYPREAKVQWKVDNA - LQSGKP 164
||| ||| ||| ||| ||| ||| ||| : | : | : |
Db 139 PPSSEQLTSGGASVVFLLNFFPKDINVKKIDGSEKONGVLN 181

RESULT 9
S68212
IG kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68212
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-214 <TAK>
A:Cross-references: EMBL:D29668
C:Superfamily: immunoglobulin V region; immunoglobulin homology

	Query Match	61.8%	Score 524.5	DB 2	Length 214
	Best Local Similarity	59.9%	Pred. No. 3.7e-33		
	Matches 100	Conservative 30	Mismatches 30	Indels 7	Gaps 2
Qy	5	DIOLTQSPSLSASVGDRTVITICRASGGI-----SIYLAWFQQRPGKAPKSLIYAASSL	58		
Db	1	DIWMTQPSLWASVGGKVTLMCKSSQSLNSRNQKYLAWYQKQPGSKLLVTFVASTR	60		
Qy	59	QSGVPKSGSGSGTDFTLTISLSQPEDFATYICQYNSYPFTFGPGTKVDIKRTVAAPS	118		
Db	61	ESGVPRDFIGSGSGTDFTLTISTVQAEADLADYFCQHQVSTPYTFEGGKTKLEIKRADAAPT	120		
Qy	119	VTFPPSPDEOLKSGTASVCLLNFTPREAKVQWKVDNA-LQSKPN	164		
Db	121	VSTFPSPSEOLTSGGASVGLNFNFPKQINNAWKIDGSRQNGVLN	167		

```

RESULT 10
A49134
IG kappa chain V-I region (ISE) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49134; S25115
R:Rocca, A.; Khanlichi, A.A.; Aucouturier, P.; Noel, L.H.; Denoroy, L.; Preud'homme, J.L.
Clin. Exp. Immunol. 91, 506-509, 1993
A:Title: Primary structure of a variable region of the V kappa I subgroup (ISE) in light
A:Reference number: A49134; MUID:93185310; PMID:7680298
A:Accession: A49134
A:Status: preliminary
A:Molecule type: mRNA; protein
A:Residues: 1-141 <POC>
A:Cross-references: EMBL:X67322; NID:G33268; PIDN:CAA47736.1; PID:G33269
A:Note: sequence extracted from NCBI backbone (NCBIP:127088)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:38-112/Domain: immunoglobulin homology <IMM>

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[illegible]

A:Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin
A:Reference number: JC5810; MUID:98063277; PMID:9398605
A:Accession: JC5810
A:Molecule type: protein
A:Residues: 1-218 <AKA>
C:Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-94/Domain: immunoglobulin homology <IMM>

Query Match	60.0%;	Score	509.5;	DB	2;	Length	218;
Best Local Similarity	59.4%;	Pred. NO.	5.2e-32;				
Matches	98;	Conservative	27;	Mismatches	35;	Indels	5;
						Gaps	2;

Qy	5	DIQLTQSPSSLSASVGDRTTITCRASQGIS----	IYLAWFOORPKAPKSLIYAASSLQS	60
Db	1	NIVLTQSPASLAVSLGQRTATISCRASKSVASGYIMHWYQQKPKLISLASNLES	60	
Qy	61	GVPSKFGSGSGTDFTLTITSLQPEDFATYYCQQVNSYPFTFGPCTKVDIKRTVAAPSVF	120	
Db	61	GVPARFSGSGSGTDFTLTINHPVEEDVATYYCQHSRELPLTFGAGTKLELRADRAFTVS	120	
Qy	121	IFPPSDEQLKSGTASVVCCLNNFYPREAKVQMKVDNA-LQSGKPN	164	
Db	121	IFPPSSEQLTSGGASVVCFLNNFYPKDINVWKIDGSRQNGVLN	165	

Search completed: March 8, 2005, 07:13:12
Job time : 41 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 06:36:06 ; Search time 174 Seconds
(without alignments)
482.649 Million cell updates/sec

Title: US-09-784-950-41

Perfect score: 849

Sequence: 1 GRLDQLTQSPSLASVG.....PREAKVQKVDNALQSGKN 164

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	771	90.8	236	2 Q6GMX8	Q6gmX8 homo sapien
2	756	89.0	236	2 Q7Z3Y4	Q7z3Y4 homo sapien
3	748	88.1	236	2 Q6GMX9	Q6gmX9 homo sapien
4	742	87.4	236	2 Q6PIH7	Q6piH7 homo sapien
5	730	86.0	236	2 Q6GMW1	Q6gmW1 homo sapien
6	711	83.7	236	2 Q6GMX0	Q6gmX0 homo sapien
7	710	83.6	234	2 Q7Z4Y3	Q7z4Y3 homo sapien
8	709	83.5	236	2 Q6P1T5	Q6piT5 homo sapien
9	693	81.6	236	2 Q6PIH4	Q6piH4 homo sapien
10	642.5	75.7	235	2 Q6PJF2	Q6pjF2 homo sapien
11	632	74.4	236	2 Q6PII8	Q6piI8 homo sapien
12	630.5	74.3	235	2 Q6GMW0	Q6gmW0 homo sapien
13	625.5	73.7	235	2 Q6GMV9	Q6gmV9 homo sapien
14	624	73.5	236	2 Q6P5S8	Q6p5S8 homo sapien
15	568.5	67.0	239	2 Q8TCD0	Q8tcd0 homo sapien
16	559.5	65.9	236	2 Q7TS98	Q7ts98 mus musculus
17	552.5	65.1	239	2 Q6P491	Q6p491 homo sapien
18	549.5	64.7	239	2 Q6NEK0	Q6neK0 homo sapien
19	545	64.2	240	2 Q6PIH6	Q6piH6 homo sapien
20	504.5	59.4	238	2 Q66JS7	Q66jS7 mus musculus
21	497	58.5	108	2 Q9UL70	Q9ul70 homo sapien
22	492	58.0	108	1 KV1L_HUMAN	P04430 homo sapien
23	473	55.7	237	2 Q7SZ36	Q7sz36 xenopus lae
24	472.5	55.7	107	1 KV1D_HUMAN	P01596 homo sapien
25	472	55.6	219	2 Q65ZC0	Q65zc0 mus musculus
26	468	55.1	244	2 Q65ZC8	Q65zc8 homo sapien
27	467	55.0	108	2 Q9UL77	Q9ul77 homo sapien
28	466	54.9	116	2 Q96PP6	Q96pf6 homo sapien
29	462	54.4	108	1 KV1R_HUMAN	P01610 homo sapien
30	462	54.4	117	1 KV1L_HUMAN	P01601 homo sapien
31	461.5	54.4	107	2 Q96SA9	Q96sa9 homo sapien

32	461	54.3	108	1 KV1G_HUMAN	P01599 homo sapien
33	460	54.2	108	1 KV1I_HUMAN	P03062 homo sapien
34	460	54.2	240	2 Q65ZC9	Q65zc9 homo sapien
35	457.5	53.9	243	2 Q6NTU5	Q6ntU5 xenopus lae
36	457	53.8	108	1 KV1H_HUMAN	P01600 homo sapien
37	457	53.8	108	1 KV1L_HUMAN	P01604 homo sapien
38	455	53.6	108	2 Q9UL79	Q9ul79 homo sapien
39	453.5	53.4	107	2 Q9UL81	Q9ul81 homo sapien
40	452	53.2	108	1 KV1P_HUMAN	P01608 homo sapien
41	451	53.1	108	1 KV1S_HUMAN	P01611 homo sapien
42	450	53.0	129	1 KV1W_HUMAN	P04431 homo sapien
43	447.5	52.7	241	2 Q63ZK4	Q63zk4 mus musculus
44	446	52.5	108	1 KV1E_HUMAN	P01597 homo sapien
45	445	52.4	108	1 KV1W_HUMAN	P01605 homo sapien

ALIGNMENTS

RESULT 1

ID	Q6GMX8	PRELIMINARY;	PRT;	236 AA.
AC	Q6GMX8;			
DT	05-JUL-2004 (TrEMBLrel. 27, Created)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)			
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)			
DB	Hypothetical protein.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RX	MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;			
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,			
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,			
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,			
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,			
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,			
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,			
RA	Brownstein M.J., Uadin T.B., Toehiyuki S., Carninci P., Prange C.,			
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,			
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,			
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,			
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,			
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,			
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,			
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,			
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,			
RA	Krzywinski M.I., Skalska U., Smailus D.E., Schnrerch A., Schein J.E.,			
RA	Jones S.J., Marra M.A.;			
RT	"Generation and initial analysis of more than 15,000 full-length human			
RT	and mouse cDNA sequences."			
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Primary B-Cells;			
RA	Strausberg R.;			
RL	EMBL; BC073764; AAH73764.1; -.			
DR	InterPro; IPR003599; Ig.			
DR	InterPro; IPR007110; Ig-like.			
DR	InterPro; IPR003597; Ig cl.			
DR	InterPro; IPR003006; Ig MHC.			
DR	InterPro; IPR003596; Ig v.			
DR	Pfam; PF07654; Cl-set; 1.			
DR	Pfam; PF00047; Ig; 2.			
DR	SMART; SM00409; IG; 2.			
DR	SMART; SM00407; IGcl; 1.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS50835; IG_LIKE; 2.			
DR	PROSITE; PS00290; IG_LIKE; 1.			

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KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
Query Match 90.8%; Score 771; DB 2; Length 236;
Best Local Similarity 91.9%; Pred. No. 4.5e-65;
Matches 146; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFQQRPGKAPKLLIYAASLSQS 60
DB 19 GSRCDIQMTQSPSSVSASVGDRTVITCRASQGISIYLAWFQQRPGKAPKLLIYAASLSQS 78
QY 61 GVPKSGSGSGGTDFTLTISLQPEDPATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 120
DB 79 GVPKSGSGSGGTDFTLTISLQPEDPATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 138
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161
DB 139 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 179

RESULT 2
Q6GMX9 PRELIMINARY; PRT; 236 AA.
AC Q6GMX9
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal Muscle;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005332; AAH05332.1; -.
DR HSSP; P01834; 1HEZ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25702 MW; 7FBFB4ED23084BC6 CRC64;
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KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25707 MW; 4FC8E14B6559EFC9 CRC64;
Query Match 89.0%; Score 756; DB 2; Length 236;
Best Local Similarity 91.3%; Pred. No. 1.2e-63;
Matches 147; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFQQRPGKAPKLLIYAASLSQS 60
DB 19 GARCIDIQMTQSPSSLSASVGDRTVITCRASQGISIYLAWFQQRPGKAPKLLIYAASLSQS 78
QY 61 GVPKSGSGSGGTDFTLTISLQPEDPATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 120
DB 79 GVPKSGSGSGGTDFTLTISLQPEDPATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 138
QY 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161
DB 139 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 179

RESULT 3
Q6GMX9 PRELIMINARY; PRT; 236 AA.
AC Q6GMX9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073763; AAH73763.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; C1-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
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SQ SEQUENCE 236 AA; 25924 MW; FDE2093DC560CFF7 CRC64;
Query Match 88.1%; Score 748; DB 2; Length 236;
Best Local Similarity 89.4%; Pred. No. 6.8e-63;
Matches 144; Conservative 7; Mismatches 10; Indels 0; Gaps 0;

QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQISIIYLAWFOORPKAPKSLIYAASSLQS 60
Db 19 GARDIQMTQSPSSLSASVGRVITTCRASQNVSRWLAWYQORPEKAPKSLIYATSSLHS 78
QY 61 GVPKFSGSGSGTDFTLTISSLPQEDFATYYCQYNSVPFTFGPTKVDIKRTVAAPSVF 120
Db 79 GVPKFSGSGSGTDFTLTISSLPQEDFATYYCQYNTPLTFGGTKVEIKRTVAAPSVF 138
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 161
Db 139 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 179

RESULT 4
Q6PIH7 PRELIMINARY; PRT; 236 AA.
ID Q6PIH7
AC Q6PIH7
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC034141; AAH34141.1; -.
RA HSSP; P01607; IAR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGcl; 1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25603 MW; 8BC561106861213F CRC64;
Query Match 87.4%; Score 742; DB 2; Length 236;
Best Local Similarity 90.1%; Pred. No. 2.5e-62;
Matches 145; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQISIIYLAWFOORPKAPKSLIYAASSLQS 60
Db 19 GARDIQMTQSPSSLSASVGRVITTCRASQISIIYLAWYQORPEKAPKSLIYAASSLQS 78
QY 61 GVPKFSGSGSGTDFTLTISSLPQEDFATYYCQYNSVPFTFGPTKVDIKRTVAAPSVF 120
Db 79 GVPKFSGSGSGTDFTLTISSLPQEDFATYYCQYNSPPFTFGGTKEIKRTVAAPSVF 138
QY 121 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 161
Db 139 IFPPSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 179

RESULT 5
Q6GMW1 PRELIMINARY; PRT; 236 AA.
ID Q6GMW1
AC Q6GMW1
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA EMBL; BC073791; AAH73791.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00407; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGcl; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00835; IG_LIKE; 2.
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DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25751 MW; 5BFEGA087AFAC437 CRC64;

Query Match 86.0%; Score 730; DB 2; Length 236;
Best Local Similarity 88.8%; Pred. No. 3.5e-61;
Matches 143; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPKAPKSLIIYAASSLSQ 60
Db 19 GARCAIQMTQSPSSLSASVGDRTVITCRASQISNDLIGWQQRKAPKLIIIYAASSLSQ 78
QY 61 GVPKFSGSGSGTDFLTITSSLPQEPATYCCQYNSYPTFGTGVKDVTKRTVAAPSVF 120
Db 79 GVPKFSGSGSGTDFLTITSSLPQEPATYCCQYNSYPTFGTGVKDVTKRTVAAPSVF 138
QY 121 IFPPSDQLKSGTGASVVCLLNFPYKQVQKVDNALQSG 161
Db 139 IFPPSDQLKSGTGASVVCLLNFPYKQVQKVDNALQSG 179

RESULT 6
Q6GMX0 PRELIMINARY; PRT; 236 AA.
AC Q6GMX0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RL EMBL; BC073775; AAH73775.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003006; IG MHC.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
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DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25807 MW; 864EA08C7E92BF8F CRC64;

Query Match 83.7%; Score 711; DB 2; Length 236;
Best Local Similarity 85.7%; Pred. No. 2.2e-59;
Matches 138; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPKAPKSLIIYAASSLSQ 60
Db 19 GARCAIQMTQSPSSLSASVGDRTVITCRASQISNNLNNYQLRPGKAPNLIYAASSLSQ 78
QY 61 GVPKFSGSGSGTDFLTITSSLPQEPATYCCQYNSYPTFGTGVKDVTKRTVAAPSVF 120
Db 79 GVPKFSGSGSGTDFLTITSSLPQEPATYCCQYNSYPTFGTGVKDVTKRTVAAPSVF 138
QY 121 IFPPSDQLKSGTGASVVCLLNFPYKQVQKVDNALQSG 161
Db 139 IFPPSDQLKSGTGASVVCLLNFPYKQVQKVDNALQSG 179

RESULT 7
Q7Z473 PRELIMINARY; PRT; 234 AA.
AC Q7Z473;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22398257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
RA Strausberg R.;
RL EMBL; BC056256; AAH56256.1; -.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003006; IG MHC.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
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KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C359BAB51BC0F CRC64;
Query Match 83.6%; Score 710; DB 2; Length 234;
Best Local Similarity 84.5%; Pred. No. 2.8e-59;
Matches 136; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQIGISYILAWFOORPKAPKSLIYAASLSQS 60
DB 17 GARCAIRLTQSPSSLSASVGDRTVITCRASQIGISYILAWFOORPKAPKSLIYAASLSQS 76
QY 61 GVPKFSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGTGVKVDIKRTVAAPSVF 120
DB 77 GVPKFSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGTGVKVDIKRTVAAPSVF 136
QY 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161
DB 137 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 177
RESULT 8
Q6PITS PRELIMINARY; PRT; 236 AA.
AC Q6PITS
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC029444; AAH29444.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG_LIKE; 2.

DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25741 MW; BD50AF071FBEES351 CRC64;
Query Match 83.5%; Score 709; DB 2; Length 236;
Best Local Similarity 85.1%; Pred. No. 3.5e-59;
Matches 137; Conservative 11; Mismatches 13; Indels 0; Gaps 0;
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQIGISYILAWFOORPKAPKSLIYAASLSQS 60
DB 19 GARCAIQLTQSPSSLSASVGDRTVITCRASQIGISYILAWFOORPKAPKSLIYAASLSQS 78
QY 61 GVPKFSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGTGVKVDIKRTVAAPSVF 120
DB 79 GVPKFSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGTGVKVDIKRTVAAPSVF 138
QY 121 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161
DB 139 IFPPSDQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 179
RESULT 9
Q6PIH4 PRELIMINARY; PRT; 236 AA.
AC Q6PIH4
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034146; AAH34146.1; -.
DR HSSP; P01607; 1AR2.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG-cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.


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DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25834 MW; 6647A9E77A3C0053 CRC64;

Query Match
Best Local Similarity 74.4%; Score 632; DB 2; Length 236;
Matches 121; Conservative 15; Mismatches 18; Indels 2; Gaps 2;

Qy 8 LTQSPSLASVGDRTVITCRASQGI-SIYLAWFQORPGKAPKSLIYAASSLQSGVPSKF 66
Db 24 LTQSPGLSLSPGRATLSKCRASQSLSSYLAWFQORPGAPRLIYGVSRATGIDRF 83
Qy 67 SGSGSGDTFTLTISLQPEDFATYCCQY-NSYFPTFGPGTKVDIKRTVAAPSFIIPPS 125
Db 84 SGSGSGDTFTLTISLQPEDFATYCCQY-NSYFPTFGPGTKVDIKRTVAAPSFIIPPS 143
Qy 126 DEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 161
Db 144 DEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 179

RESULT 12
Q6GMW0 PRELIMINARY; PRT; 235 AA.
ID Q6GMW0
AC Q6GMW0
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073792; AAH792.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF007654; C1-set; 1.
DR Pfam; PF000047; Ig; 2.
```

```
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25765 MW; 4360C36B6D4133F5 CRC64;

Query Match
Best Local Similarity 74.3%; Score 630.5; DB 2; Length 235;
Matches 120; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

Qy 5 DIQLTQSPSLASVGDRTVITCRASQGISIYLAWFQORPGKAPKSLIYAASSLQSGVPS 64
Db 21 EIVMTQSPATLSVSPGERATLSKCRASQSLSSYLAWFQORPGAPRLIYGVSRATGIDRF 80
Qy 65 KFGSGSGDTFTLTISLQPEDFATYCCQVNSY-PFTFGPGTKVDIKRTVAAPSFIIP 123
Db 81 RFGSGSGDTFTLTISLQPEDFATYCCQVNSY-PFTFGPGTKVDIKRTVAAPSFIIP 140
Qy 124 PSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 161
Db 141 PSDEQLKSGTASVCLNNFYPREAKVQWKVDNALQSG 178

RESULT 13
Q6GMV9 PRELIMINARY; PRT; 235 AA.
ID Q6GMV9
AC Q6GMV9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
OX [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073793; AAH73793.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF007654; C1-set; 1.
```



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DR PIR; S42267; S42267.
DR PIR; S42268; S42268.
DR HSP; P01834; 1172.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig v.
DR Pfam; PF07654; Cl-set; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26234 MW; FAGEDC3A3B03871D CRC64;

Query Match 67.0%; Score 568.5; DB 2; Length 239;
Best Local Similarity 66.0%; Pred. No. 7.8e-46;
Matches 107; Conservative 22; Mismatches 28; Indels 5; Gaps 1;

Qy 5 DIQLTQSPSSLSASVGRVTITCRASQGI-----SIVLWFOQRPGKAPKSLIYAASLQ 59
Db 21 DVNMTQGLPLDVTIGQPASISCRSTOSLVYSDGNTLYLWFFQRPQSPRLIYKVNRD 80

Qy 60 SGVPSKPSGSGSGTDFTLTITSSLOPEDFATYYCOQYNSYPFTFGTKVDIKRTVAAPSV 119
Db 81 SGVDPDRFSGSGSGTDFTLKITREAEADVGVYFCMQGTHWPSFTFGQTKLEIKRTVAAPSV 140

Qy 120 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161
Db 141 FIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 182

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Search completed: March 8, 2005, 07:12:26
Job time : 175 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 8, 2005, 06:17:32 ; Search time 164 Seconds
(without alignments)
386.760 Million cell updates/sec

Title: US-09-784-950-41

Perfect score: 849

Sequence: 1 GIBLDLTQSPSSLSASVG.....PREAKVQKVDNALQSGKPN 164

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	849	100.0	164	2 AAY34317	Aay34317 IGF antib
2	777	91.5	224	4 AAB75040	Aab75040 TRO005 Hu
3	763	89.9	233	8 ADR46823	Adr46823 Human ant
4	761	89.6	214	7 ADF11431	Adf11431 18B2 anti
5	754	88.8	236	3 AAY96297	Aay96297 Human IGF
6	753	88.7	214	3 AAY93735	Aay93735 The kappa
7	753	88.7	214	6 AAE35890	Aae35890 Human 11.
8	753	88.7	234	8 ADS84446	Ads84446 Human ant
9	753	88.7	234	8 ADS84464	Ads84464 Human ant
10	753	88.7	234	8 ADR68588	Adr68588 Human ant
11	753	88.7	234	8 ADR68606	Adr68606 Human ant
12	751	88.5	236	5 AAU74297	Aau74297 Anti-huma
13	746	87.9	214	7 ADF11423	Adf11423 2B11 anti
14	746	87.9	234	5 ADM47073	Adm47073 Mouse ant
15	746	87.9	236	5 ABG77164	Abg77164 Germline
16	746	87.9	236	8 ADR28586	Adr28586 Human ant
17	745	87.8	233	8 ADL93655	Adl93655 Human CD4
18	745	87.8	236	5 ABG77160	Abg77160 Germline
19	745	87.8	236	8 ADR28582	Adr28582 Human ant
20	743.5	87.6	234	2 AAR38162	Aar38162 Human imm
21	742	87.4	224	4 AAB75043	Aab75043 TRO005 Hu
22	740	87.2	224	4 AAB75044	Aab75044 TRO005 Hu
23	739	87.0	214	8 ADF11669	Adf11669 anti-CD11
24	739	87.0	224	4 AAB75041	Aab75041 TRO005 Hu
25	737	86.8	184	8 ADS84439	Ads84439 Human ant

26	737	86.8	184	8	ADR68581	Adr68581 Human ant
27	737	86.8	234	7	ADE28413	Ade28413 Human ant
28	737	86.8	234	8	ADS84452	Ads84452 Human ant
29	737	86.8	234	8	ADR68594	Adr68594 Human ant
30	736	86.7	223	6	ABJ36940	Abj36940 Anti-CD40
31	736	86.7	234	8	ADR84470	Adr84470 Human ant
32	736	86.7	234	8	ADS84476	Ads84476 Human ant
33	736	86.7	234	8	ADR68618	Adr68618 Human ant
34	736	86.7	234	8	ADR68612	Adr68612 Human IGF
35	733.5	86.4	237	3	AAY96298	Aay96298 Human imm
36	733.5	86.4	241	4	AAB82912	Aab82912 Human imm
37	733	86.3	212	6	AAQ31100	Aao31100 Human A2-
38	733	86.3	214	2	AAY08600	Aay08600 JP1112785
39	733	86.3	234	2	AAR20058	Aar20058 Light cha
40	733	86.3	234	7	ADE28429	Ade28429 Human ant
41	733	86.3	236	8	ADP07905	Adp07905 Human imm
42	731	86.1	152	8	ADK52390	Adk52390 Human ant
43	730	86.0	212	8	ADF76324	Adf76324 M16-L lig
44	730	86.0	234	8	ADS84458	Ads84458 Human ant
45	730	86.0	234	8	ADR68600	Adr68600 Human ant

ALIGNMENTS

RESULT 1
AAY34317
ID AAY34317 standard; protein; 164 AA.

XX AC AAY34317;

XX DT 19-NOV-1999 (first entry)

XX DE IGF antibody 2.6.1 kappa chain sequence.

XX KW Antibody; CD147; IGM; ABX-CBL; activated T-cell killing; leukaemia;
KW activated B-cell; monocyte; graft versus host disease; therapy; cancer;
KW organ transplant rejection disease; lymphoma; pancreatic disease;
KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX OS Homo sapiens.

XX PN WO9945031-A2.

XX PD 10-SEP-1999.

XX PF 03-MAR-1999; 99WO-US004583.

XX PR 03-MAR-1998; 98US-00034607.

XX PP 03-FEB-1999; 99US-00244253.

XX PA (ABGE-) ABGENIX INC.

XX PI Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

XX PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX N-PSDB; AAZ20418.

XX PT New monoclonal antibody, used for treating e.g. graft versus host

XX PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX PS Claim 61; Fig 33; 245pp; English.

XX CC This sequence represents the kappa chain of an antibody of the invention.
CC The antibody is a monoclonal antibody (MAB) with an isotype that fixes
CC complement and a variable region that binds to the epitope on CD147 bound
CC by the IGM MAB ABX-CBL, providing that the antibody is not CBL1. The MAB
CC can selectively kill activated T-cells, activated B-cells or resting or
CC activated monocytes. The products and methods can be used for treating
CC diseases involving activated T-cells or B-cells or monocytes, e.g. graft
CC versus host disease (GVHD), organ transplant rejection diseases (e.g.
CC renal transplant, ocular transplant), cancers (e.g. cancers of the blood

CC	(e.g. leukaemia's and lymphomas) and pancreatic), autoimmune diseases
CC	(e.g. lupus), and inflammatory diseases (e.g. arthritis)
XX	
SQ	Sequence 164 AA;
	Query Match 100.0%; Score 849; DB 2; Length 164;
	Best Local Similarity 100.0%; Pred. No. 2.8e-48;
	Matches 164; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GIRLDIQLTQSPSSLSASVGRDVITTCRASQGISIYLAWFQORPGKAPKSLIYAASSLOS 60
Db	1 GIRLDIQLTQSPSSLSASVGRDVITTCRASQGISIYLAWFQORPGKAPKSLIYAASSLOS 60
QY	61 GVPSKFSGSGSGTDTLTITSSLQPEDFATYYCQYNSYPTFGTGKVDIKRTVAAPSVF 120
Db	61 GVPSKFSGSGSGTDTLTITSSLQPEDFATYYCQYNSYPTFGTGKVDIKRTVAAPSVF 120
QY	121 IFPPSDEQLKSGTASVVCLLNFPREAKVQWKVDNALQSGKEN 164
Db	121 IFPPSDEQLKSGTASVVCLLNFPREAKVQWKVDNALQSGKEN 164
RESULT 2	
AAB75040	
ID	AAB75040 standard; protein; 224 AA.
XX	XX AAB75040;
XX	XX AC
DT	19-JUL-2001 (first entry)
DE	TRO005 HuMab kappa chain protein sequence 3E2K.
XX	XX Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW	Human antibody phage display library; immunisation; transgenic animal.
OS	Homo sapiens.
OS	Synthetic.
PN	WO200125492-A1.
XX	XX 12-APR-2001.
XX	XX 02-OCT-2000; 2000WO-US027237.
PF	XX 02-OCT-1999; 99US-0157415P.
PR	PR 01-DEC-1999; 99US-00453234.
XX	XX (BIOS-) BIOSITE DIAGNOSTICS INC.
PA	(GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX	XX Buechler J, Valkirs G, Gray J, Lonberg N;
PI	XX WPI; 2001-335567/35.
DR	XX
XX	XX
PT	Producing a human antibody phage display library comprises providing a
PT	transgenic animal whose genome comprises human immunoglobulin genes and
PT	isolating nucleic acids encoding antibody chains from lymphatic cells.
XX	
PS	Example 37; Page 121-122; 161pp; English.
XX	
CC	The present invention describes a method (M1) for producing a human
CC	antibody phage display library (I), comprising: (1) providing a nonhuman
CC	transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC	(2) isolating nucleic acids encoding human antibody chains (III) from
CC	lymphatic cells; and (3) forming a library of display packages whose
CC	members comprise a nucleic acid encoding (III) which is displayed from
CC	the package. The method is used for producing a human antibody display
CC	library, e.g., a Fab phage display library. The display method may be
CC	used to screen nucleic acids encoding antibody chains obtained from
CC	immunised nonhuman transgenic animals, and from this a population of
CC	antibodies may be prepared. Production of a human monoclonal antibodies
CC	display library using this method means there is no need to immunise
CC	humans with antigens, and the difficulties faced with immortalising B

CC	cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC	represent sequences used in the exemplification of the present invention
XX	
SQ	Sequence 224 AA;
	Query Match 91.5%; Score 777; DB 4; Length 224;
	Best Local Similarity 94.9%; Pred. No. 1.9e-43;
	Matches 149; Conservative 6; Mismatches 2; Indels 0; Gaps 0
QY	5 DIQLQTSPSSLSASVGRVTTITCRASQISYIYLAWFQORPGKAPKSLIYAASSLQSGVPS 64
DB	1 NIQWTSPPSSLSASVGRVTTITCRASQISISLAWYQKPEKAPKSLIYAASSLQSGVPS 60
QY	65 KFGSGSGTDTFTLTISLQPEDFATYYCQQNSVPFTFEGPTKVDIKRTVAAPSVPFIPP 124
DB	61 RFSGSGSGTDTFTLTISLQPEDFATYYCQQNSVPFTFEGPTKVDIKRTVAAPSVPFIPP 120
QY	125 SDEOLKSGTASWCLLNFPYPREAKVQWKVDNALQSG 161
DB	121 SDEOLKSGTASWCLLNFPYPREAKVQWKVDNALQSG 157
RESULT 3	
ADRA6823	
ID	ADRA6823 standard; protein; 233 AA.
XX	AC ADR46823;
XX	AC
XX	18-NOV-2004 (first entry)
DT	
XX	
DE	Human antibody B11 light chain variable region protein SEQ ID NO:6.
XX	molecular conjugate; monoclonal antibody; human antigen presenting cell;
KW	antigen presenting cell; APC; human; beta human chorionic gonadotropin;
KW	betahCG; beta chorionic gonadotropin; antibody;
KW	T cell-mediated immune response; immunisation; cytostatic; antimicrobial;
KW	immunosuppressive; anti-HIV; hepatotropic; virucide; antimalarial;
KW	CD8 agonist; vaccine; autoimmune disorder; cancer; infectious disease;
KW	melanoma; fibrosarcoma; leukaemia; HIV; hepatitis; malaria; herpes;
KW	antibody B11; light chain variable region.
XX	
OS	Homo sapiens.
XX	
XX	WO2004074432-A2.
XX	
PD	02-SEP-2004.
XX	
XX	30-JAN-2004; 2004WO-US002725.
XX	
PR	31-JAN-2003; 2003US-0443979P.
XX	
PA	(MEDA-) MEDAREX INC.
XX	
PI	Keler T, Endres M, He L, Ramakrishna V;
XX	
DR	WPI; 2004-635555/61.
DR	N-PSDB; ADR46822.
XX	
PT	New molecular conjugate having a monoclonal antibody that binds to human
PT	APCs linked to a beta human chorionic gonadotropin, useful for inducing a
PT	Cytotoxic T cell response in cancers and infectious diseases.
XX	
PS	Claim 14; SEQ ID NO 6; 82pp; English.
XX	
CC	The present invention describes a molecular conjugate comprising a
CC	monoclonal antibody that binds to human antigen presenting cells (APCs)
CC	linked to beta human chorionic gonadotropin (betahCG), where the antibody
CC	comprises a heavy and/or light chain variable region derived from a human
CC	VH5-51 or VK-L15 germline sequence with the 98 or 95 amino acid sequences
CC	of SEQ ID NO:30 or 32 (ADRA46847, or ADRA46849), respectively. Also
CC	described: (1) a molecular conjugate comprising a human antibody heavy
CC	chain and a human antibody light chain, where either or both chains are
CC	linked to betahCG; (2) a molecular conjugate comprising a human single

PA (AMGE-) AMGEN INC.

Key	Location/Qualifiers
FT	1..22
FT	/label= signal_peptide
FT	23..236
FT	/label= IGFAM-9
FT	38..112
FT	/label= Ig_domain
FT	149..218
FT	/label= Ig_domain
FT	192..235

```

FT  /label= Ig_domain
XX WO200029583-A2.
XX
XX
XX 25-MAY-2000.
XX
XX 19-NOV-1999; 99WO-US027566.
XX
XX 19-NOV-1998; 98US-00195853.
XX 22-DEC-1998; 98US-0113635P.
XX 07-APR-1999; 99US-0128194P.
XX
XX (INCY-) INCYTE PHARM INC.
XX
XX Yue H, Tang YT, Corley NC, Guegler KJ, Gorgone GA, Baughn MR;
XX Lu DAM, Lal P, Hillman JL, Yang J;
XX
XX WPI; 2000-387796/33.
XX N-PSDB; AAA27389.
XX
XX Immunoglobulin superfamily proteins, the agonist and antagonist of the
XX protein is useful for preventing and treating disorders associated with
XX altered levels of the protein such as cancer, immune system disorders.
XX
XX Claim 1; Page 85; 105pp; English.
XX
XX The present sequence is the human immunoglobulin superfamily protein
XX IGFAM-9. Its gene was isolated from a cDNA library of breast tumour
XX tissue. It is expressed in reproductive, gastrointestinal and immune and
XX haematopoietic tissue, where cancer and inflammation are common. The
XX gene, protein, its antibodies, agonists and antagonists are suitable for
XX diagnosing and treating many diseases, including cancer, immune system
XX disorders (such as inflammation, AIDS, allergies, anaemia, Crohn's
XX arteriosclerosis, asthma, atherosclerosis, cholecystitis, Graves'
XX disease, diabetes mellitus, emphysema, rheumatoid arthritis, hepatitis,
XX multiple sclerosis, psoriasis, rheumatoid arthritis, scleroderma,
XX systemic lupus erythematosus and ulcerative colitis), complications of
XX cancer, haemodialysis and extracorporeal circulation, trauma and
XX haematopoietic cancer (such as leukaemia) and infections caused by
XX bacteria, viruses, fungi or parasites
XX
XX Sequence 236 AA;
XX
Query Match 88.8%; Score 754; DB 3; Length 236;
Best Local Similarity 90.7%; Pred. No. 6.4e-42;
Matches 146; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
QY 1 GIRLDIQTQSPSSLSASVGDRTVITCRASQGISIYLAWFQQRPGKAPKSLIYAASLSQS 60
DB 19 GARCDIQMTQSPSSLSASVGDRTVITCRASQDISNYLAWFQQRPGTAPKSLIYDTSLSQS 78
QY 61 GVPSKFGSGSGTDTLTITISLQPEDFATYCCQYNSYPTFFGPGTKVDIKRTVAAPSVF 120
DB 79 GVPSKFGSGSGTDTLTITISLQPEDFATYCCQYNSYPTFFGPGTKVDIKRTVAAPSVF 138
QY 121 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 161
DB 139 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 179
RESULT 6
AAV93735
ID AAV93735 standard; protein; 214 AA.
XX
XX AAV93735;
AC
XX
XX 03-OCT-2000 (first entry)
DT
XX
XX The kappa chain of immunoglobulin clone 11.2.1.
DE
XX
XX Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
XX hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
XX proliferative disorder; cancer; immunodeficient disorder.
XX

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XX Homo sapiens.
XX OS
XX WO200037504-A2.
XX
XX 29-JUN-2000.
XX
XX 23-DEC-1999; 99WO-US030895.
XX
XX 23-DEC-1998; 98US-0113647P.
XX
XX (PFIZ ) PFIZER INC.
XX (ABGE-) ABGENIX INC.
XX
XX Hanson DC, Neveu MJ, Mueller MJ, Hanke EE, Gilman SC, Davis CG;
XX Corvalan JR;
XX
XX WPI; 2000-442647/38.
XX N-PSDB; AAA46899.
XX
XX Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
XX -4 containing specified heavy and light chain sequences, useful for
XX treating, e.g. immune disorders.
XX
XX Claim 3; Fig 22a; 157pp; English.
XX
XX The present sequence represents a kappa chain of an antibody of the
XX invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
XX -4. Antibodies of the invention are composed of a heavy chain variable
XX region, comprising a modified contiguous sequence from a FRI-PR3 sequence
XX encoded by a human VH3-33 family gene. The modifications are contained in
XX CDR1, CDR2 and/or framework regions. The antibodies may be used to
XX inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
XX disorders (e.g. autoimmune disease, diabetes and graft rejection) and
XX proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
XX used to up-regulate immune system to up-regulate immunodeficient
XX disorders
XX
XX Sequence 214 AA;
XX
Query Match 88.7%; Score 753; DB 3; Length 214;
Best Local Similarity 92.4%; Pred. No. 6.8e-42;
Matches 145; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
QY 5 DIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFQQRPGKAPKSLIYAASLSQSVPS 64
DB 1 DIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFQQRPGKAPKSLIYAASLSQSVPS 60
QY 65 KFGSGSGSGTDTLTITISLQPEDFATYCCQYNSYPTFFGPGTKVDIKRTVAAPSVFIFPP 124
DB 61 RFSGSGSGTDTLTITISLQPEDFATYCCQYNSYPTFFGPGTKVDIKRTVAAPSVFIFPP 120
QY 125 SDEQLKSGTASVCLNNFYPRKQVQKVDNALQSG 161
DB 121 SDEQLKSGTASVCLNNFYPRKQVQKVDNALQSG 157
RESULT 7
AAE35890
ID AAE35890 standard; protein; 214 AA.
XX
XX AAE35890;
AC
XX
XX 17-JUN-2003 (first entry)
DT
XX
XX Human 11.2.1 anti-CTLA-4 antibody mature kappa chain.
DE
XX
XX Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
XX cancer.
XX
XX Homo sapiens.
XX
XX EP1262193-A1.
XX

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XX PD 04-DEC-2002.
 XX PF 23-MAY-2002; 2002EP-00253652.
 XX PR 23-MAY-2001; 2001US-0293042P.
 XX PA (PFIZ) PFIZER PROD INC.
 XX PI Hanson DC, Mueller EE;
 XX DR WPI; 2003-131215/13.
 XX DR N-PSDB; AAD54350.
 XX PT Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
 PT preparation of medicament for the treatment of cancer.
 XX PS Disclosure; Fig 1S; 76pp; English.
 XX CC The invention relates to the use of human anti-cytotoxic T lymphocyte
 CC antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
 CC the treatment of cancer such as bone cancer, pancreatic cancer, skin
 CC cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
 CC cancer, cancer of the anal region, stomach cancer, breast cancer,
 CC testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
 CC The present sequence is human anti-CTLA-4 antibody mature kappa chain
 XX SQ Sequence 214 AA;
 Query Match 88.7%; Score 753; DB 6; Length 214;
 Best Local Similarity 92.4%; Pred. No. 6.8e-42;
 Matches 145; Conservative 6; Mismatches 6; Indels 0; Gaps 0;
 QY 5 DIQQTQSPSSLSASVGRVITTCRASQGISIYLAWFQORPKAPKSLIYAASSLSQGVPS 64
 DB 1 DIQMTQSPSSLSASVGRVITTCRASQGISIYLAWFQORPKAPKSLIYAASSLSQGVPS 60
 QY 65 KFGSGSGTDFTLTISLQPEDFATYCCQVNSYPTFGPGTKVDIKRTVAAPSVFIPPP 124
 DB 61 RFSGSGSGTDFTLTISLQPEDFATYCCQVNSYPTFGPGTKVDIKRTVAAPSVFIPPP 120
 QY 125 SDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 161
 DB 121 SDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 157
 RESULT 8
 ADS84446
 ID ADS84446 standard; protein; 234 AA.
 XX AC ADS84446;
 XX DT 18-NOV-2004 (first entry)
 XX DE Human anti-EPO-R antibody Ab198 light chain SEQ ID NO:85.
 XX KW human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianaemic; neuroprotective; vulnerable; gene therapy; aplasia; anaemia;
 KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
 XX OS Homo sapiens.
 XX PN W02004035603-A2.
 XX PD 29-APR-2004.
 XX PF 14-OCT-2003; 2003WO-US032243.
 XX PR 14-OCT-2002; 2002US-00269711.
 PR 10-OCT-2003; 2003US-00684109.

XX PA (ABBO) ABBOTT LAB.
 XX PI Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 XX DR WPI; 2004-348433/32.
 XX DR N-PSDB; ADS84444, ADS84445.
 XX PT New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.
 XX PS Disclosure; SEQ ID NO 85; 192pp; English.
 XX CC The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence; and (5) an isolated and
 CC purified amino acid sequence, and their fragments. The EPO receptor
 CC binding antibody has antianaemic, neuroprotective and vulnerary
 CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from
 CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence represents a human anti-EPO-R antibody light
 CC chain, which is given in the exemplification of the present invention.
 XX SQ Sequence 234 AA;
 Query Match 88.7%; Score 753; DB 8; Length 234;
 Best Local Similarity 88.8%; Pred. No. 7.4e-42;
 Matches 143; Conservative 11; Mismatches 7; Indels 0; Gaps 0;
 QY 1 GIRLDIQLTQSPSSLSASVGRVITTCRASQGISIYLAWFQORPKAPKSLIYAASSLSQ 60
 DB 17 GSRCDIQMTQSPSSVSASIGDRVITTCRASQGISIYLAWFQORPKAPKSLIYAASSLSQ 76
 QY 61 GVPKFSFGSGSGTDFTLTISLQPEDFATYCCQVNSYPTFGPGTKVDIKRTVAAPSVF 120
 DB 77 GVPKFSFGSGSGTDFTLTISLQPEDFATYCCQVNSYPTFGPGTKVDIKRTVAAPSVF 136
 QY 121 IFPPSDBQLKSGTASVCLLNFPYKQVQKVDNALQSG 161
 DB 137 IFPPSDBQLKSGTASVCLLNFPYKQVQKVDNALQSG 177
 RESULT 9
 ADS84464
 ID ADS84464 standard; protein; 234 AA.
 XX AC ADS84464;
 XX DT 18-NOV-2004 (first entry)
 XX DE Human anti-EPO-R antibody Ab430 light chain SEQ ID NO:103.
 XX KW human; erythropoietin receptor; EPO receptor;
 KW erythropoietin receptor binding antibody; EPO receptor binding antibody;
 KW antianaemic; neuroprotective; vulnerable; gene therapy; aplasia; anaemia;

KW wound healing; neural cell damage protection;
 KW neural tissue damage protection; brain injury; spinal cord injury;
 KW stroke; anti-erythropoietin receptor antibody; anti-EPO-R antibody.
 XX
 OS Homo sapiens.
 XX WO2004035603-A2.
 XX
 PN 29-APR-2004.
 XX
 PD
 XX
 XX 14-OCT-2003; 2003WO-US032243.
 PF
 XX 14-OCT-2002; 2002US-00269711.
 PR
 XX 10-OCT-2003; 2003US-00684109.
 PR
 XX (ABBO) ABBOTT LAB.
 PA
 XX
 XX Devries PJ, Green LL, Ostrow DH, Reilly EB, Wieler J;
 PI WPI; 2004-348433/32.
 XX
 DR N-PSDB; ADS84462, ADS84463.
 DR
 XX
 XX New antibodies that bind to or activate an endogenous human
 PT erythropoietin receptor, useful for diagnosing, preventing or treating
 PT disorders associated with dysfunctional erythropoietin receptor, e.g.
 PT anemia.
 PT
 XX
 PS Disclosure; SEQ ID NO 103; 192pp; English.
 XX
 CC The present invention describes an antibody or its fragment that binds to
 CC or activates an endogenous activity of a human erythropoietin (EPO)
 CC receptor in a mammal, but does not interact with a peptide having a
 CC sequence of 30 amino acids (SEQ ID NO:1, ADS84362). Also described: (1)
 CC methods of modulating or activating an endogenous activity of a human EPO
 CC receptor in a mammal, comprising administering to the mammal a
 CC therapeutic amount of the above antibody or its fragment to modulate or
 CC activate the receptor; (2) a method of treating a mammal suffering from
 CC aplasia, comprising administering to the mammal a therapeutic amount of
 CC the above antibody or its fragment to modulate or activate the receptor;
 CC (3) a pharmaceutical composition comprising a therapeutic amount of the
 CC above antibody or antibody fragment, and a pharmaceutical excipient; (4)
 CC an isolated and purified polynucleotide sequence, and their fragments,
 CC complements and degenerate codon equivalents; and (5) an isolated and
 CC purified amino acid sequence, and their fragments. The EPO receptor
 CC binding antibody has antianaemic, neuroprotective and vulnerary
 CC activities, and can be used in gene therapy. The compositions and methods
 CC from the present invention can be used for modulating an endogenous
 CC activity of a human EPO receptor or for treating mammals suffering from
 CC aplasia or anaemia. They may also be used for identifying mammals having
 CC a dysfunctional EPO receptor. The composition may also be used in
 CC promoting wound healing or in protecting against neural cell and/or
 CC tissue damage resulting from brain/spinal cord injury, stroke and the
 CC like. The present sequence represents a human anti-EPO-R antibody light
 CC chain, which is given in the exemplification of the present invention.
 XX
 SQ Sequence 234 AA;
 Query Match 88.7%; Score 753; DB 8; Length 234;
 Best Local Similarity 90.7%; Pred. No. 7.4e-42;
 Matches 146; Conservative 6; Mismatches 9; Indels 0; Gaps 0;
 QY 1 GIRLDIQLTQSPSLASVGDRTVITCRASQGISYILAWFOQRPKAPKSLIYAASLSQS 60
 DB 17 GARCIDIQMTQSPSLASVGDRTVITCRASQGINRDLGWQQRPGKAPKSLIYAASLSQS 76
 QY 61 GVPSKFGSGSGTGDTFTLTISLSQPEDFATYYCQYNSYPTFFGTGKVDIKRTVAAPSVF 120
 DB 77 GVPSRFSGSGSGTEFTLTISLSQPEDFATYYCLQHSYPTFFGTGKVDIKRTVAAPSVF 136
 QY 121 IFPPSDQLKSGTASVYVCLLNFFPRAKQVQKVDNALQSG 161
 DB 137 IFPPSDQLKSGTASVYVCLLNFFPRAKQVQKVDNALQSG 177

RESULT 10
 ADR68588
 ID ADR68588 standard; protein; 234 AA.
 XX
 AC ADR68588;
 XX
 XX 02-DEC-2004 (first entry)
 DT
 XX
 XX Human antibody Ab198 light chain polypeptide seqid 85.
 DE
 XX
 XX antianaemic; respiratory; vulnerary; gene therapy; vaccine;
 KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
 KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
 KW wound healing; neural cell damage; tissue damage; brain injury;
 KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;
 KW AB198.
 XX
 XX Homo sapiens.
 OS
 XX
 PN US2004175379-A1.
 XX
 PD 09-SEP-2004.
 XX
 XX 10-OCT-2003; 2003US-00684109.
 PF
 XX
 XX 14-OCT-2002; 2002US-0418031P.
 PR
 XX (DEVIR/) DEVRIES P J.
 PA (OSTR/) OSTROW D H.
 PA (REIL/) REILLY E B.
 PA (GREE/) GREEN L L.
 PA (WIEL/) WIELER J.
 XX
 PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
 XX WPI; 2004-661369/64.
 XX N-PSDB; ADR68586.
 DR
 DR
 XX New antibody or its antibody fragment that activates an endogenous
 PT activity or is capable of binding to a human erythropoietin receptor in a
 PT mammal, useful for treating a mammal suffering aplasia or anemia.
 PS Disclosure; SEQ ID NO 85; 156pp; English.
 XX
 CC The invention describes an antibody or its fragment that activates an
 CC endogenous activity or capable of binding to a human erythropoietin
 CC receptor in a mammal, or that comprises at least one heavy or light chain
 CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
 CC ID NO: 3 or 5) given in the specification or its fragment, but does not
 CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
 CC given in the specification. Also described are: a method of activating or
 CC modulating an endogenous activity of a human erythropoietin receptor in a
 CC mammal; a pharmaceutical composition comprising a therapeutic amount of
 CC an antibody or antibody fragment above and a pharmaceutical excipient; an
 CC isolated and purified polynucleotide sequence selected from 28 sequences
 CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
 CC the specification, and their fragments, complements, and degenerate codon
 CC equivalents; and an isolated and purified amino acid sequence selected
 CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
 CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
 CC their fragments. The antibody or its antibody fragment that activates or
 CC modulates the activity of the receptor is useful in a method of treating
 CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
 CC treating disorders characterised by decreased or subnormal levels of
 CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
 CC hypoxia and/or diseases characterised by inadequate blood circulation or
 CC reduced blood flow. They are also useful for promoting wound healing or
 CC for protecting against neural cell and/or tissue damage, resulting from
 CC brain/spinal cord injury, stroke and the like. The antibodies are also
 CC useful for identifying or diagnosing mammals having dysfunctional
 CC erythropoietin receptor. This sequence represents a human Ab198 antibody
 CC light chain polypeptide.

```
XX SQ Sequence 234 AA;
Query Match 88.7%; Score 753; DB 8; Length 234;
Best Local Similarity 88.8%; Pred. No. 7.4e-42;
Matches 143; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRGKAPKSLIYAASSLSQS 60
Db 17 GSRCDIQMTQSPSSVSASIGDRVSIITCRASQGISIYLAWFOQRGKAPKSLIYAASSLSQS 76

Qy 61 GVPKFSGSGSGTDTLTISLQPEDFATYICQOYNSYPTFFGPTKVDIKRTVAAPSVF 120
Db 77 GVPKFSGSGSGTDTLTISLQPEDFATYICQOYNSYPTFFGPTKVDIKRTVAAPSVF 136

Qy 121 IFPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 161
Db 137 IFPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 177

RESULT 11
ADR68606
ID ADR68606 standard; protein; 234 AA.
AC ADR68606;
XX
DT 02-DEC-2004 (first entry)
XX
DE Human antibody Ab430 light chain polypeptide seqid 103.
XX
KW antianemic; respiratory; vulnerary; gene therapy; vaccine;
KW erythropoietin receptor; EPO-R; anti-EPO-R-antibody; aplasia; anaemia;
KW hypoxaemia; chronic tissue hypoxia; blood circulation; blood flow;
KW wound healing; neural cell damage; tissue damage; brain injury;
KW spinal cord injury; stroke; human; anti-EPO-R-antibody; light chain;
KW AB430.
XX
OS Homo sapiens.
XX
XX US2004175379-A1.
XX
PD 09-SEP-2004.
XX
PF 10-OCT-2003; 2003US-00684109.
XX
PR 14-OCT-2002; 2002US-0418031P.
XX
PA (DEVV/) DEVRIES P J.
PA (OSTR/) OSTROW D H.
PA (REIL/) REILLY E B.
PA (GREEN/) GREEN L L.
PA (WIEL/) WIELER J.
XX
PI Devries PJ, Ostrow DH, Reilly EB, Green LL, Wieler J;
XX
DR WPI; 2004-661369/64.
DR N-ESDB; ADR68604.
XX
PT New antibody or its antibody fragment that activates an endogenous
PT activity or is capable of binding to a human erythropoietin receptor in a
PT mammal; useful for treating a mammal suffering aplasia or anemia.
XX
PS Disclosure; SEQ ID NO 103; 156pp; English.
XX
XX The invention describes an antibody or its fragment that activates an
CC endogenous activity or capable of binding to a human erythropoietin
CC receptor in a mammal, or that comprises at least one heavy or light chain
CC variable region having a sequence comprising 116 or 107 amino acids (SEQ
CC ID NO: 3 or 5) given in the specification or its fragment, but does not
CC interact with a peptide comprising 30 amino acids (SEQ ID NO: 1) also
CC given in the specification. Also described are: a method of activating or
CC modulating an endogenous activity of a human erythropoietin receptor in a
CC mammal; a pharmaceutical composition comprising a therapeutic amount of
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CC an antibody or antibody fragment above and a pharmaceutical excipient; an
CC isolated and purified polynucleotide sequence selected from 28 sequences
CC comprising 322-370 bp (even SEQ ID NOS between SEQ ID NO: 2-56) given in
CC the specification, and their fragments, complements, and degenerate codon
CC equivalents; and an isolated and purified amino acid sequence selected
CC from 39 sequences comprising 27-552 amino acids (odd SEQ ID NOS between
CC SEQ ID NO: 3-57, and SEQ ID NO: 58-68) given in the specification or
CC their fragments. The antibody or its antibody fragment that activates or
CC modulates the activity of the receptor is useful in a method of treating
CC a mammal suffering aplasia or anaemia. The antibodies are also useful for
CC treating disorders characterised by decreased or subnormal levels of
CC oxygen in the blood or tissue such as hypoxaemia or chronic tissue
CC hypoxia and/or diseases characterised by inadequate blood circulation or
CC reduced blood flow. They are also useful for promoting wound healing or
CC for protecting against neural cell and/or tissue damage, resulting from
CC brain/spinal cord injury, stroke and the like. The antibodies are also
CC useful for identifying or diagnosing mammals having dysfunctional
CC erythropoietin receptor. This sequence represents a human Ab430 antibody
CC light chain polypeptide.
XX
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SQ Sequence 234 AA;

Query Match 88.7%; Score 753; DB 8; Length 234;
Best Local Similarity 90.7%; Pred. No. 7.4e-42;
Matches 146; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

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Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRGKAPKSLIYAASSLSQS 60
Db 17 GARCIDIQMTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRGKAPKSLIYAASSLSQS 76

Qy 61 GVPKFSGSGSGTDTLTISLQPEDFATYICQOYNSYPTFFGPTKVDIKRTVAAPSVF 120
Db 77 GVPKFSGSGSGTDTLTISLQPEDFATYICQOYNSYPTFFGPTKVDIKRTVAAPSVF 136

Qy 121 IFPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 161
Db 137 IFPPSDEQLKSGTASVCLLNFPYKQVQKVDNALQSG 177
```

RESULT 12
AAU74297

ID AAU74297 standard; protein; 236 AA.

AC AAU74297;

XX

DT 12-MAR-2002 (first entry)

XX

DE Anti-human AILIM monoclonal antibody clone Jmab-136, light chain.

XX

XX Human; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;

XX antiallergic; antiulcer; neuroprotective; antithyroid; vasotropic;

XX immunosuppressive; dermatological; antiinflammatory; hepatotropic;

XX activation inducible lymphocyte immunomodulatory molecule; AILIM;

XX monoclonal antibody; allergy; rheumatoid arthritis; diabetes mellitus;

XX multiple sclerosis; autoimmune thyroiditis; psoriasis; hepatitis;

XX allergic contact-type dermatitis; chronic inflammatory dermatosis;

XX systemic lupus erythematosus; autoimmune disorder; inflammation;

XX graft versus host reaction; immune rejection; intestinal immunity;

XX ulcerative colitis; pneumonia; nephritis; vasculitis; pancreatitis.

XX

OS Homo sapiens.

XX

XX WO200187981-A2.

XX

XX 22-NOV-2001.

XX

XX 15-MAY-2001; 2001WO-JP004035.

XX

XX 18-MAY-2000; 2000JP-00147116.

XX

XX 30-MAR-2001; 2001JP-00099508.

XX

XX (NISB) JAPAN TOBACCO INC.

XX

PI Teuji T, Tezuka K, Hori N;
 XX WPI; 2002-075313/10.
 DR N-PSDB; AAS99473.
 XX
 XX New human monoclonal antibody that binds to activation inducible
 PT lymphocyte immunomodulatory molecule, useful for treating rheumatoid
 PT arthritis, multiple sclerosis and inflammation.
 XX
 XX Claim 30; Page 270-271; 300pp; English.
 XX
 XX The invention relates to a novel human antibody (I), preferably a human
 CC monoclonal antibody which binds to an activation inducible lymphocyte
 CC immunomodulatory molecule (AIIIM). (I) is useful for modulating signal
 CC transduction into a cell mediated by AIIIM, for modulating proliferation
 CC of AIIIM-expressing cells, for modulating production of a cytokine from
 CC AIIIM-expressing cells, and for inducing antibody-dependent cytotoxicity
 CC against AIIIM-expressing cells and/or immune cytolysis or apoptosis of
 CC AIIIM-expressing cells. (I) is useful for treating, preventing or
 CC prophylaxis of delayed type allergy. (I) is useful for treating and
 CC preventing various diseases associated with AIIIM-mediated costimulatory
 CC transduction, and for inhibiting the onset and/or advancement of the
 CC diseases. (I) is useful for suppression, prevention and/or treatment of
 CC rheumatoid arthritis, multiple sclerosis, autoimmune thyroiditis,
 CC allergic contact-type dermatitis, chronic inflammatory dermatosis,
 CC systemic lupus erythematosus, insulin-dependent diabetes mellitus,
 CC psoriasis, autoimmune or allergic disorders, inflammation, disorders
 CC caused by abnormal intestinal immunity, specifically inflammatory
 CC intestinal disorders such as ulcerative colitis, pneumonia, hepatitis,
 CC nephritis, vasculitis, and pancreatitis. (I) induces no serious
 CC immunorejection due to antigenicity to human, i.e., human anti-mouse
 CC antigenicity (HAMA) in a host. AAU74296-AAU74301 represent anti-human
 CC AIIIM monoclonal antibody amino acid sequences of the invention
 XX
 SQ Sequence 236 AA;

Query Match 88.5%; Score 751; DB 5; Length 236;
 Best Local Similarity 90.1%; Pred. No. 1e-41;
 Matches 145; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLASVGDRTVITCRASGSIYILAWFOORPGKAPKSLIYAASLSQS 60
 Db 19 GSRCDIQMTQSPSSVASVGDRTVITCRASGSIISRLLAWYQQKPKAPKLLIYVASSLSQS 78
 Qy 61 GVPKSGSGSGTDTFTLTISLQPEDFATYCCQYNSVPFTFGPTKVDIKRTVAAPSVF 120
 Db 79 GVPKSGSGSGTDTFTLTISLQPEDFATYCCQANSFPWTFGGTKVETIKRTVAAPSVF 138
 Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSG 161
 Db 139 IFPPSDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSG 179

RESULT 13
 ADF11423
 ID ADF11423 standard; protein; 214 AA.
 XX
 AC ADF11423;
 XX
 XX 12-FEB-2004 (first entry)
 DT
 XX
 XX 2E11 anti-OPGL antibody light chain SEQ ID NO:36.
 DE
 XX human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;
 KW osteopathic; antiarthritic; cytostatic; gene therapy; bone disorder;
 KW osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.
 XX
 OS Homo sapiens.
 XX
 XX WO2003086289-A2.
 PN
 XX 23-OCT-2003.
 PD

XX 07-APR-2003; 2003WO-US010749.
 PF
 XX 05-APR-2002; 2002US-0370407P.
 PR
 XX (AMGE-) AMGEN INC.
 PA
 XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;
 PI WPI; 2003-845253/78.
 XX N-PSDB; ADF11422.
 DR
 DR New isolated antibody that specifically binds osteoprotegerin ligand,
 XX useful for diagnosing or treating bone disorders, such as osteoporosis,
 PT bone loss from arthritis, Paget's disease or osteopenia.
 PT
 XX Claim 18; SEQ ID NO 36; 156pp; English.
 PS
 XX The present invention describes an isolated human antibody (I) that
 CC specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a
 CC pharmaceutical composition comprising a pharmaceutical carrier and a
 CC therapeutic amount of (I); (2) methods of treating an osteopenic disorder
 CC in a patient, comprising administering to a patient the pharmaceutical
 CC composition of (1) or a pharmaceutical amount of (I); and (3) a method
 CC for detecting OPGL in a biological sample, comprising contacting the
 CC sample with (I) under conditions that allow for binding of the antibody
 CC to OPGL, and measuring the level of bound antibody in the sample. (I) has
 CC osteopathic, antiarthritic and cytostatic activities, and can be used in
 CC gene therapy. The composition and methods are useful in diagnosing or
 CC treating bone disorders, such as osteoporosis, bone loss from arthritis,
 CC Paget's disease or osteopenia. The antibody (I) may also be used for
 CC detecting OPGL in biological samples and in identifying cells or tissues
 CC that produce the protein. The present sequence represents a sequence
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 214 AA;

Query Match 87.9%; Score 746; DB 7; Length 214;
 Best Local Similarity 91.7%; Pred. No. 1.9e-41;
 Matches 144; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 5 DIQLTQSPSSLASVGDRTVITCRASGSIYILAWFOORPGKAPKSLIYAASLSQS 64
 Db 1 DIQLTQSPSSLASVGDRTVITCRASGSIISRLLAWYQQKPKAPKSLIYAASLSQS 60
 Qy 65 KFGSGSGTDTFTLTISLQPEDFATYCCQYNSVPFTFGPTKVDIKRTVAAPSVF 124
 Db 61 RFSGSGSGTDTFTLTISLQPEDFATYCCQYNSVPFTFGPTKVDIKRTVAAPSVF 120
 Qy 125 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSG 161
 Db 121 SDEQLKSGTASVVCLLNNFYPREAKVQKVDNALQSG 157

RESULT 14
 ADF47073
 ID ADF47073 standard; protein; 234 AA.
 XX
 AC ADF47073;
 XX
 XX 03-JUN-2004 (first entry)
 DT
 XX
 XX Mouse anti-human G-CSF antibody light chain protein.
 DE
 XX methylothroph yeast; mammalian sugar chain; OCH1; alpha-1;
 KW 6-mannosyl transferase; alpha-1; 2-mannosidase;
 KW orotidin-5'-phosphate decarboxylase; URA3;
 KW phosphoribosyl-amino-imidazole succinocarboxamide synthase; ADE1;
 KW imidazole-glycerol-phosphate dehydratase; HIS3;
 KW 3-isopropyl malate dehydrogenase; LEU2; proteinase A; proteinase B; PRB1;
 KW PEP4; YPS1; KTR1; MN9; AOX; GAPDH; mannosyl transferase;
 KW glyceraldehyde 3-phosphate dehydrogenase; mannose glycoprotein.
 XX


```

OS Mus sp.
XX WO2003091431-A1.
XX
XX PD 06-NOV-2003.
XX
XX PF 28-APR-2003; 2003WO-JP005464.
XX
XX PR 26-APR-2002; 2002JP-00127677.
XX
XX PA (KIRI ) KIRIN BEER KK.
XX
XX PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
XX FI Kobayashi K, Kitagawa Y, Kameda T, Kawashima N, Jigami Y;
XX
XX FI Chiba Y;
XX
XX DR WPI; 2003-854401/79.
XX
XX PT Producing methylotrophic yeast that expresses mammalian sugar chains by
XX
XX PT disrupting the OCH1 gene and inserting an alpha-1,2-mannosidase gene.
XX
XX PS Example 28; SEQ ID NO 92; 247pp; Japanese.
XX
XX CC The invention relates to the production of a methylotrophic yeast that
XX
XX CC produces mammalian sugar chains, comprising disrupting the OCH1 gene in
XX
XX CC the yeast that encodes for alpha-1,6-mannosyl transferase and inserting
XX
XX CC and expressing the alpha-1,2-mannosidase gene. The specification also
XX
XX CC includes DNA sequences encoding: (a) orotidin-5'-phosphate decarboxylase
XX
XX CC (URA3); (b) phosphoribosyl-amino-imidazole succinocarboxamide synthase
XX
XX CC (ADE1); (c) imidazole-glycerol-phosphate dehydratase (HIS3); (d) 3-
XX
XX CC isopropyl malate dehydrogenase (LEU2); (e) alpha-1,6-mannosyl transferase
XX
XX CC (OCH1); (f) proteinase A (PEP4); (g) proteinase B (PRB1); and (h)
XX
XX CC aspartic protease (YPS1), mannosyl transferase (KTR1 or MNN9), alcohol
XX
XX CC oxidase (AOX) and glyceraldehyde 3-phosphate dehydrogenase (GAPDH) gene
XX
XX CC sequences. The yeast is used for the production of human and mammalian
XX
XX CC high mannose glycoproteins with high yield and purity. The method is also
XX
XX CC useful for producing hybrid or complex sugar chains containing mammalian
XX
XX CC type chains. This sequence represents a mouse anti-human G-CSF antibody
XX
XX CC light chain used in the invention.
XX
XX SQ Sequence 234 AA;
Query Match 87.9%; Score 746; DB 7; Length 234;
Best Local Similarity 90.1%; Pred. No. 2.1e-41;
Matches 145; Conservative 8; Mismatches 8; Indels 0; Gaps 0;
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASOGISYILAWFOORPKAPKSLIYAASLSQS 60
DB 17 GARCIDIQMTQSPSSVSASVGDRTVITCRASQVSSWLAWYQQKPKAPKRLIYAASLSQS 76
QY 61 GVPKFSFGSGSGTDFTLTISSLPEDFATYYCQQYNSYPFFGPGTKVDIKRTVAAPSVF 120
DB 77 GVPKFSFGSGSGTDFTLTISSLPEDFATYYCQQANSFPFFGPGTKVEIKRTVAAPSVF 136
QY 121 IFPPSDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSG 161
DB 137 IFPPSDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSG 177
RESULT 15
ABG77164
ID ABG77164 standard; protein; 236 AA.
XX
XX AC ABG77164;
XX
XX DT 24-OCT-2002 (first entry)
XX
XX DE Germline protein sequence of anti-IGF-1R antibody AJ30/Jk1.
XX
XX KW Insulin-like growth factor I receptor; antibody; human; cytostatic;
XX
XX KW osteopathic; antiatherosclerotic; antipsoriatic; IGF-1R; tumour;
XX
XX KW anti-neoplastic; anti-tumour; anti-angiogenic; neuropathy; osteoporosis;
XX
XX KW acromegaly; gigantism; psoriasis; atherosclerosis.

```

```

XX Homo sapiens.
XX OS
XX FN WO200253596-A2.
XX
XX PD 11-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-US051113.
XX
XX PR 05-JAN-2001; 2001US-0259927P.
XX
XX PA (PFIZ ) PFIZER INC.
XX
XX PA (ABGE-) ABGENIX INC.
XX
XX FI Cohen BD, Beebe J, Miller PE, Moyer JD, Corvalan JR, Gallo M;
XX
XX XX WPI; 2002-575410/61.
XX
XX PT Novel humanized, chimeric monoclonal antibody that specifically binds to
XX
XX PT insulin-like growth factor I (IGF-I) receptor useful for inhibiting
XX
XX PT binding of IGF-I or IGF-II to receptor and for treating cancer in humans.
XX
XX PS Disclosure; Fig 198; 172pp; English.
XX
XX CC This invention relates to a novel humanised, chimeric or human monoclonal
XX
XX CC antibody or its antigen binding portion that specifically binds to
XX
XX CC insulin-like growth factor I receptor (IGF-IR). The antibodies of the
XX
XX CC invention can act as an inhibitor of binding of IGF-I or IGF-II with IGF-
XX
XX CC IR and can inhibit in vivo tumour growth and IGF-IR tyrosine
XX
XX CC phosphorylation. The antibodies of the invention are useful for
XX
XX CC diagnosing the presence or location of an IGF-IR-expressing tumour in a
XX
XX CC subject. The antibody or its antigen-binding portion is also useful for
XX
XX CC treating cancer in a human. The method for this further involves an anti
XX
XX CC neoplastic, anti-tumour, anti-angiogenic or chemotherapeutic agent. The
XX
XX CC antibodies may also be useful for increasing IGF-IR activity and thus
XX
XX CC restoring IGF-IR activity in a condition characterised by low IGF-IR
XX
XX CC levels e.g. neuropathy, or osteoporosis. An antibody of the invention is
XX
XX CC also useful for inducing apoptosis of specific cells in a patient, and to
XX
XX CC treat non-cancerous states or disease, e.g. acromegaly, gigantism,
XX
XX CC psoriasis and atherosclerosis. Fully human anti-IGF-IR antibodies
XX
XX CC minimise the immunogenic and allergic responses intrinsic to mouse or
XX
XX CC mouse-derivatised monoclonal antibodies and thus increase the efficacy
XX
XX CC and safety of the administered antibodies. The present sequence
XX
XX CC represents an anti-insulin-like growth factor I receptor antibody of the
XX
XX CC invention
XX
XX SQ Sequence 236 AA;
Query Match 87.9%; Score 746; DB 5; Length 236;
Best Local Similarity 89.4%; Pred. No. 2.1e-41;
Matches 144; Conservative 8; Mismatches 9; Indels 0; Gaps 0;
QY 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASOGISYILAWFOORPKAPKSLIYAASLSQS 60
DB 19 GARCIDIQMTQSPSSLSASVGDRTVITCRASQVSSWLAWYQQKPKAPKRLIYAASLSQS 78
QY 61 GVPKFSFGSGSGTDFTLTISSLPEDFATYYCQQYNSYPFFGPGTKVDIKRTVAAPSVF 120
DB 79 GVPKFSFGSGSGTDFTLTISSLPEDFATYYCQQNSYPFFGPGTKVEIKRTVAAPSVF 138
QY 121 IFPPSDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSG 161
DB 139 IFPPSDEQLKSGTASVVCLLNFPYPRKAVQWKVDNALQSG 179
Search completed: March 8, 2005, 07:09:26
Job time : 165 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 8, 2005, 07:06:05 ; Search time 133 Seconds
(without alignments)
405.739 Million cell updates/sec

Title: US-09-784-950-41
Perfect score: 849
Sequence: 1 GIRLDIQLTQSPSLASVG.....PREAKVQKVDNALQSKPN 164

Scoring table: BLOSUM62DX

Gapop 10.0 , Gapext 0.5

Searched: 1391452 seqs, 32904822 residues

Total number of hits satisfying chosen parameters: 1391452

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*

18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	761	89.6	214	15	US-10-408-901-44
2	753	88.7	214	14	US-10-153-382-19
3	753	88.7	234	16	US-10-684-109-85
4	753	88.7	234	16	US-10-684-109-103
5	751	88.5	236	9	US-09-859-053-30
6	751	88.5	236	16	US-10-625-105-30
7	746	87.9	214	15	US-10-408-901-36
8	746	87.9	236	15	US-10-038-591-52
9	745	87.8	233	16	US-10-663-244-150
10	745	87.8	236	15	US-10-038-591-48
11	739	87.0	214	15	US-10-423-299-3
12	737	86.8	184	16	US-10-684-109-78
13	737	86.8	234	15	US-10-292-088-24
					Sequence 44, Appl
					Sequence 19, Appl
					Sequence 85, Appl
					Sequence 103, Appl
					Sequence 30, Appl
					Sequence 30, Appl
					Sequence 36, Appl
					Sequence 52, Appl
					Sequence 150, Appl
					Sequence 48, Appl
					Sequence 3, Appl
					Sequence 78, Appl
					Sequence 24, Appl

14	737	86.8	234	16	US-10-684-109-91	Sequence 91, Appl
15	736	86.7	223	16	US-10-693-629-66	Sequence 66, Appl
16	736	86.7	234	16	US-10-684-109-109	Sequence 109, Appl
17	736	86.7	234	16	US-10-684-109-115	Sequence 115, Appl
18	733.5	86.4	241	14	US-10-221-945-1	Sequence 1, Appl
19	733	86.3	212	14	US-10-320-231A-77	Sequence 77, Appl
20	733	86.3	234	15	US-10-292-088-48	Sequence 48, Appl
21	730	86.0	234	16	US-10-684-109-97	Sequence 97, Appl
22	730	86.0	363	15	US-10-291-265-335	Sequence 335, Appl
23	729.5	85.9	211	9	US-09-974-449-36	Sequence 36, Appl
24	729	85.9	367	15	US-10-291-265-899	Sequence 899, Appl
25	723	85.2	213	16	US-10-379-392-135	Sequence 135, Appl
26	723	85.2	214	15	US-10-364-953-1	Sequence 1, Appl
27	723	85.2	237	14	US-10-020-786-10	Sequence 10, Appl
28	722	85.0	208	15	US-10-634-581-1	Sequence 1, Appl
29	722	85.0	214	9	US-09-949-559-128	Sequence 128, Appl
30	722	85.0	214	10	US-09-875-221A-128	Sequence 4, Appl
31	722	85.0	214	14	US-10-310-454-4	Sequence 113, Appl
32	722	85.0	214	17	US-10-728-420B-113	Sequence 62, Appl
33	721	84.9	223	16	US-10-693-629-62	Sequence 137, Appl
34	720	84.8	213	16	US-10-379-392-137	Sequence 100, Appl
35	720	84.8	237	9	US-09-056-160B-100	Sequence 100, Appl
36	720	84.8	237	14	US-10-234-671-100	Sequence 2, Appl
37	720	84.8	491	13	US-10-011-125-2	Sequence 155, Appl
38	719	84.7	213	16	US-10-379-392-155	Sequence 2, Appl
39	717	84.5	215	16	US-10-462-040A-2	Sequence 68, Appl
40	716	84.3	233	15	US-10-404-724-68	Sequence 47, Appl
41	715	84.2	236	15	US-10-038-591-47	Sequence 88, Appl
42	715	84.2	502	16	US-10-679-620-88	Sequence 245, Appl
43	714	84.1	153	15	US-10-309-762-245	Sequence 21, Appl
44	714	84.1	164	15	US-10-364-743-21	Sequence 23, Appl
45	714	84.1	164	15	US-10-364-743-23	

ALIGNMENTS

RESULT 1

US-10-408-901-44

; Sequence 44, Application US/10408901

; Publication No. US20040023313A1

; GENERAL INFORMATION:

; APPLICANT: Boyle, William

; APPLICANT: Huang, Haichun

; APPLICANT: Elliot, Robin

; APPLICANT: Sullivan, John

; APPLICANT: Medlock, Eugene

; APPLICANT: Martin, Francis

; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway

; TITLE OF INVENTION: Inhibitors

; FILE REFERENCE: MBHB 01-1145-A

; CURRENT APPLICATION NUMBER: US/10/408,901

; CURRENT FILING DATE: 2003-04-07

; NUMBER OF SEQ ID NOS: 76

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 44

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-901-44

Query Match	89.6%	Score 761	DB 15	Length 214	
Best Local Similarity	93.6%	Pred. No. 3.8e-48			
Matches 147	Conservative 6	Mismatches 4	Indels 0	Gaps 0	
Qy	5	DIQLTQSPSLASVGDVRVITCRASQGISYILAWFOORCKAPKSLIYRASSLSQSGVPS	64		
Db	1	DIQMTQSPSLASVGDVRVITCRASQGISYILAWFOORCKAPKSLIYRASSLSQSGVPS	60		
Qy	65	KFGSGSGTDTLTITISSLPQEDFATYCCQVNSVPTFGPGTKVDIKRTVAAPSVFIFPP	124		
Db	61	RFGSGSGTDTLTITISSLPQEDFATYCCQVNSVPTFGPGTKVDIKRTVAAPSVFIFPP	120		


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; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-30

Query Match      88.5%; Score 751; DB 9; Length 236;
Best Local Similarity 90.1%; Pred. No. 2.3e-47;
Matches 145; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOORPGKAPKSLIYVAASLSQS 60
Db 19 GSRCDIQMTQSPSSVSASVGDRTVITCRASQGISRLAWYQKPGKAPKLLIYVASSLSQS 78

Qy 61 GVPKPSGSGSGTDTLTITISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 120
Db 79 GVPKPSGSGSGTDTLTITISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 138

Qy 121 IFPPSDQLKSGTASVCLNNFYPREAKVQKVDNALQSG 161
Db 139 IFPPSDQLKSGTASVCLNNFYPREAKVQKVDNALQSG 179

RESULT 6
US-10-625-105-30
; Sequence 30, Application US/10625105
; Publication No. US20040180052A1
; GENERAL INFORMATION:
; APPLICANT: Tsuji, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, Nobuaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/10/625,105
; CURRENT FILING DATE: 2003-07-22
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-625-105-30

Query Match      88.5%; Score 751; DB 16; Length 236;
Best Local Similarity 90.1%; Pred. No. 2.3e-47;
Matches 145; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOORPGKAPKSLIYVAASLSQS 60
Db 19 GSRCDIQMTQSPSSVSASVGDRTVITCRASQGISRLAWYQKPGKAPKLLIYVASSLSQS 78

Qy 61 GVPKPSGSGSGTDTLTITISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 120
Db 79 GVPKPSGSGSGTDTLTITISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 138

Qy 121 IFPPSDQLKSGTASVCLNNFYPREAKVQKVDNALQSG 161
Db 139 IFPPSDQLKSGTASVCLNNFYPREAKVQKVDNALQSG 179

RESULT 7
US-10-408-901-36
; Sequence 36, Application US/10408901
; Publication No. US20040023313A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Boyle, William
; APPLICANT: Huang, Haichun
; APPLICANT: Elliot, Robin
; APPLICANT: Sullivan, John
; APPLICANT: Medlock, Eugene
; APPLICANT: Martin, Francis
; TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway
; TITLE OF INVENTION: Inhibitors
; FILE REFERENCE: MBHB 01-1145-A
; CURRENT APPLICATION NUMBER: US/10/408,901
; CURRENT FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 36
; LENGTH: 214
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-408-901-36

Query Match      87.9%; Score 746; DB 15; Length 214;
Best Local Similarity 91.7%; Pred. No. 4.8e-47;
Matches 144; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Qy 5 DIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOORPGKAPKSLIYAAASSLSQGVPS 64
Db 1 DIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWYQKPEKAPKSLIYAAASSLSQGVPS 60

Qy 65 KFGSGSGTDTLTITISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVFIPPP 124
Db 61 RFSGSGSGTDTLTITISLQSEDATYYCQYNSYPFTFGQTRLEIKRTVAAPSVFIPPP 120

Qy 125 SDQLKSGTASVCLNNFYPREAKVQKVDNALQSG 161
Db 121 SDEQLKSGTASVCLNNFYPREAKVQKVDNALQSG 157

RESULT 8
US-10-038-591-52
; Sequence 52, Application US/10038591
; Publication No. US20040086503A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Bruce D.
; APPLICANT: Beebe, Jean
; APPLICANT: Miller, Penelope E.
; APPLICANT: Moyer, James D.
; APPLICANT: Corvalan, Jose R.
; APPLICANT: Gallo, Michael
; TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR
; FILE REFERENCE: ABX-PF2
; CURRENT APPLICATION NUMBER: US/10/038,591
; CURRENT FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: 60/259,927
; PRIOR FILING DATE: 2001-01-05
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 52
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-038-591-52

Query Match      87.9%; Score 746; DB 15; Length 236;
Best Local Similarity 89.4%; Pred. No. 5.3e-47;
Matches 144; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOORPGKAPKSLIYVAASLSQS 60
Db 19 GARDIQMTQSPSSLSASVGDRTVITCRASQGISRLAWYQKPGKAPKLLIYVAASLSQS 78

Qy 61 GVPKPSGSGSGTDTLTITISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 120
Db 79 GVPKPSGSGSGTDTLTITISLQPEDFATYYCQYNSYPFTFGPGTKVDIKRTVAAPSVF 138
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; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78
; LENGTH: 184
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-78

Query Match
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Matches 143; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 3 RLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPGKAPKSLIYAASLSQGV 62
Db 21 KLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPGKAPKSLIYAASLSQGV 80
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Db 81 PSRPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVFIF 140
Qy 123 PPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSG 161
Db 141 PPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSG 179

RESULT 13
US-10-292-088-24
; Sequence 24, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
; APPLICANT: BEDIAN, VAHE
; APPLICANT: GLADUE, RONALD P.
; APPLICANT: CORVALAN, JOSE
; APPLICANT: JIA, XIAO-CHI
; APPLICANT: FENG, XIAO
; TITLE OF INVENTION: ANTIBODIES TO CD40
; FILE REFERENCE: ABX-PF/3 US
; CURRENT APPLICATION NUMBER: US/10/292,088
; CURRENT FILING DATE: 2003-03-14
; PRIOR APPLICATION NUMBER: 60/348,980
; PRIOR FILING DATE: 2001-11-09
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-292-088-24

Query Match
Best Local Similarity 86.8%; Score 737; DB 15; Length 234;
Matches 142; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPGKAPKSLIYAASLSQ 60
Db 17 GSRCDIQWTSQSPSSASVGDRTVITCRASQGISIYLAWFOQRPGKAPKSLIYAASLSQ 76
Qy 61 GVPKPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 120
Db 77 GVPKPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 136
Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSG 161
Db 137 IFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSG 177

RESULT 14
US-10-684-109-91
; Sequence 91, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
; APPLICANT: DeVries, Peter J.
; APPLICANT: Green, Larry L.
; APPLICANT: Ostrow, David H.
; APPLICANT: Reilly, Edward B.
; APPLICANT: Wieler, James
; TITLE OF INVENTION: Erythropoietin Receptor Binding
; FILE REFERENCE: 6989-US-02
; CURRENT APPLICATION NUMBER: US/10/684,109
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 10/269,711
; PRIOR FILING DATE: 2002-10-14
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-684-109-91

Query Match
Best Local Similarity 86.8%; Score 737; DB 16; Length 234;
Matches 142; Conservative 9; Mismatches 10; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPGKAPKSLIYAASLSQ 60
Db 17 GSRCDIQWTSQSPSSLSASVGDRTVITCRASQGISIYLAWFOQRPGKAPKSLIYAASLSQ 76
Qy 61 GVPKPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 120
Db 77 GVPKPSGSGSGTDFLTITSSLOPEDFATYCCQYNSYPTFGPGTKVDIKRTVAAPSVF 136
Qy 121 IFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSG 161
Db 137 IFPPSDEQLKSGTASVVCLLNNFYPRKAVQWKVDNALQSG 177

RESULT 15
US-10-693-629-66
; Sequence 66, Application US/10693629
; Publication No. US20040120948A1
; GENERAL INFORMATION:
; APPLICANT: KIRIN BEER KABUSHIKI KAISHA
; APPLICANT: MIKAYAMA, Toshifumi
; APPLICANT: YOSHIDA, Hitoshi
; APPLICANT: FORCE, Walker, R.
; APPLICANT: CHEN, Xingjie
; APPLICANT: TAKAHASHI, Nobuaki
; TITLE OF INVENTION: ANTI CD40 MONOCLONAL ANTIBODY
; FILE REFERENCE: 021286-0306473
; CURRENT APPLICATION NUMBER: US/10/693,629
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: PCT/US01/13672
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US09/844,684
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: JP2001/142482
; PRIOR FILING DATE: 2001-05-11
; PRIOR APPLICATION NUMBER: JP2001/310535
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: US10/040,244
; PRIOR FILING DATE: 2001-10-26
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 223
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-693-629-66

Query Match
Best Local Similarity 86.7%; Score 736; DB 16; Length 223;
Matches 142; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
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OM protein - protein search, using sw model

Run on: March 8, 2005, 05:54:19 ; Search time 42 Seconds
(without alignments)
291.487 Million cell updates/sec

Title: US-09-784-950-41

Perfect score: 849

Sequence: 1 GIRLDIQLTQSPSSLSASVG.....PREAKVQKVDNALQSKPN 164

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	753	88.7	214	4	US-09-472-087-71
2	751	88.5	236	4	US-09-859-053-30
3	729	85.9	236	1	US-08-157-101A-5
4	720	84.8	491	4	US-10-011-125A-2
5	715	84.2	233	2	US-07-934-373C-25
6	715	84.2	233	3	US-08-437-642B-25
7	715	84.2	233	4	US-08-146-206C-25
8	715	84.2	233	4	US-09-705-686-25
9	715	84.2	233	4	US-09-705-392A-25
10	715	84.2	233	4	US-09-705-398-25
11	715	84.2	233	5	PCT-US93-07832-25
12	713	84.0	233	4	US-08-030-175-43
13	713	84.0	234	4	US-09-740-002-24
14	711	83.7	224	4	US-09-456-090A-48
15	711	83.7	224	4	US-09-453-234-48
16	710	83.6	214	2	US-07-934-373C-39
17	710	83.6	214	3	US-08-437-642B-39
18	710	83.6	214	5	PCT-US93-07832-39
19	709.5	83.6	233	3	US-08-812-586-45
20	709.5	83.6	233	4	US-09-535-832A-42
21	709	83.5	218	2	US-08-887-352B-13
22	709	83.5	218	3	US-08-466-151-9
23	709	83.5	218	3	US-09-109-207C-13
24	709	83.5	218	3	US-09-296-005-13
25	709	83.5	218	3	US-08-466-163B-9
26	709	83.5	218	3	US-09-920-171-13
27	709	83.5	218	4	US-09-802-096-9

28	709	83.5	218	4	US-09-802-077-9	Sequence 9, Appli
29	709	83.5	218	4	US-09-716-028-13	Sequence 13, Appl
30	709	83.5	218	4	US-10-113-996-13	Sequence 13, Appl
31	709	83.5	218	5	PCT-US96-13152-2	Sequence 2, Appli
32	708	83.4	214	2	US-07-934-373C-40	Sequence 40, Appl
33	708	83.4	214	2	US-08-788-800-11	Sequence 11, Appl
34	708	83.4	214	2	US-08-437-642B-40	Sequence 40, Appl
35	708	83.4	214	3	US-09-097-309-2	Sequence 2, Appli
36	708	83.4	214	3	US-09-097-171A-2	Sequence 2, Appli
37	708	83.4	214	3	US-09-460-587-2	Sequence 2, Appli
38	708	83.4	214	4	US-09-940-166A-2	Sequence 2, Appli
39	708	83.4	214	5	PCT-US93-07832-40	Sequence 40, Appl
40	708	83.4	237	3	US-09-097-309-6	Sequence 6, Appli
41	708	83.4	237	3	US-09-097-171A-10	Sequence 10, Appl
42	708	83.4	237	3	US-09-422-712B-2	Sequence 2, Appli
43	708	83.4	237	3	US-09-607-756-2	Sequence 2, Appli
44	708	83.4	237	3	US-09-460-587-6	Sequence 6, Appli
45	708	83.4	237	4	US-09-940-166A-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-472-087-71

; Sequence 71, Application US/09472087

; Patent No. 6682736

; GENERAL INFORMATION:

; APPLICANT: HANSON, DOUGLAS C.

; APPLICANT: NEVEU, MARK J.

; APPLICANT: MUELLER, ELLEN B.

; APPLICANT: HANKE, JEFFREY H.

; APPLICANT: GILMAN, STEVEN C.

; APPLICANT: DAVIS, C. GEOFFREY

; APPLICANT: CORVALAN, JOSE R.

; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

; FILE REFERENCE: ABX-PF1

; CURRENT APPLICATION NUMBER: US/09/472,087

; CURRENT FILING DATE: 1999-12-23

; PRIOR APPLICATION NUMBER: 60/113,647

; PRIOR FILING DATE: 1998-12-23

; NUMBER OF SEQ ID NOS: 147

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 71

; LENGTH: 214

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-472-087-71

Query Match 88.7%; Score 753; DB 4; Length 214;

Best Local Similarity 92.4%; Pred. No. 2.4e-59;

Matches 145; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 5 DIQLTQSPSSLSASVGRVTITCRASQGISLYLAWFOORCGKAPKSLIYAASSLSQSGVPS 64

Db 1 DIQMTQSPSSLSASVGRVTITCRASQGISLYLAWFOORCGKAPKLLIYAASSLSQSGVPS 60

Qy 65 KFGSGSGSTDTFTLISSILQPEDFATYTCQQYNSYPTFGPGTKVDIKETVAAPSVFIFPP 124

Db 61 RFSGSGSGTDTFTLISSILQPEDFATYTCQQYNSYPTFGPGTKVEIKETVAAPSVFIFPP 120

Qy 125 SDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSG 161

Db 121 SDEQLKSGTASVCLLNFFYPREAKVQKVDNALQSG 157

RESULT 2

US-09-859-053-30

; Sequence 30, Application US/09859053

; Patent No. 6803039

; GENERAL INFORMATION:

; APPLICANT: Tsuji, Takashi

; APPLICANT: Tezuka, Tatsunari

```
; APPLICANT: Hori, No. 6803039uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILIM AND
; TITLE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 236
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-859-053-30

Query Match      88.5%; Score 751; DB 4; Length 236;
Best Local Similarity 90.1%; Pred. No. 4e-59;
Matches 145; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIYAASLSQS 60
Db 19 GSRCDIQMTQSPSSVSASVGDRTVITTCRASQGISRLAWYQKPGKAPKLLIYVASSLSQS 78

Qy 61 GVPSKFGSGSGDTFTLTISLQPEDFATYYCOQYNSYPFTFGTGKVDIKRTVAAPSVF 120
Db 79 GVPSRFSGSGGTFTLTISLQPEDFATYYCOQANSFPWTFGGTGKVEIKRTVAAPSVF 138

Qy 121 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 139 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 179

RESULT 3
US-08-157-101A-5
; Sequence 5, Application US/08157101A
; Patent No. 5808032
; GENERAL INFORMATION:
; APPLICANT: KURIHARA, TATSUYA
; APPLICANT: MATSUKURA, SHIGEKAZU
; APPLICANT: TSURUOKA, NOBUO
; APPLICANT: ARIMA, KENJI
; APPLICANT: NISHIHARA, TATSURO
; TITLE OF INVENTION: ANTI-HBS ANTIBODY GENES AND EXPRESSION
; TITLE OF INVENTION: PLASMIDS THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PILLSBURY, MADISON & SUTRO
; STREET: 1100 NEW YORK AVENUE, N.W.
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/157,101A
; FILING DATE: 05-APR-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: TITUS, MARLANA K
; REGISTRATION NUMBER: 35843
; REFERENCE/DOCKET NUMBER: 9437/204199
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-861-3711
; TELEFAX: 202-822-0944
; TELEX: 6714627 CUCH
```

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; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-157-101A-5

Query Match      85.9%; Score 729; DB 1; Length 236;
Best Local Similarity 85.7%; Pred. No. 3.6e-57;
Matches 138; Conservative 11; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIYAASLSQS 60
Db 19 GARCIDIQMTQSPSAMAASVGDRTVITTCRASQGISGNLYLWVWFQKPGKPKLLIYAASLSQS 78

Qy 61 GVPSKFGSGSGDTFTLTISLQPEDFATYYCOQYNSYPFTFGTGKVDIKRTVAAPSVF 120
Db 79 GVPSRFSGSGGTFTLTISLQPEDFATYYCLHNNYPLSFGGTGKVEIKRTVAAPSVF 138

Qy 121 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 139 IFPPSDQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 179

RESULT 4
US-10-011-125A-2
; Sequence 2, Application US/10011125A
; Patent No. 6828121
; GENERAL INFORMATION:
; APPLICANT: Chen, Christina Yu-Ching
; TITLE OF INVENTION: BACTERIAL HOST STRAINS
; FILE REFERENCE: P1804R1
; CURRENT APPLICATION NUMBER: US/10/011,125A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/256,162
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 12
; SEQ ID NO 2
; LENGTH: 491
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized.
; Patent No. 6828121
; US-10-011-125A-2

Query Match      84.8%; Score 720; DB 4; Length 491;
Best Local Similarity 88.5%; Pred. No. 5.2e-56;
Matches 139; Conservative 8; Mismatches 10; Indels 0; Gaps 0;

Qy 5 DIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIYAASLSQSVPS 64
Db 24 DIQLTQSPSSLSASVGDRTVITTCRASQDISNYLWYQQKPGKAPKLLIYFTSSLHSGVPS 83

Qy 65 KFGSGSGSGDTFTLTISLQPEDFATYYCOQYNSYPFTFGTGKVDIKRTVAAPSVFIFPP 124
Db 84 RFGSGSGSGDTFTLTISLQPEDFATYYCOQYNSYPFTFGGTGKVEIKRTVAAPSVFIFPP 143

Qy 125 SDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 144 SDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 180

RESULT 5
US-07-934-373C-25
; Sequence 25, Application US/07934373C
; Patent No. 5821337
; GENERAL INFORMATION:
; APPLICANT: Paul J. Carter
; APPLICANT: Leonard G. Presta
; TITLE OF INVENTION: Immunoglobulin Variants
```

NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA: US/07/934,373C
FILING DATE: 21-Aug-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-07-934-373C-25

Query Match 84.2%; Score 715; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 6.2e-56;
Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASOGISIVLAWFOQRGKAPKSLIYVAASLIQS 60
Db 16 GVHSDIQMTQSPSSLSASVGDRTVITCRASODINNLYNWYQQRGKAPKLLIYTTSLHS 75
Qy 61 GVPKFSGSGGTDTLTITSSLOPEDPATYCCQYNSVPFTFGTKVDIKRTVAAPSVF 120
Db 76 GVPKFSGSGGTDTLTITSSLOPEDPATYCCQYNSVPFTFGTKVDIKRTVAAPSVF 135
Qy 121 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 161
Db 136 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 176

RESULT 6
US-08-437-642B-25
Sequence 25, Application US/08437642B
Patent No. 6054297
GENERAL INFORMATION:
APPLICANT: Paul J. Carter
APPLICANT: Leonard G. Presta
TITLE OF INVENTION: Immunoglobulin Variants
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA: US/08/437,642B
FILING DATE: 09-May-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934373
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/146206
FILING DATE: 17-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05126
FILING DATE: 15-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/715272
FILING DATE: 14-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P0709P2C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-437-642B-25

Query Match 84.2%; Score 715; DB 3; Length 233;
Best Local Similarity 85.7%; Pred. No. 6.2e-56;
Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITCRASOGISIVLAWFOQRGKAPKSLIYVAASLIQS 60
Db 16 GVHSDIQMTQSPSSLSASVGDRTVITCRASODINNLYNWYQQRGKAPKLLIYTTSLHS 75
Qy 61 GVPKFSGSGGTDTLTITSSLOPEDPATYCCQYNSVPFTFGTKVDIKRTVAAPSVF 120
Db 76 GVPKFSGSGGTDTLTITSSLOPEDPATYCCQYNSVPFTFGTKVDIKRTVAAPSVF 135
Qy 121 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 161
Db 136 IFPPSDEQLKSGTASVVCLLNFPYREAKVQWKVDNALQSG 176

RESULT 7
US-08-146-206C-25
Sequence 25, Application US/08146206C
Patent No. 6407213
GENERAL INFORMATION:
APPLICANT: Carter, Paul J.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method for Making Humanized Antibodies
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA: US/08/146,206C
APPLICATION NUMBER: 17-No. 6407213-1993
FILING DATE: 17-No. 6407213-1993

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;
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-146-206C-25

Query Match      84.2%; Score 715; DB 4; Length 233;
Best Local Similarity 85.7%; Pred. No. 6.2e-56;
Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIIYAASLQS 60
Db 16 GVHSDIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNWYQKPGKAPKLLIYTTSLHS 75
Qy 61 GVPSKFGSGSGDTFTLTISLQPEDFATYYCOQYNSYPFTFGTKVDIKRTVAAPSVF 120
Db 76 GVPSRFGSGSGDTFTLTISLQPEDFATYYCQGNLTLPFTFGQTKVEIKRTVAAPSVF 135
Qy 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 136 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 176

RESULT 8
US-09-705-686-25
; Sequence 25, Application US/09705686
; Patent No. 6639055
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705.686
; FILING DATE: 02-No. 6639055-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-705-686-25

Query Match      84.2%; Score 715; DB 4; Length 233;
Best Local Similarity 85.7%; Pred. No. 6.2e-56;
Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIIYAASLQS 60
Db 16 GVHSDIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNWYQKPGKAPKLLIYTTSLHS 75
Qy 61 GVPSKFGSGSGDTFTLTISLQPEDFATYYCOQYNSYPFTFGTKVDIKRTVAAPSVF 120
Db 76 GVPSRFGSGSGDTFTLTISLQPEDFATYYCQGNLTLPFTFGQTKVEIKRTVAAPSVF 135
Qy 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 136 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 176

RESULT 9
US-09-705-392A-25
; Sequence 25, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705.392A
; FILING DATE: 02-No. 6719971-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-705-392A-25

Query Match      84.2%; Score 715; DB 4; Length 233;
Best Local Similarity 85.7%; Pred. No. 6.2e-56;
Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-705-686-25

Query Match      84.2%; Score 715; DB 4; Length 233;
Best Local Similarity 85.7%; Pred. No. 6.2e-56;
Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIIYAASLQS 60
Db 16 GVHSDIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNWYQKPGKAPKLLIYTTSLHS 75
Qy 61 GVPSKFGSGSGDTFTLTISLQPEDFATYYCOQYNSYPFTFGTKVDIKRTVAAPSVF 120
Db 76 GVPSRFGSGSGDTFTLTISLQPEDFATYYCQGNLTLPFTFGQTKVEIKRTVAAPSVF 135
Qy 121 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 161
Db 136 IFPPSDEQLKSGTASVVCLNNFYPREAKVQWKVDNALQSG 176

RESULT 9
US-09-705-392A-25
; Sequence 25, Application US/09705392A
; Patent No. 6719971
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; Presta, Leonard G.
; TITLE OF INVENTION: Method for Making Humanized Antibodies
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/705.392A
; FILING DATE: 02-No. 6719971-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/146206
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: 07/715272
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0709P1D1 REVISED
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-1994
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-09-705-392A-25

Query Match      84.2%; Score 715; DB 4; Length 233;
Best Local Similarity 85.7%; Pred. No. 6.2e-56;
Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
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Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIYAASLSQS 60
 Db 16 GVHSDIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNWYQQKPGKAPKLLIYTTSLHS 75
 Qy 61 GVPSKFGSGSGDTFTLTISLQPEDPATYCCQYNSYPTFGPTKVDIKRTVAAPSVF 120
 Db 76 GVPSRFGSGSGDTYLTITSLQPEDPATYCCQGNLTPTTFGGTKVEIKRTVAAPSVF 135

Qy 121 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 161
 Db 136 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 176

RESULT 10

US-09-705-398-25
 ; Sequence 25, Application US/09705398
 ; Patent No. 6800738
 ; GENERAL INFORMATION:
 ; APPLICANT: Carter, Paul J.
 ; TITLE OF INVENTION: Method for Making Humanized Antibodies
 ; NUMBER OF SEQUENCES: 26
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatIn (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09705398
 FILING DATE: 02-Nov-1993
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/146206
 FILING DATE: 17-NOV-1993
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Lee, Wendy M.
 REGISTRATION NUMBER: 40,378
 REFERENCE/DOCKET NUMBER: P0709P1D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1994
 TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 233 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 25:
 US-09-705-398-25

Query Match 84.2%; Score 715; DB 4; Length 233;
 Best Local Similarity 85.7%; Pred. No. 6.2e-56;
 Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIYAASLSQS 60
 Db 16 GVHSDIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNWYQQKPGKAPKLLIYTTSLHS 75

Qy 61 GVPSKFGSGSGDTFTLTISLQPEDPATYCCQYNSYPTFGPTKVDIKRTVAAPSVF 120
 Db 76 GVPSRFGSGSGDTYLTITSLQPEDPATYCCQGNLTPTTFGGTKVEIKRTVAAPSVF 135

Qy 121 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 161
 Db 136 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 176

RESULT 11
 PCT-US93-07832-25
 ; Sequence 25, Application PC/TUS9307832
 ; GENERAL INFORMATION:
 ; APPLICANT: Genentech, Inc.
 ; TITLE OF INVENTION: Immunoglobulin Variants
 ; NUMBER OF SEQUENCES: 40
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 460 Point San Bruno Blvd
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080

COMPUTER READABLE FORM:
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/07832
 FILING DATE: 19930820
 CLASSIFICATION:

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/715272
 FILING DATE: 14-JUN-1991
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US92/05126
 FILING DATE: 15-JUN-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/934373
 FILING DATE: 21-AUG-1992
 ATTORNEY/AGENT INFORMATION:

NAME:
 REGISTRATION NUMBER:
 REFERENCE/DOCKET NUMBER: 709P2PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE:
 TELEFAX: 415/952-9881

TELEX: 910/371-7168
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 233 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 PCT-US93-07832-25

Query Match 84.2%; Score 715; DB 5; Length 233;
 Best Local Similarity 85.7%; Pred. No. 6.2e-56;
 Matches 138; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

Qy 1 GIRLDIQLTQSPSSLSASVGDRTVITTCRASQGISIYLAWFQORPGKAPKSLIYAASLSQS 60
 Db 16 GVHSDIQMTQSPSSLSASVGDRTVITTCRASQDINNLYNWYQQKPGKAPKLLIYTTSLHS 75

Qy 61 GVPSKFGSGSGDTFTLTISLQPEDPATYCCQYNSYPTFGPTKVDIKRTVAAPSVF 120
 Db 76 GVPSRFGSGSGDTYLTITSLQPEDPATYCCQGNLTPTTFGGTKVEIKRTVAAPSVF 135

Qy 121 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 161
 Db 136 IFPPSDQLKSGTASVCLNNFYPRKQVQKVDNALQSG 176

RESULT 12
 US-08-030-175-43
 ; Sequence 43, Application US/08030175
 ; Patent No. 6767996
 ; GENERAL INFORMATION:
 ; APPLICANT: Gorman, Scott D.
 ; APPLICANT: Clark, Michael R.

APPLICANT: GenPharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIOR APPLICATION NUMBER: US 60/157,415
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 224
TYPE: PRT
ORGANISM: Homo. sapiens
OTHER INFORMATION: MI-21L
US-09-453-234-48

Query Match 83.7%; Score 711; DB 4; Length 224;
Best Local Similarity 89.7%; Pred. No. 1.3e-55;
Matches 140; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
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2 IRMTQSPSFLSASVGDRTTTCRASQSISSYLNWYQKPGKAPKLLIYAASSLSQGVPSR 61
Qy 66 FSGSGSGTDFTLTISSLQPEDFATYCCQYNSYDFTGPGTKVDIKRTVAAPSVFIFPPS 125
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62 FVSGSGGTDFTLTISSLQPEDFATYCCQGYSTPTFTGPGTKVDIKRTVAAPSVFIFPPS 121
Qy 126 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 161
Db |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSG 157

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Job time : 43 secs

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